# KWARA STATE UNIVERSITY

## THE SIXTH (6TH) INAUGURAL LECTURE

# DECODING THE SECRET OF LIFE: PLANT, SEX AND SUSTAINABLE FOOD PRODUCTION

**By**

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**The Vice Chancellor**
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Gentlemen of the Press,
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Great KWASUITES,
Ladies and Gentlemen,

## 1. Preamble

I am highly honoured today Wednesday 13th November 2019 to be given the privilege to deliver the 6th Inaugural Lecture of the Kwara State University. It is the first both from the College of Agriculture and from the Department of Crop Production of this University. By tradition, an inaugural lecture is expected to lead the audience into the

mind of the lecturer by giving a brief account of his/her voyage into the discipline where he or she is professing. This lecture will not be different. I had wanted to study pharmacy, but by providence I was offered admission to study B.Sc. Botany, twice. Through wise counsel of my academic father, Prof. Bayo Lawal, then of the Department of Statistics, University of Ilorin, and now of the Kwara State University, who sarcastically asked "*ti o ba se pharmacy, o ta ju oogun lo ni?"*, meaning "you won't sell more than drugs with your insistence on pharmacy*".* He went further to encourage that I should accept the offer but be determined to excel in the discipline. To excel in Botany! "By the way", I asked myself, "What is Botany and what are the prospects of this course?" Attempts to find answers to these questions made me to contact Professor P.D.S. Caligari, then Head, Department of Agricultural Botany, University of Reading, United Kingdom. He did not only encourage me to study Botany but his response stimulated my interest in the course and helped me in the choice of my specialty, Genetics and Plant Breeding, later in life. Mr. Ag. Vice Chancellor Sir, after my National Youth Service Corps (NYSC), I got admission and a fellowship for a 2-year Master of Philosophy (M.Phil.) degree in Genetics and Plant Breeding, jointly organised by the University of Birmingham and University of Reading, United Kingdom, through the recommendation of Prof. Caligari. Unfortunately, before my resumption for study in UK, my fellowship was cancelled because of the suspension of Nigeria from the Commonwealth during the military regime of General Sanni Abacha. I finally settled for postgraduate studies at the University of Ilorin

as an alternative. Shortly after obtaining M.Sc., I was offered an appointment as a Research Officer 1 (Plant Breeding) by the Cocoa Research Institute of Nigeria, Ibadan. To the glory of Almighty God, I worked hard and rose to become a Chief Research Officer (Plant Breeding and Biotechnology) within nine years of my engagement at that Institute. I later went further to distinguish myself as a scientist and a scholar of repute in Germany. These experiences are what led to my invitation to join in the development of Kwara State University in 2010 and by the grace of Allah, I was appointed full Professor in 2016. Today, I will give brief accounts of some of my contributions as a Plant Breeder and Molecular Geneticist in the course of this lecture. But before that, I will give a brief introduction about genetics and plant breeding as a discipline and its relevance to the society.

## 2. Introduction

Genetics is often defined as the study of heredity, but hereditary is an old phenomenon that predates biology or genetics as a scientific discipline as we know today. For several thousand years, the ancient people had improved plant crops and domesticated animals for food and selection of individuals for breeding. But genetics as a set of principles and analytical practice started in 1860 when Gregor Mendel reported the results of crossing experiment on *Pisium* and pointed to the existence of biological elements, now called genes. The word "genetics" comes from "gene". Genetics is therefore the study of genes. Advances in genetics have moved from the selection and inter-mating of individuals in the past to recent developments in molecular genetics and

biotechnology in which genes can now be transferred across genetically diverse genomes. This advancement was facilitated by the discovery of Deoxyribonucleic acid (DNA) in 1953.

DNA is the hereditary materials containing genetic instructions (code) for growth, function, development and reproduction of every organism. It is assembled in thread-like form on the chromosome and composed of two chains that coiled around each other to form a double helix. It is also composed of two nucleotides strands held together by complimentary hydrogen bonding of A (adenine) with Thymine (T) and Guanine (G) with Cytosine (C). Human has 3.2 billion nucleotides while maize genome comprises 2.3 billion base sequences with 32,000 protein coding genes. Today, huge resources are being committed to sequencing genome of major crop plants in order to decode the secret of their lives and use it as manuals for their improvement. Below is a quote from Richard Wilson, the Director of the Genome Center at Washington University in St Louis, Missouri, after successful sequencing of maize genome:

> What we have here is a crucial part of the instruction manual for how you breed a better corn plant. You can now find where genes that underlie certain traits are located, and, thus, you have the tools for how you go off and breed those desired traits into new generations of plants (cited in Dolgin, 2009).

With advancement in technology, it is now possible to extract the DNA from tissues of plants (dead or living) and regenerate new individuals. On July 21, 2019, the New York Times reported a successful cloning of cat

from dead by Sinogene, a commercial pet-cloning company based in Beijing, at a cost of about $35,000 (N12.6M) and a duration of seven months. This is possible because the secret of life in cat has been decoded. In short, with God, many things are now possible through genetics today. With climate change and its consequence on food security, the survival of human race largely depends on the understanding of the secret coded in plant and animal genomes. That is why the society needs geneticists and breeders to decode these secrets for sustainable food production.

Ag. Vice Chancellor Sir, my research mostly focusing on decoding the secret of life in plants have been published in over 50 articles in highly reputable journals. They can also be categorised into three (3) major areas, namely: (i) genetic improvement of cashew, (ii) investigation into genetic evolution and stability of apomixis in plants and (iii) cowpea improvement. Since my most recent works are on apomixis, I will start this lecture with that.

## 3. What is Apomixis?

Ag. Vice Chancellor Sir, before going into the kernel of this lecture, please permit me to define apomixis and explain why it is an important tool for the future of agriculture and sustainable food production in the world. Apomixis in flowering plants is simply defined as asexual seed production from maternal tissues of the ovule in plants by circumventing meiosis (reductional division) and fertilization to produce embryos (offsprings/seeds) that are genetically identical to the mother plant (true copies of mother) (Figure 1). This

natural form of seed production involves three major biological developmental steps: (i) *apomeiosis*, (ii) *parthenogenesis*, and (iii) *pseudogamy/autonomous endosperm formation* (Koltunow & Grossniklaus, 2003; Aliyu, Schranz, et al., 2010) (Figure 1). In basic term, apomixis could be liken to "Single Mother Plant". Sex on the other hand involves fusion of reduced gametes (products of meiosis) to produce highly variable progenies (i.e. not true copies of the mother). This therefore brings about wide variability in forms, characters and most importantly, yield in plants.

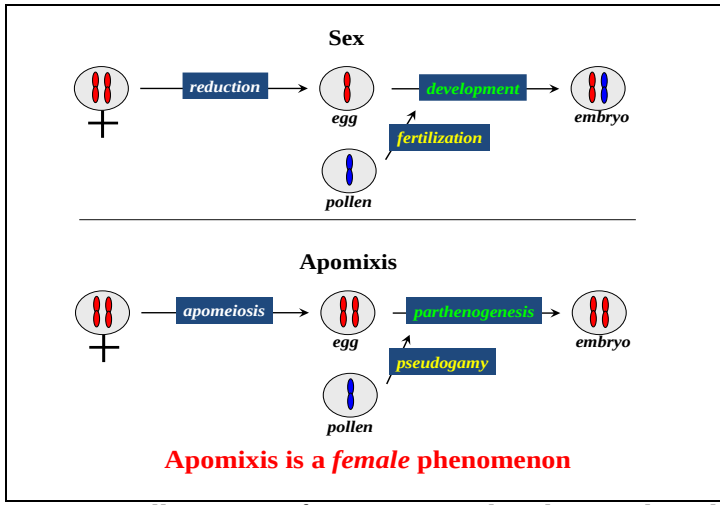



Figure 1: Illustration of process sexual and asexual seed formation in flowering plants.

