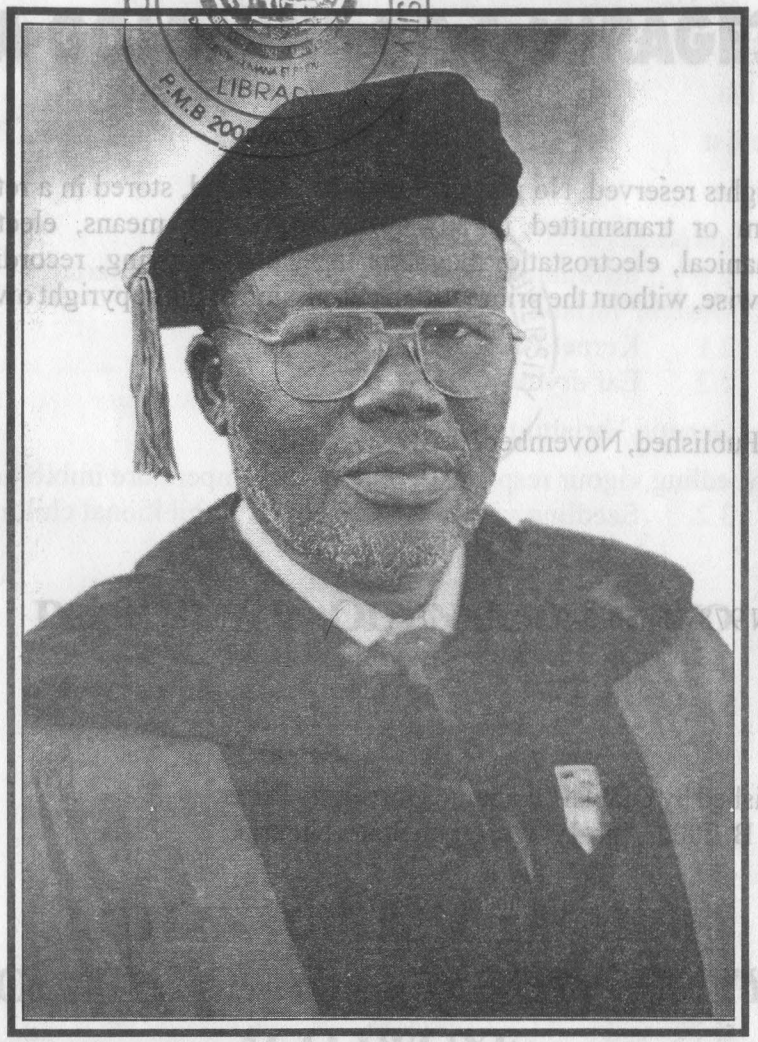

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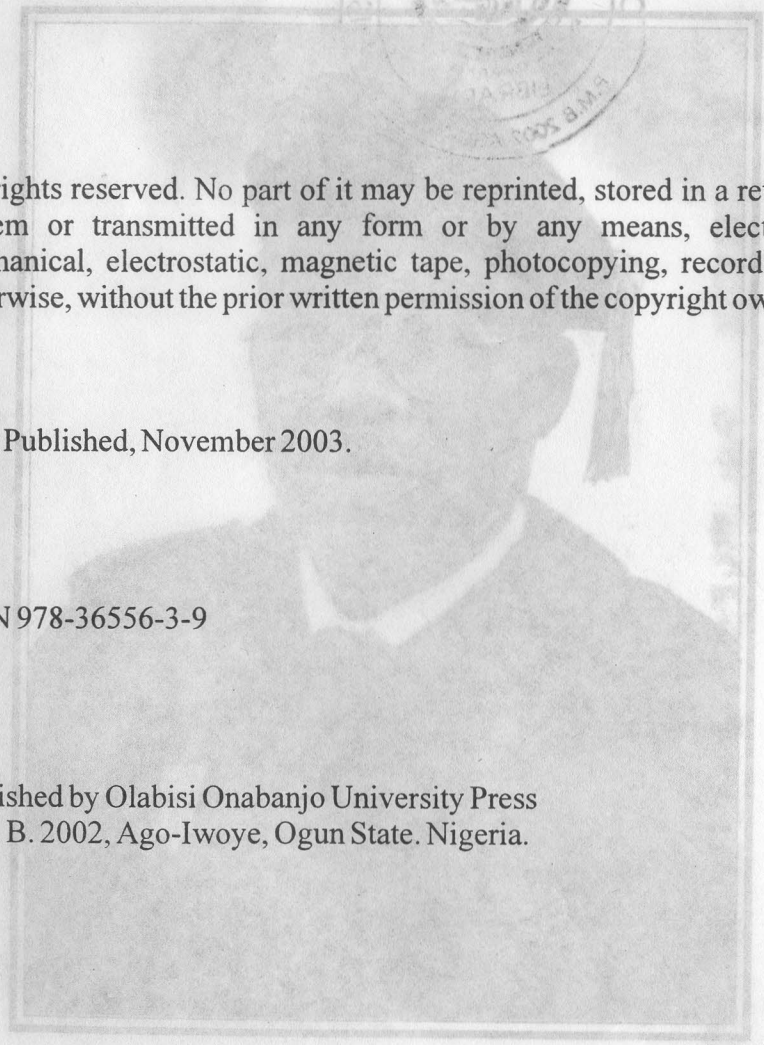