## 4. Importance of Apomixis Technology to Sustainable Food Production

Ag. Vice Chancellor Sir, the availability of quality seed is an essential component of crop production.

Understanding the biological mechanisms involved in seed developmental process is critical to advancement in quality yield and for sustainable global food production. Sexual seed production has continued to receive greater attention but its progenies are genetically varied because of recombination during gametogenesis (meiosis). In contrast, asexual (apomixis) seeds are 100% replica of the mother genetic constitution, but it is still a rare occurrence, mostly in the wild relatives. Apomixis is considered a key enabling technology that could facilitate the fixation of hybrid vigor (heterosis) in a single generation, thereby significantly reducing the costs associated with hybrid seed production in crops like maize, wheat, rice, etc. Successful transfer of apomixis into crop plants will considerably increase seed yield and allow farmers to reuse hybrid seeds over generations (Spillane et al., 2004) (Figure 2). Understanding the genetic mechanisms underpinning this natural switch from sexual to asexuality is of great importance to agriculture and could bring significant economic and social benefits to the society (Barcaccia & Albertini, 2013). Searching for the secret (genes and genetic mechanism) behind this biological phenomenon in plants was the major goal of Apomixis research at the Institute of Plant Genetics and Crop Research (IPK), Germany, where I spent about a decade as a scientist and scholar.

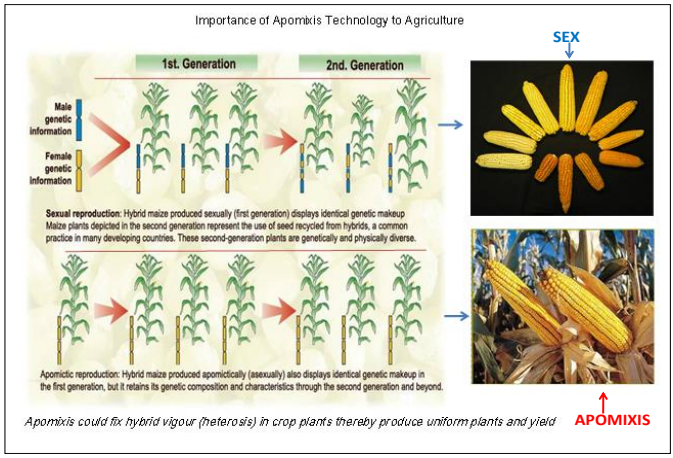



Figure 2: Illustration of how apomixis can fix hybrid vigour through generations and produce uniform plants and quality yield in maize. Sexual hybrid seeds in the upper part will produce variable plants and yield at the 2nd generation.

## 5. Development of a High-Throughput System for Rapid Plant Analysis

Ag. Vice Chancellor Sir, my sojourn to apomixis world started in 2006 with an offer of a two-year position as a postdoctoral scientist in IPK, Germany. My first task was to develop a high throughput method for flow cytometry in plant system. I must confess that before this appointment, I have never seen a flow cytometer as all my experience had been about cytology and/or cytogenetics. However, during my interview for the position, I cleverly separated the word “cytometry” into two, cyto (cell) and metric (measurement) and showed proof that I have carried out a number of studies in cytology, and that cytometry would be a variant of

cytology. Twenty-four (24) hours after the interaction, I was recommended for the position and that marked beginning of my induction and venture into the world of apomixis.

Flow cytometry is a powerful tool for the investigation of many parameters at the single cell level, and it has the advantage of rapidly processing a high number of individual cells. In polyploid and apomixis studies, the determination of relative nuclear content (ploidy) of individual plant and the identification of apomictic individuals has relied on the evaluation of leaf and seed tissues DNA ploidy and/or the screening for embryo to endosperm C-value ratios in a large number of seeds. Such screening method using conventional nuclei preparation protocols is labour and time intensive, and represents a bottleneck which is not readily amenable to automation.

Ag. Vice Chancellor, I have optimised and automated sample preparation procedure through the use of a genogrinder, in conjunction with a two-step buffer system supplemented with a reducing agent for the rapid isolation of sufficient nuclei for FCM analysis (Figure 3). With this improved method, ninety-six (96) samples can be prepared and analysed within 2.5 hours and about 300 - 350 samples/day (Aliyu, Schranz, et al., 2010) against conventional chopping technique (Galbraith et al., 1983). In the course of this work, a 96-well filter system was also developed. This is about 7- 8 folds of the conventional method. Besides saving considerable time, it allows the experimenter to do other tasks while the analysis is on automation.

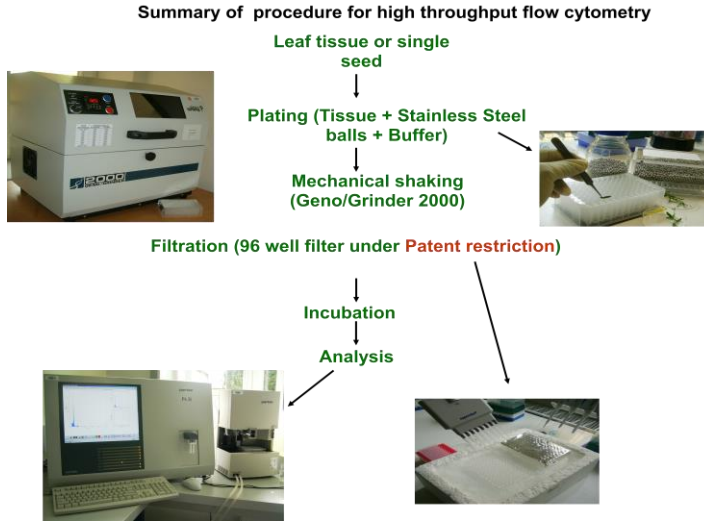



Figure 3: Step-by-step procedure for High-Throughput Flow Cytometry (Aliyu & Sharbel, 2007).

The protocols have produced reliable results for both dicots (*Hypericum perforatum* and *Boechera* spp) and monocots (*Poa parentesis*) for DNA content (ploidy) determination, and have enabled us to measure quantitative variation in apomictic and sexual seed productions between individuals. This improved method has the potential for large scale application in the seed industry, apomixis research and crop improvement programmes (Aliyu & Sharbel, 2007).

## 6. Application of High-Throughput Method to Research and Industry

Ag. Vice Chancellor Sir, besides the application of this improved method to apomixis research and analysing

plant samples for some institutions, I have trained a number of staff of seed companies in Germany (Eurograss GbH and Sateen Union GbH) on the application of this procedure to quality control, especially in double haploid plant production and screening for somaclonal variation in plant tissue culture.

I have also trained many postgraduate students on its application to research in evolution and population genetics. I have enjoyed conference sponsorships from Partec GbH, and Beckman Coulter because I have adapted their cytometers to the high throughput and have done some proof-of-concept for their use in plant research. Ag. Vice Chancellor Sir, this high throughput method has been very impactful because it exposes the secret of sex in plants at a very rapid rate, thus, adding to crop improvement technology for future sustainable food production.

## 7. Quantitative Variation for Asexual Seed Production in *Boechera*

Ag. Vice Chancellor, the improved protocol has been used to analyse a total of 22,480 single seeds, each from 243 *Boechera* individuals comprising of 62 diploids and 9 triploids from 17 different taxa in our study on the quantitative variation for apomixis expression in *Boechera* (Aliyu, Schranz, et al., 2010). The goal was to identify obligate apomicts (individual with 100% asexual seed production). A complimentary karyotype study of *Boeachera* accessions has shown that the sexual diploids have somatic chromosome number of 2n = 14, while diploid apomicts and triploids have 2n = 15 and 3n = 21 respectively (Plate 1) (Voigt et al., 2007).

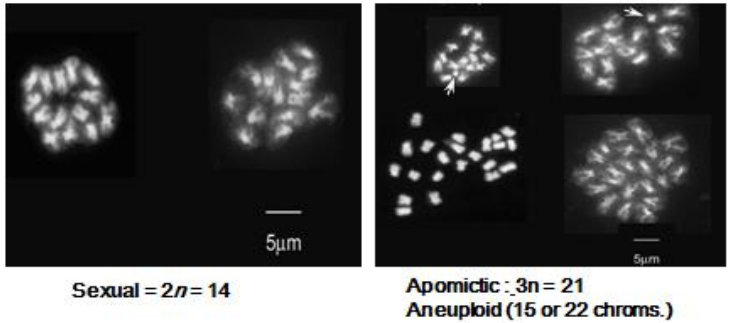



Plate 1: Karyotypic studies in sexual and apomictic *Boechera spp*

Ag. Vice Chancellor Sir, seed screening data of all diploid *Boechera* showed four different reproductive modes based on the frequency of apomeiosis expression, while all triploids were 100% apomeiotic (Figure 4). Besides obligate sexual (i.e. individuals without apomeiosis) and obligate apomictic accessions (individuals without sex), two groups of facultative apomicts were identified based on low or high levels of apomeiosis expression (Figure 4). From this data we were able to identify obligate apomictic individuals with 100% apomixis expression that are good candidates for further works on the identification of the genes controlling apomixis and molecular mechanism of Apomixes in *Boechera* (Aliyu et al., 2013; Corral et al., 2013; Mau et al., 2013).

The complete absence of intermediate apomeiosis frequencies (Figure 4) therefore shed light upon the mechanism behind apomixis in *Boechera* and complex gene regulatory changes associated with apomeiosis (Sharbel et al., 2009, 2010). Thus, while low frequency

apomeiosis accessions (1-3%) are *sensu stricto* facultative apomictic, their population-level dynamics (*e.g.* gene flow) reflect that of sexuality rather than apomixis (Aliyu, Schranz, et al., 2010; Lovell et al., 2013).

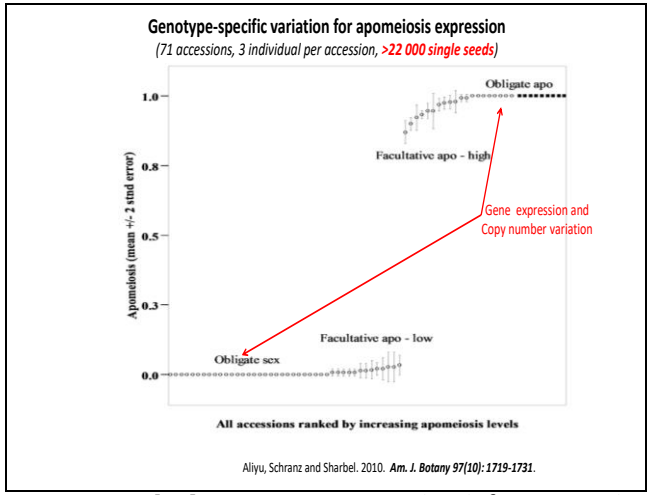



Figure 4: Ranked mean apomeiosis (apo) frequency (± 2 SE) for 62 diploid (circles) and nine triploid (squares) *Boechera* accessions. (Aliyu, Schranz, et al., 2010).

Strong correlation between apomeiosis (absence of meiosis) and parthenogenesis (autonomous development of egg cell) in a number of apomictic species has led to the conclusion that they are tightly linked, and/or under common expression regulation, or that parthenogenesis is a secondary (*i.e.* pleiotropic) result of apomeiosis expression (Savidan, 2000). Importantly, the lower frequencies of parthenogenesis and pseudogamy, relative to apomeiosis levels in each *Boechera* accession, suggest that apomeiosis is the key step upon which the subsequent developmental steps depend.

In angiosperm, fertilization of the bipolar central nuclei, consisting of two maternally (2m) derived genomes with one paternally (1p) derived copy genome from pollen, is essential for proper endosperm development in sexual plants. This ratio must be balanced for normal development of endosperm during seed development. In this study, Ag. Vice Chancellor Sir, most seeds from diploid and triploid apomictic *Boechera* had 2C:6C and 3C:9C embryo to endosperm ratio respectively, thus demonstrating that parthenogenetic development of unreduced egg cells with pseudogamously derived endosperm (*i.e.* fertilization of unreduced bipolar central by unreduced male pollen) and *2 maternal* : *1 paterna*l genome ratio are favoured during apomictic seed development. The pervasiveness of pseudogamy across apomictic genotypes underscores the importance of the fertilization of central cells for endosperm development in apomictic *Boechera.* In a lay man language, despite the fact that apomictic *Boechera unreduced egg has the capacity to develop without fertilization by the pollen from a father* (Parthenogenesis), *there was a strong evidence that the accompanying endosperm requires a father's contribution (fertilization of central cells by pollen, Pseudogamy) for development.* However, 3 diploid apomictic taxa were found to be genotype-specific for production of high frequencies of pentaploid (5C) endosperms, which is a clear evidence of the relaxation on the constraint of 2 maternal: 1 paternal genome balance during endosperm formation of seeds from these individuals. Importantly, the high levels of pseudogamously derived endosperm in both diploid (4m+2p) and triploid (6m+3p) apomicts, suggests strong influence of genomic imprinting during endosperm

development in sexual and apomictic *Boechera* (Naumova et al., 2001). In addition to the prevalence of pseudogamy, there were relatively low levels of autonomous endosperm formation recorded in diploid and triploid apomicts, confirming that fertilization-independent-endosperm-development is possible in *Boechera* apomictic phenotypes (Voigt et al., 2007; Aliyu, Schranz, et al., 2010).

Ag. Vice Chancellor Sir, this deep analysis was not only unprecedented but it has revealed some secrets about apomixis in *Boechera* and has disapproved previous concept of apomixis as a female phenomenon. This study has become a standard reference for apomixis and polyploidy studies since it was published (Aliyu, Schranz, et al., 2010). This data set has revealed the secret about sexuality and asexuality in the life of *Boechera* and has provided germane information for the transmission of apomixis into crop plants.

## 8. Gene Copy Number Variation in Boechera

Ag. Vice Chancellor Sir, an attempt to find answer to the mystery behind continuous evolution and survival of apomictic individuals, despite perturbed meiosis has led to the study of mutation accumulation (copy number variation) in the transcribed genomic regions of 10 sexual and 10 apomictic plants selected based on 100% sexuality and apomictic expression (Figure 4, Aliyu, Schranz, et al., 2010), using a double-validated analysis of comparative genomic hybridization (CGH) of a high-density (>700K) custom microarray (Springer et al., 2009). From 719,345 probes present on the tiling-array, a total of 313,568 probes showed copy number polymorphism across the apomictic and sexual genomes,

the most significant of which were depletions (n = 304,593; 97%) compared to the enrichment (n = 8975 probes; 3%; Table 1). The low frequencies of enrichment for all *Boechera* genotypes, irrespective of reproductive mode (Table 1), strongly suggest that their accumulation (CNV) is counter selective (Le Rouzic et al., 2007). There were differences between reproductive modes, with the most probes (67%) showing CNV in the sexual genotypes, compared to the 33% in apomicts (Table 1).