GENETIC VARIABILITY: A GOLDMINE OR A MIRAGE?

BY

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28TH INAUGURAL LECTURE
OLABISI ONABANJO UNIVERSITY
AGO-IWOYE.

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GENETIC VARIABILITY: A GOLDMINE OR A MIRAGE?

The Vice-Chancellor,
Principal Officers of the University,
Provosts of Colleges and Deans of Faculties,
Our Royal Fathers,
Distinguished Ladies and Gentlemen,
Gentlemen and Ladies of the Press here present,
Great OOUITES!

PREAMBLE

It is my pleasure to welcome you all to this 28th inaugural lecture. It is the fourth of its series from the College of Agricultural Sciences, the second from both the Faculty of Agricultural Production and Renewable Resources and the Department of Crop Production respectively and, the first from the Genetics Component of the Improvement Option of the Crop Production Department of this citadel of knowledge.

This lecture focuses in part on the experiences accumulated in the pursuit of the noble and painstaking profession of plant breeding (applied genetics). Unlike very many other experiences in plant breeding and genetics, it draws mainly on activities in permanent (long gestation) economic crops in exploring the general applicability of basic genetic principles and their existence therein. This is related to recent developments in plant breeding and the pertinent efforts of the unravelling field of biotechnology. All these are focused in the context of a developing nation with a view to fostering suggestions on how to best use modern scientific innovations within the limits of the resources available to the nation locally and globally.

At first glance, the subject, Genetics, induces "stomach upset" in many Natural and Applied Biology students. I had similar predicament some 35 40 years before I later discovered quoting the words of Naustradamus in his book "The Man who saw tomorrow" that "beyond the

perceived turbulence came a peaceful, a suiting and a more friendly environment". In view of this and with the assumed divergence in background knowledge of the audience before me, I crave your indulgence to delve into some introductory information.

1.0. INTRODUCTION

Let everyone assume himself/herself as an experimental organism and hazard a guess at the number of basic units (cells) his/her body contains. The year 2000 updates provide the following statistics

Table I: Analysis of Human Genome Discoveries

Human body	
Total number of cells	6×10^{13}
Genetic code	6×10^{9} base pairs or 1.5 gigabytes (only 3% or 45m bytes of that is active)
Summated length of chromosome DNA chains in all cells chromosome copy operations (Prenatal + 1st Year)	1.2×10^{14}m (4.6 light days) 240 Tbytes or 1000,000 ultrawide SCSI
Power Consumption (adult)	90 100 watts (2000 kilocals / day) 1.6 pw/cell

(After Vadim Gerasimov 2000)

Each human being with respect to cell number and the genetic code is therefore more than a trillionaire and thus an intricate factory with multifunctions. Each unit, the cell, represents an elaborate chemical computer, with its own power management structures, read only and

random access memory. It communicates with neighbours and environment. A cell thus is an individual organism and under certain conditions may live outside the collective set up. Each cell (with some exceptions) has a complete copy of the genetic information and theoretically is capable of recreating the whole human body (totipotency). The magnitude of information processing activity inside the human body is amazing. The cell reproduction processes require tetrabytes of chromosome DNA information gadgets to be copied every second. Beside protein synthesis and other functions in cells, it can be several orders of magnitude more information-intensive. Power consumption of a single cell corresponds to about 10^{7} chemical reactions per second. (Gerasimov, 2000). The base pairs are on 23 pairs of chromosomes a set of which comes from each parent at fertilization after coition. Very similar situations obtain in other forms of diploid animal species and plants with appropriate differences in the naturally bestowed number of chromosome pairs.

1.1. INFORMATION TRENDS ON THE HEREDITARY MATERIAL

Before the 19th century, the idea that "life" began "de novo" was nursed. The century saw convincing proof that life gave birth to life but pre-nursed the hypothesis that this was effected via preformationism (i.e. one of the reproducing cells gametes contained the miniature organism while the contribution from the other parent was purely nourishing.) (Fig 1a.)