Table 1: Number of probes showing copy number variation (CNV) in apomictic and sexual *Boechera*. Aliyu et al. (2013).

| **Characteristics of CNV** | **Mode of Reproduction** | | **Total** |
|---|---|---|---|
| | **Apomictic** | **Sexual** | |
| **Deletions** | 99 795 (32.76%) | 204 798 (67.24%) | 304 593 (97.14%) |
| **Duplications** | 5 200 (57.94%) | 3 775 (42.06%) | 8 975 (2.86%) |
| **All probes with CNV** | 104 995 (33.48%) | 208 573 (66.52%) | 313 568 (100%) |

Based on the genome-wide patterns of depletion and enrichment, five lineages (i.e., four clusters and the divergent *B. schistaceae*-Sex-9 sample) were identified from the genotypes studied (Figure 5). Three of the clusters (lineages 1, 3, and 4) were characterized by both sexual and apomictic genotypes (Figure 5; Aliyu et al., 2013). Considering that apomixis is derived from sexuality in *Boechera* (Schranz et al., 2006; Mau et al., 2015), these data are consistent with at least three independent origins of apomixis from different sexual backgrounds (Lovell et al., 2013; Mau et al., 2015).

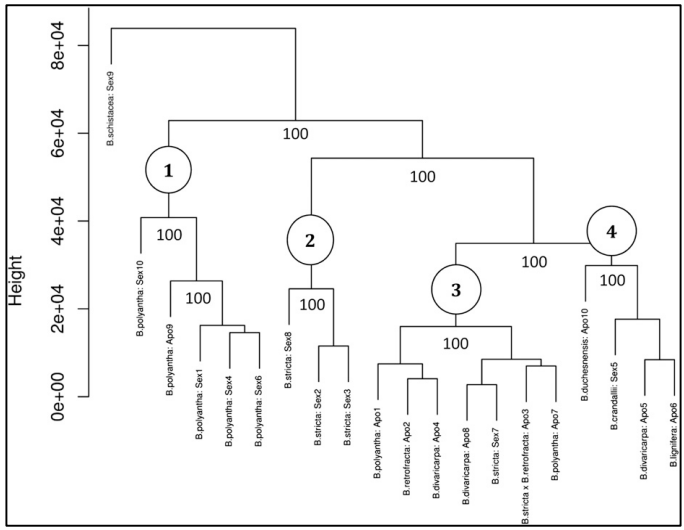



Figure 5: Hierarchical clustering of 10 sexual and 10 apomictic Boechera genotypes gene copy number from cDNA microarray probes (see Aliyu et al., 2013).

Strong evidence of low level of facultative apomixis obtained in some diploid apomictics (Aliyu, Schranz, et al., 2010) perhaps enables the perpetuation of apomictic lineages through gene flow and introgression from sexual lineage (Van Dijk & Vijverberg, 2005). Low-frequency facultative apomicts represent an ancestral "pre-condition", for the evolutionary success of apomixis in *Boechera* and this is related to regulatory changes induced by hybridization (Kantama et al., 2007; Sharbel et al., 2009, 2010; Mau et al., 2015), leading to increase in the expression of apomeiosis in multiple hybrid lineages. Thus, multiple origins of apomictic lineages from different sexual ancestors through time are a likely explanation for their long-term evolutionary success,

despite Muller's ratchet. *Apomixis evolves from sexuals and each apomictic maintain linkage with its ancestral counterparts for hybridization (sex) in case of selection pressure due to mutational load*.

Furthermore, gene ontology analysis of 110 array probes (corresponding to 64 cDNAs) showing progressive reduction in the accumulation of depletions from sexual to apomictic genotypes showed that they are predominantly transposable elements (TEs). BLAST analysis of *Boechera* cDNA sequences of array probes with significant CNV showed that TEs of all families have undergone higher levels of depletion compared with enrichment in both sexual and apomictic *Boechera* genotypes across all lineages. TEs are genomic parasites that could contribute to eventual lineage extinction in apomictics because of their deleterious effects (Dolgin & Charlesworth 2006). However, mating system has shown differential purifying selection for TEs insertions. Thus, the probability of recombination and syngamy leading to loci that are homozygous for deleterious recessive alleles wil be higher in sexual than in apomictic plants because of their hybrid origin and this applies to both TE insertions and other types of mutation. CNV data showed a clear evidence that substantial mutations in transcriptionally active region of the *Boechera* genome are genomic parasite (TEs) and counter selected through purifying selection (deletion). Prevalence of depleted CNVs in sexuals compared to apomictics suggests sex as a major biological mechanism for eliminating such deleterious mutation from the genome and hybrid origin of apomicts with the absence of meiosis and syngamy,

will reduce the frequencies of individuals with homozygous deleterious alleles in apomictic genotypes.

In addition, a gene ontology (GO) analysis for overrepresentation of particular classes of genes showing CNV demonstrated a similar pattern of significant classes between sexuals and apomicts. Most of the genes characterized by depletions in both reproductive classes were involved in regulatory, transporter, or catalytic activity. Interestingly, pollen–pistil interactions were overrepresented for enriched genes with higher significance level in apomicts (Aliyu et al., 2013). Gene duplication (enrichment) may be providing a polyploidy-like mechanism whereby deleterious mutations are buffered by extra allele copies (Tanaka et al., 2009).

Ag. Vice Chancellor Sir, through this gene copy number variation study, the secret of survival of apomictic *Boechera* was revealed. The hybrid nature of the asexual species, recurrent hybridization with ancestral sexual types, multiple origins of the asexual lineages, and presence duplicate (extra) genes involving in reproductive process are the key factors responsible for the continuous evolution of apomixis in *Boeachera.* This information will be useful in the development of apomictic clonal hybrid crops.

## 9. Apollo (Apoallele) is the Candidate Gene for Apomeiosis in *Boechera* Ovule

Ag. Vice Chancellor Sir, a gene expression analysis (designed by Agilent Technologies, 105K genus *Boechera* microarray) from micro-dissected live ovules of seven diploid sexual genotypes and 10 different diploid or triploid apomictic genotypes, based upon

previous quantitative variation study (Figure 4; Aliyu, Schranz, et al., 2010) was performed to identify gene controlling apomeiosis in *Boechera* (Corral et al., 2013). Candidate probes with significantly differential expression ($P < 0.05$) between apomictic and sexual plants led to the identification of four different spots with oligonucleotide sequences matching perfectly to ESTs belonging to the same genus *Boechera* gene (APOLLO) when blasted (Corral et al., 2013). This amino acid sequence showed high similarities (BLASTp) to the DEDDh (for Aspartate Glutamate Aspartate Aspartate histidine) exonucleases from *Arabidopsis lyrata, A. thaliana,* and *Brassica rapa* (Corral et al., 2013).

When the gene (APOLLO) was cloned and sequenced in 18 *Boechera* genotypes, it shows highly polymorphism at different levels between sexual and apomictic haplotypes (Corral et al., 2013). Apomixis-specific polymorphisms were identified in all the 10 apomictic genotypes but not in any sexual genotype (Corral et al., 2013). Sexual plants were homozygous for APOLLO sexalleles, whereas all apomictic plants were heterozygous for both sexalleles and apoalleles. While sexallele transcripts contribute to gene expression in sexual plants, APOLLO was significantly down-regulated in sexual ovules (Corral et al., 2013). In contrast, APOLLO was significantly up-regulated in apomictic ovules when compared to sexuals ($P<0.001$), an indication of preferential apoallele expression (Corral et al., 2013).

Searching for the molecular function of this gene, the Plant PAN analysis of all cloned APOLLO 59 UTRs revealed that the 20-nucleotide apomixis-specific

polymorphism (TGGCCCGTGAAGTTTATTCC) was characterized by a plus-strand transcription factor-binding site (TBS; agtTTATTc) for the ATHB-5 (for ARABIDOPSIS THALIANA HOMEOBOX PROTEIN5) transcription factor. This is present in apoalleles but absent in all sexalleles (Corral et al., 2013). Furthermore, this study also revealed gene copy number variation (CNV) for APOLLO between the sexual and apomictic *Boechera spp*. While two copies of APOLLO were found in all sexual genotypes and all copies corresponded to sexalleles, APOLLO copies (i.e. CNV), vary from four to six copies in diploid apomictic plants and five to eight copies in triploids (Corral et al., 2013), thereby validating the claims of Aliyu et al. (2013). All apomictic plants are heterozygous for APOLLO with one copy of both apoalleles and sexalleles, confirming hybrid nature of apomictic *Boechera* (Aliyu et al., 2013; Corral et al 2013). Indeed, PCR (qPCR) validation of APOLLO in ovules, anthers, and leaves showed that these gene codes for a DEDD 39→59 exonuclease and have an important role in chromosomal replication (Corral et al., 2013).

## 10. UPGRADE2 (*BspUPG2*) Gene Involved in the Formation of Unreduced Pollen in *Boechera*

Mr. Ag. Vice Chancellor Sir, while we have phenotypic proof from the quantitative variation study that apomixis (apomeiosis) occurred in both female (egg) and male (pollen) parts (Aliyu, Schranz, et al., 2010), and APOLLO (apoallele) as gene responsible for apomeiotic expression in apomictic *Boechera* ovule, another parallel study was set up to find candidate gene involved in

apomeiosis in the pollen. To this end, a detailed quantitative analysis of the process of microsporogenesis was carried out to identify suitable anthers for comparative RNA expression between reduced (sexual) and unreduced (apomictic) pollen formation in seven sexual and seven apomictic genotypes (Mau et al., 2013). This gene expression microarray-based analysis of diploid sexual versus diploid apomictic *Boechera spp*. genotypes has led to the identification of *BspUPG2* gene that is up-regulated in apomictic genotypes but down regulated in sexual types (Mau et al., 2013). qRT-PCR validation showed strong apomeiosis specific up-regulation of BspUPG2 in reproductive tissues of apomictic *Boechera spp*, and the transcriptional activity of this locus has correlation with meiotic non-reduction during male sporogenesis (Figure 6, Mau et al., 2013).

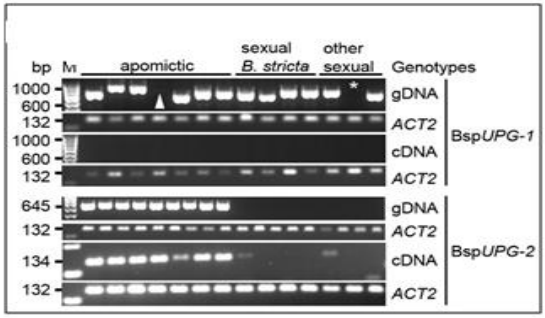



Figure 6: PCR with primers the apo-specific presence of BspUPG2, whereas BspUPG1 is present in both sexual and apomictic genomes (Mau et al., 2013).

The identification of a transcript unique to apomictic *Boechera* spp. UPGRADE2 *(BspUPG2)*, which is highly

up-regulated in pollen is a further proof that apomixis is not only a female phenomenon as believed in the past. *BspUPG2* is highly conserved among apomictic *Boechera spp*. genotypes but has no homolog in sexual *Boechera spp*. or in any other taxa (Mau et al., 2013).

Mr. Ag. Vice Chancellor Sir, when these two genes (*APOLLO* and *UPGRADE2*) were tested in the 73 genotypes analyzed by Aliyu, Schranz, et al. (2010), both had 100% correlation with both high-level facultative and obligate apomicts (Corral et al., 2013; Mau et al., 2013). We have successfully used these genes to transform sexual *Boechera* into apomict and in collaboration with the University of Nebraska, there is an on-going industry partner project for the transformation of Arabidopsis, maize and tobacco with APOLLO and UPGRADE 2 genes.

## 11. Genomic Studies in *Hypericum spp.*

Mr. Ag. Vice Chancellor Sir, I have also been involved in the development of eleven (11) microsatellite (simple sequence repeat, SSR) markers for genetic evaluation of *Hypericum perforatum* L. because of its pharmaceutical values (Corral et al., 2011). These markers were used in our genome-wide scale study of biogeographical distribution and variation of *H. perforatum* in North America and Europe (Molins et al. 2014). We have established Europe as the centre of the origin of this plant with multiple introductions to North America. Frequent gene flow between different gene pools accounts for the phylogenetic similarity of plants from these two regions (Molins et al. 2014).

## 12. Cashew Improvement

Mr. Ag. Vice Chancellor Sir, cashew was introduced into Africa the same period with India i.e. about 16th century through trade mission by the Portuguese explorers (Mitchell & Mori, 1987). It is now an important commodity export crop with economic and health benefits in many third world countries in Asia and Africa (Ohler, 1979; Aliyu & Yahaya, 2001; Yahaya et al., 2010). Detailed historical account, evolution and development of cashew in Nigeria have been documented (see Ohler, 1979; Akinwale & Esan, 1989; Aliyu and Hammed, 2008a; Aliyu, 2012b). Currently, cashew can grow effectively in about twenty-seven (27) out of the thirty-six (36) states of Nigeria with the major production in the north central states (Aliyu, 2012b). World production of raw nuts stands at about 4.0 million tonnes of raw cashew nuts in 2017 (FAO, 2017) and about one-third of this world production comes from Africa. Nigeria accounts for 42% of the continent exports. Nigeria is reported to have production capacity of about 800,000 tonnes but currently exports about 220,000 tonnes, valued at N145 billion ($405m). Kwara State, located in the guinea savannah ecology, is endowed with the ideal climate and soil characteristics suitable for the production of high quality cashew (Aliyu, 2012b).

## 13. Pollen Longevity in Cashew

Mr. Ag. Vice Chancellor Sir, the need to carry out hybridization between distant parents has led to a study on longevity of pollen after the collection and determination of the appropriate medium for its

germination *in vitro*. Flower panicles at pre-anthesis with different stalk lengths were collected from five different genotypes and inserted in beakers (1000ml) containing sterile water, and stored both under humid condition at room temperature and at $6^{o}$ C in the refrigerator. As expected, pollen grain viability reduces with the period of storage (0 -7 days) (Aliyu et al., 2001). However, panicles with stalk dip in water retain 50% pollen grain viability in 96 hours (4 days) after being separated from mother plants (Aliyu et al., 2001). Pollen grain viability at 50% is still suitable for hand pollination in tree crop (Aliyu, 2008). However, viability reduces to 1.6% 168 hours after detachment. In practice, pollen stored at that length of time (96 hours) can be used for hybridization among parental lines in distant locations whose blooming periods are some days apart. However, of the nine different sucrose concentrations and four different concentrations each for $H_3BO_3$, $KNO_3$, and $CaCl_2.2H_2O$ tested for *in vitro* medium for pollen germination; 5.0% sucrose supplemented with 50ppm each of $H_3BO_3$, $KNO_3$, and $CaCl_2.2H_2O$ gave highest germination (29% higher than control) (Aliyu et al., 2001) and are recommended for pollen studies in cashew.

## 14. Flowering Pattern in Cashew

Mr. Ag. Vice Chancellor Sir, my romance with cashew plants has further revealed variation in the production (quantity and time) of different types of flowers across canopy position of a tree. Two years data on floral studies across canopy positions of 5 cashew genotypes showed that southern part of canopy attained anthesis 18 days earlier than its eastern counterparts (Aliyu &

Awopetu, 2003). Similarly, the quantity of flowers in southern branches was 48% higher than the eastern part. Preponderance of productive flowers in one part of canopy than the other parts explains non-uniform fruit set often recorded across the tree canopy in cashew. Light and temperature are critical to cashew production (Masawe et al., 1999). Because cashew produces its fruits on the periphery of the canopy, farmers should use recommended genotype- and/location- specific spacing during field layout and establishment. High density planting with interlocking of branches will significantly affect yield. Mr. Ag. Vice Chancellor Sir, I have visited many cashew plantations, and have seen this error committed and investments wasted.

## 15. Tree Compatibility and Fruit Set in Cashew

Mr. Ag. Vice Chancellor Sir, as part of my efforts to address the problem of low yield, a combination of hybridization (diallel cross) and histological sectioning of pollen-stigma interaction, stylar pollen tube growth of pollinated flowers were used to investigate genetic compatibility in cashew trees (Plates 2a – d, Aliyu, 2007b; 2008). This study is similar to hysterosalpingogram (HSG) in testing the blockage of fallopian tube in medical practice. Of 21,779 pollinations carried out during the three years of this study, 11,388 (52%) adhered to stigmatic surface and 8,890 (41%) germinated through the stylar tube (Plates 2a-c, Aliyu, 2007b). However, pollen fertility of the trees was between 54% and 99%; therefore, low pollination and fertilization cannot be attributed to low pollen viability (Aliyu, 2007b). Climatic variables such as temperature

and relative humidity are critical for pollination in tropical crops in addition to availability of pollinators. There was no evidence of tube growth inhibition (blockage) based on histological examination of both cross- and self- pollinated flowers (Plate 2a-c, Aliyu, 2007b), suggestive that factors affecting fruit set can be traced to events preceding pollination and/or at fertilization and afterward.

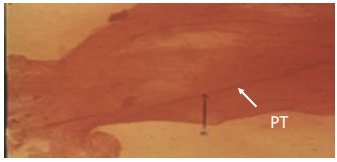



Plate 2a: Pollinated style of cross-compatible clones showing pollen tubes growth from the stigmatic position and within upper part of the style 12-hours after pollination. Mag. x400. PT: polle tube growth

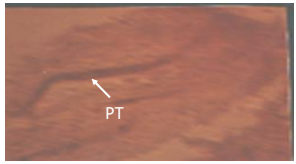



Plate 2b: Pollen tube growth within the stylar tissue of compatible clones observed 16- hour after pollination. Mag. x400. PT: pollen tube growth

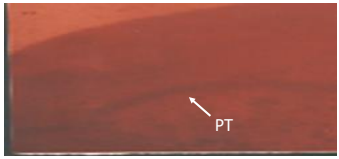



Plate 2c: Pollen tube at the base of the style of the compatible clones i.e. at the ovary 24-hours after pollination. Mag. x400. PT: pollen tube growth within the ovary.

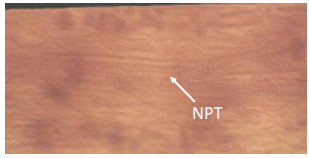



Plate 2d: Pollinated style of self-incompatible clones without pollen tube growth 12 hours after self-pollination. Mag. x400. NPT: no pollen tube growth.

Plate 2: Pollen tube growth in hand pollinated flowers in cashew

Comparing the number of pollinated flowers with the actual fruit set, the cashew genotypes exhibited 34% cross-compatibility, 51% partial cross-compatibility and 15% cross-incompatibility at fruit set, against, 50% cross-compatibility, 46% partial cross-compatibility and 4% cross-incompatibility at pollination (Table 2, Aliyu,

2007b, 2008). Significant reduction in the level of compatibility during the transition from stigma pollination to fruit development could arise from post zygotic incompatibility, hormonal imbalance, fruit abortion, pest infestation or adverse climatic condition. Nonetheless, three cashews (CC06, CC01 and CC02) demonstrated genotype-specific for broad pollen acceptability (highly compatible mothers). Also notable in the study is maximum 55% fruit set of successfully pollinated flowers, despite controlled pollination, suggestive of upper limit (carrying capacity) in cashew and maternal resource allocation (nutrition), among other factors that could have a role to play.

Table 2: Analysis of cross compatibility of fruit set obtained from m diallel cross among 11 cashew clones Aliyu (2008).

| | Cross-compatibility | | | | | |
|---|---|---|---|---|---|---|
| | Female Parents | | | Pollen Parents | | |
| Clone | + + | - + | - - | + + | - + | - - |
| CC01 | 6 | 3 | 1 | 3 | 3 | 4 |
| CC02 | 5 | 4 | 1 | 4 | 2 | 4 |
| CC03 | 2 | 7 | 1 | 3 | 6 | 1 |
| CC04 | 3 | 7 | 0 | 3 | 5 | 2 |
| CC05 | 2 | 7 | 1 | 4 | 4 | 2 |
| CC06 | 10 | 0 | 0 | 8 | 2 | 0 |
| CC07 | 2 | 5 | 3 | 2 | 7 | 1 |
| CC08 | 3 | 6 | 1 | 5 | 5 | 0 |
| CC09 | 2 | 4 | 4 | 1 | 9 | 0 |
| CC010 | 1 | 6 | 3 | 2 | 6 | 2 |
| CC011 | 1 | 7 | 2 | 2 | 7 | 1 |
| Total | 37 | 56 | 17 | 37 | 56 | 17 |
| Percentage (%) | 34 | 51 | 15 | 34 | 51 | 15 |

The 55% fruit set is comparably higher than 3-12% obtainable through open pollination in farmers' field. Mr. Ag. Vice Chancellor Sir, no wonder that only 20% of trees on the cashew field are often found productive (Martins & Kasuga, 1995; Aliyu, 2005c; Aliyu & Awopetu, 2007c; Aliyu & Awopetu, 2011). Significant variation between fruit set in hand pollinated (55%) cashews and naturally pollinated fields (<12%) is suggestive of inefficient pollination system and high cross incompatibility in cashew (Aliyu & Asogwa, 2001). Unfortunately, new cashew fields are continually being established with bulk harvest till date, without taking genetic compatibility into consideration. Such forceful co-habitation of incompatible partners will be unproductive and amount to waste of investment. It therefore becomes imperative that cashew fields should henceforth be established with certified compatible polyclonal materials.

Paired parental clones that recorded high fruit set in their crosses and reciprocals (CC08 and CC01; CC02 and CC04; CC05 and CC06) will be good candidates for the establishment of high yielding cashew fields. Selection of high-yielding materials only based on fruit set by the mother trees may turn out to be an incomplete/ineffective strategy to achieve yield improvement without recourse to identifying compatible pollen parents/trees. This simple but important step will go a long way to enhance nut yield improvement in cashew and consequently increase farmer's outputs (Aliyu, 2008).

## 16. Exogeneous Plant Hormones and Fruit Set in Cashew

With about 50% fruit set obtained in previous studies (Aliyu, 2007b; Aliyu, 2008), five exogenous hormones (Gibberellic Acid ($GA_3$) and 4 Auxins (IAA, IBA, NAA, & 2, 4-D) at seven different rates of application (0 $mgL^{-1}$, 10 $mgL^{-1}$, 25 $mgL^{-1}$, 50 $mgL^{-1}$, 100 $mgL^{-1}$, 250 $mgL^{-1}$ and 500 $mgL^{-1}$) were evaluated on cashew trees to improve yield. Of five hormones tested, $GA_3$ at 50 - 100 $mgL^{-1}$ significantly improve the quality of flowering (precocity and number of hermaphrodite flowers), fruiting, and about 69% increase in fruit retention (Aliyu, 2005b; Aliyu et al., 2011). Cashew farmers are encouraged to use exogenous hormone ($GA_3$) to improve yield in cashew.

## 17. Nut Size-Number Trade-off in Cashew

Mr. Ag. Vice Chancellor Sir, another important pitfall to avoid by cashew growers is indiscriminate planting of bold nuts (Jumbo). While it is highly probable that such nuts will produce large kernels of high premium (W180 – W240), study has shown that large nut size can be at the expense of number i.e. size-number trade-off (Aliyu, 2006; Aliyu & Awopetu, 2011). There is significant correlation between number of fruits (nuts) per individual tree and total yield (kg) per tree (r=0.98, Aliyu, 2006; r=0.84; Aliyu et al., 2014), but the correlation between nut size and total yield (kg) has shown to be genotype specific. Trees with nut size between 6.00 and 12.00g have shown significant increase in total yield with increasing size of individual nut. However, total yield decreases with increasing nuts size above (>13.00g)

(Aliyu & Awopetu, 2011). Harnessing these two characteristics (size and number) for optimum outputs is however crucial to future growth of cashew. Trees combining prolific fruiting (about 2500 nuts/trees) with 9.0 to 13.0g nut size are the most suitable for establishing productive field (Aliyu, 2005c; Aliyu & Awopetu, 2007c; Aliyu & Awopetu 2011; Aliyu et al., 2014). Such trees have the capacity to produce about 2 tonnes per hectare and will attract better price because for its premium kernels.

## 18. Genotype x Environment Interaction (Yield Stability) in Cashew

Mr. Ag. Vice Chancellor Sir, our genotype x environment data on yield components from Ibadan, Ochaja and Uhonmora, using a combination of additive main effect and multiplicative interaction (AMMI) and genotype, genotype by environment (GGE) biplot analysis has shown inverse relationship between stability and yield, as the best three yielding genotypes (KT_26, IW_222 and IW_31, remain most unstable (Aliyu et al., 2014). The interaction of genotype with the environment (location) (GxE) has brought about change in performance (ranking of genotype) between locations, and rule out the universal best genotype among the seven cashew genotypes studied (Aliyu et al., 2014). Each location has some comparative advantages over the other for some of the yield component traits. While Ibadan and Uhonmora with high relative humidity favoured flowering precocity, nut production was better in Ochaja with warm climate. Comparatively, Ochaja was the most suitable for cashew production among the three

locations. The effect of climatic and edaphic factors on flowering and yield of some tree crops are well documented. However, the data grouped the three locations into two micro-environments (ME), Ibadan and Uhonmora as micro-environment 1 (ME-1) with IW_222, as the best genotype and Ochaja as micro-environment 2 (ME-2) with MD_261 as the best genotype. In summary, with the selection of suitable genotypes for specific environment and the use of appropriate husbandry techniques, significant improvement in cashew nut yield is possible.

## 19. Genetic Diversity Studies in Cashew

Mr. Ag. Vice Chancellor Sir, I have applied a combination of morphological and molecular markers (electrophoresis and simple sequence repeats, microsatellite) to study the extent of diversity of Nigerian cashew and results have been documented (Aliyu & Awopetu, 2007a, 2007c; Aliyu, 2012b). There was a high level of concordance between these markers systems, indicating their usefulness in cashew genetic resources management. Data from these markers consistently grouped the accessions into 5 major groups that reflect breeding history and more importantly, fruiting and morphotypic characteristics of the genotypes (Aliyu & Awopetu, 2007a, 2007c). Group I comprises very high yield with intermediate quality kernels. Group II is characterized with moderate nut yield with high quality kernels. Group III combines high nut yield with small-compact tree canopy, suitable for high density planting. Group IV genotypes are predominantly large canopy type with poor nut yield. Group V is characterized with low

yield with high quality kernels (Aliyu & Awopetu, 2007a, 2007c; Aliyu, 2012b). Parents with contrasting features are candidates for hybrid development and source of introgression in a long term cashew breeding programme.

Of the ten (10) microsatellite loci used (Croxford et al., 2006) for the molecular characterization of 187 cashew accessions of different genetic introductions, eight (8) were polymorphic and could be efficiently used for characterization and management of cashew germplasm (Aliyu, 2012b). Preliminary data showed significant redundancy within the Nigerian cashew germplasm and there is the need to develop a core collection from existing materials and introduce new germplasm to broadening the genetic pool.

## 20. *In Vitro* Culture of Hybrid Cashew Embryo

Mr. Ag. Vice Chancellor Sir, the problem of fruit abscission and pilfering of apple before maturity during the development of hybrid cashew has led to this work on *in vitro* culture of hybrid embryo to regenerate plantlets (Aliyu & Awopetu, 2005). Embryos of 2-, 4-, 6- and 8-weeks old were evaluated on different media compositions, ranging from pure Murashige and Skoog (MS) agar medium (Murashige & Skoog, 1962) to modified MS medium supplemented with 1 mM each of naphthaleneacetic acid (NAA), benzyladenine (BA) and gibberellic acid ($GA_3$). In this study, embryo size (age) significantly correlated to response rate and emergent of the plantlets, with older embryos i.e. 6 weeks old and above performed better (Plate 3, Aliyu & Awopetu, 2005).

Among the media composition tested, only modified MS medium supplemented with 1 mM of gibberellic acid (MS+$GA_3$) supported the growth of young embryos of 2 weeks old (Aliyu, 2005a, Aliyu & Awopetu, 2005). Temperature, source of explants, browning, and contamination are other known factors affecting *in vitro* culture of cashew (Aliyu, 2005a).



Plate 3: *In vitro culture of cashew hybrid embryo*

## 21. Chromosome and Genome Size Studies in Cashew.

Mr. Ag. Vice Chancellor Sir, as part of the efforts to unravel the secret of life in cashew and develop genetic resources that will facilitate its improvement, chromosome and genome studies have been carried out on cashew accessions growing in Nigeria (Aliyu & Awopetu, 2007b; Aliyu, 2012a; Aliyu 2015). Mitotic spread consistently revealed 2n=42 for all cashews sampled (Plate 4a-d, Aliyu & Awopetu, 2007b) with the

total length of 51.10µm and 56.00 µm the homologous chromosomes in India and Brazilian introductions, respectively, suggesting intra-specific genome variation. Chromosome compliment of 6Asm + 1Am + 4Bsm + 5Bm + 5Cm and 6Asm + 1Am + 1Ast + 9Bm + 2Bsm + 2Cm were obtained from Indian and Brazilian accessions, respectively (Plates 4c and d, Aliyu & Awopetu, 2007b). Regular meiotic divisions with 21 bivalents and tetrads pollen mother cells were prevalent across the genotypes studied, suggestive of high fertility of the pollen grains. The diploid chromosome number of 2n = 42 and haploid of n = 21 suggest that chromosome polymorphism of 2n = 24, 30, 40, and 42 (Deckers et al., 2001) are rare in Nigerian cashew accessions, an indication of genome stability.

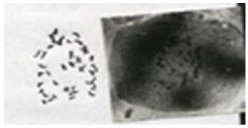


Plate 4a: Mitotic chromosome of Indian accessions . x400

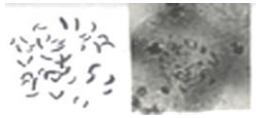


Plate 4b: Mitotic chromosome of Brazilian accessions. x400

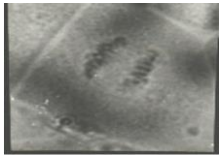


Plate 4c. Late anaphase in Indian accessions. x400

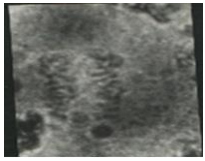


Plate 4d. Late anaphase in Brazilian accessions x400

Plate 4: Mitotic chromosome spread in cashew

Mr. Ag. Vice Chancellor Sir, the optimization of flow cytometric protocol preceded genome size determination in cashew, and data from fluorescence intensity, background yield (%), nuclear yield (nuclei $s^{-1}$ $mg^{-1}$) and coefficient of variation (%) of *G0/G1* peak of the

analysed nuclear suspension showed that Otto's buffer with 70mg leaf sample and 20 mins incubation period (Aliyu, 2012a) is most suitable for cashew. *Lycopersicon esculentum* (tomato) and *Glycime. max* (soybean) are the most ideal internal reference for genome size determination in this plant (Doležel et al., 2007; Aliyu, 2012a).

Furthermore, the determination of absolute genome size with the use of Propidium Iodide (PI) validates intra-specific variation in cashew (Aliyu & Awopetu, 2007b; Aliyu, 2012a; Aliyu, 2015). The absence of endopolyploidy from the histrogram profiles indicates stability of this plant genome (Leitch & Leitch, 2008; Aliyu, 2015). Importantly, cashew genotypes sampled have absolute genome size of 0.428 pg and 419 Mb /1C (Aliyu, 2015) with about 0.20-fold difference in the mean genome size (0.743 - 0.899 pg/2C). Genome plasticity for plant adaptation is a well-documented phenomenon in plant species (Leitch & Leitch, 2008). In addition, there was correlation between intra-specific genome variation and geographical gradients of the accessions (Aliyu, 2015).

Mr. Ag. Vice Chancellor, I believe you will agree with me that secret of life of cashew plant has been revealed from these studies. The genomic information provided has laid a solid foundation for future advance genomic research in cashew.

## 22. Propagation and Germination in Cashew

Mr. Ag. Vice Chancellor Sir, the success of any tree plantation depends partly on the process and handling of propagules at culturing. To this end, I have conducted a

number of studies to improve the propagation of cashew (layering, budding and grafting) (Hammed & Aliyu, 2002; Aliyu, 2003, 2005a, 2007a; Aliyu & Akintaro, 2007; Aliyu & Hammed, 2008b; Aliyu, Dada, et al., 2010; Hammed et al., 2014).

## 23. Cowpea Improvement Programme

Mr. Ag. Vice Chancellor Sir, as a follow up to our earlier work (Awopetu & Aliyu, 2006), recently I started the evaluation of seventy (70) cowpea lines from (IITA) Ibadan and the initial results led to the selection of three superior varietal groups viz: (i) IT10K-837-1, combines very high seed yield with early maturity and large seed, (ii), IT07K-299-6, IT10K-815-5, IT10K817-7, and IT08K-150-24, combine very high seed yield with medium maturity and large seeds, and (iii) IT11K-61-82, combines very high seed yield with early maturity and medium seeds (Aliyu & Makinde, 2016). Further yield stability trials across three locations in Kwara State identifies two lines (IT07K-299-6 and IT11K-61-82) that combine precocity with stable high seed yield across the three trial locations (Aliyu et al., 2019). Other parallel studies with my students have also led to the identification of potential drought tolerant candidates and that application of phosphorus fertilizer at the rate of 20kg/ha $P_2O_5$ (P20) is capable of increasing seed yield by about 43%.

## 24. Conclusions and Recommendations

Mr. Ag. Vice Chancellor Sir, it has been opined that the number of people on earth will increase from 7.7 to 10 billion by 2050 and to meet the world food demand

agricultural production must increase by 80%. To achieve this task, innovative breeding technologies for improving existing crops for better adaptation, efficient utilization of resources, improved yield and nutritional values are required. Apomixis technology offers a great opportunity because it is capable of fixing hybrid vigour (heterosis) in a single generation, thereby allowing stable high yield over generations and enabling farmers to reuse their seeds.

In the course of this lecture, I have enumerated my contributions that can facilitate the process of successful transformation of crop plants with apomixis thereby increasing yield and enhancing sustainable global food production. I have enumerated how the development of high throughput method for rapid screening of apomixis expression has led to the discovery of APOLLO and UPGRADE2 as genes controlling apomeiosis (sex avoidance), and gene duplication and hybridization as biological mechanisms for continuous evolution of apomixis. In areas of cashew improvement, Mr. Ag. Vice Chancellor Sir, I have also enumerated a lot of my contributions that significantly address the problem of low yield, thereby leading to the identification of cashew genotypes with stable high yield (1.5 – 2.5 tonnes/ha), and quality nuts for sustainable production and investment in the industry. My works also provided genome information necessary for advance genomic research and genetic transformation of cashew. My recent efforts in cowpea improvement have shown a promising trend of significant increase in seed yield by two cowpea lines for the southern guinea savannah ecology.

Mr. Ag. Vice Chancellor Sir, there is the urgent need for the Federal Government to give priority to research by providing resources for functional laboratories, equipped with modern technologies and training of manpower that will carry out advanced research in agricultural production for sustainable food security. The governments should upgrade existing genetic facilities in some of our institutions to the status of the centres of excellence in genomic research. The government should also strengthen the capacity of Nigerian scientists to embark on genetic engineering of our major food crops in addition to the conventional system being used. The government should put in place monitoring mechanism to prevent the influx of GMO crops into the country because of its effect on biodiversity of our plant and animal resources. Our national breeding programmes on cereals and grain legumes should consider integrating the use of apomixis technology for hybrid seed development because of its potential to revolutionized agriculture.

Mr. Ag. Vice Chancellor Sir, advances in genetic research is moving at jet speed and there is urgent need to review the training curriculum in plant breeding and genetics for our students in Nigerian universities to reflect current realities. Ph.D. training in genetics and plant breeding should include at least 6 months mandatory placement (government funded) in advance plant genomic laboratories to build capacity our future breeding practitioners and make them relevant/competitive in the global scientific community.

Furthermore, there is urgent need for professors of genetics and practicing breeders to develop teaching materials that will facilitate learning and comprehension

of the subject. Students run away from the discipline because they can hardly comprehend our jargons. Using local examples from our research findings will assist learning greatly.

The government through the Cocoa Research Institute of Nigeria should establish polyclonal seed gardens as sources of improved planting materials for future cashew establishment. Farmers should embark on rejuvenation of old moribund cashew with improved materials. Farmers should adopt the integrated crop management technology, including the use of improved planting materials and synthetic hormones/pesticides at recommended rates to improve yield in crop. The government should as a matter of policy discourage export of raw nuts from the country to create job, especially for youth and women who are mostly engaged in the cashew processing.

Mr. Ag. Vice Chancellor Sir, with increase in cashew production in many West African countries in the recent time, it is high time that the governments of Economic Community of West Africa States (ECOWAS) come up with a regional cashew development plan to be tagged "West African Cashew Development Agenda". This is to be supported by the African Development Bank to address myriads of challenges confronting cashew industry in the region. Such initiative stands to boost production, processing, export, and largely transform the economy of cashew industry and improve livelihood of the rural households.

Mr. Ag. Vice Chancellor Sir, cashew has the potential to transform the economy of Kwara State if the sector is properly organized and the industry is

supported. There is urgent need for the Kwara State Government to develop a ten-year strategic plan for the transformation of the agricultural commodity, especially cashew, where it has competitive advantage. I am aware that the state government initiated a farmer-ownership cashew project that targeted 5000 hectares per local government area with processing plants in each senatorial district in 2005, but this project was aborted before takeoff. The current administration can revisit this as part of the effort to lay a solid foundation for a sustainable economy of our dear state. The state government should partner with the federal government to stop illegal shipment of nuts across porous borders to the neighbouring countries.

Mr. Ag. Vice Chancellor Sir, this is my little contribution in the attempt to decode the secret of life in plants. I have worked extensively on sex organ in plant (flower), process (compatibility) and product of sex (fruit set), and lately, how to avoid sex (apomixis) because of the many sins (variability in yield and disease transmission), all towards sustainable food production.

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