Figure 1a

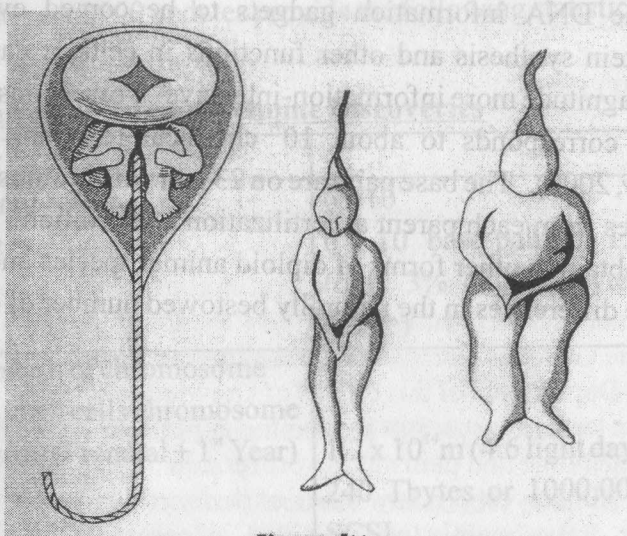


Figure 1(a)
"Homunculi" presumed to be seen in human sperm. (After Singer, from Hartsoeker and Delenpatius.)

This was later replaced by the idea that tissues, organs and not miniature organisms were the factors responsible for the transfer of life (epigenesis). Following this came the hypothesis of pangenesis which indicated that gemules were transferred in the blood stream to the sex organs from where these were separated out during development into paternal and maternal organs. The views of pangenesis were favoured by evolutionists since they provided them with plausible explanations of evolutionary process.

By the end of the 19th century, details of cell structure, cell division were known and the roles of the germ cell nuclei in fertilization were clearly understood. By the turn of the 20th century, the role and materials involved in body cell division (mitosis) and gamete formation (meiosis) were understood, setting the stage for the comprehension of the 19th century quantified knowledge of the hereditary substance by Mendel (1822 - 1824) now referred to as chromosomes.

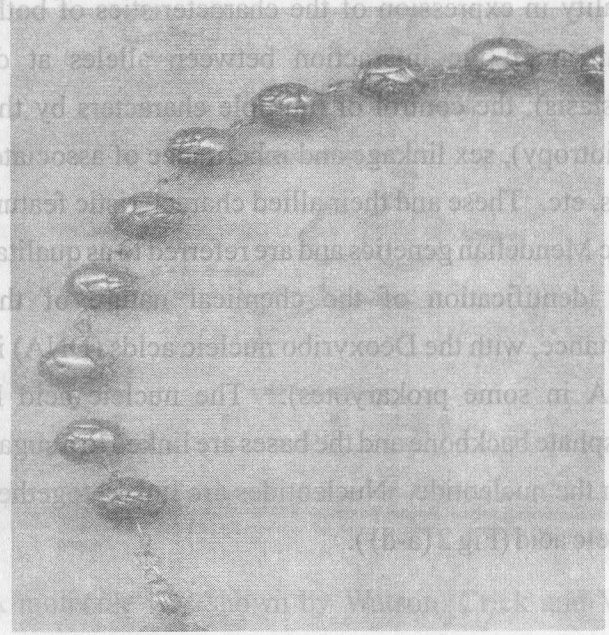


Fig 1(b): The Mendelian concept of the genes on chromosomes

Progressive contributions to knowledge in the field of genetics and related subject areas have elucidated the structure (physical and chemical) and the functioning of this hereditary information complex. Those pertinent to the basic understanding of this lecture are enumerated as follows:

(1) the existence of articulate bead-like components (genes) at loci on strings (chromosomes)(Fig 1b) which make for exactness in inheritance and majorly explains similarities between parents and offsprings (Fig 1b).These have also provided a basis for understanding the phenomena of the expression of a character (dominant) controlled by an allele (dominance) over a trait that is suppressed (recessiveness) by an allele at the same locus; the equality in expression of the characteristics of both alleles (co-dominance); the interaction between alleles at different loci (epistasis); the control of multiple characters by the same gene (pleiotropy), sex linkage and inheritance of associated sex linked traits, etc. These and their allied characteristic features constitute basic Mendelian genetics and are referred to as qualitative traits.

(2) The identification of the chemical nature of the hereditary substance, with the Deoxyribo nucleic acids (DNA) in eukaryotes (RNA in some prokaryotes). The nucleic acid has a sugar-phosphate backbone and the bases are linked to a sugar molecule to form the nucleotide. Nucleotides are linked together to form the nucleic acid (Fig 2 (a-d)).

Fig. 2: Nucleic acid and components

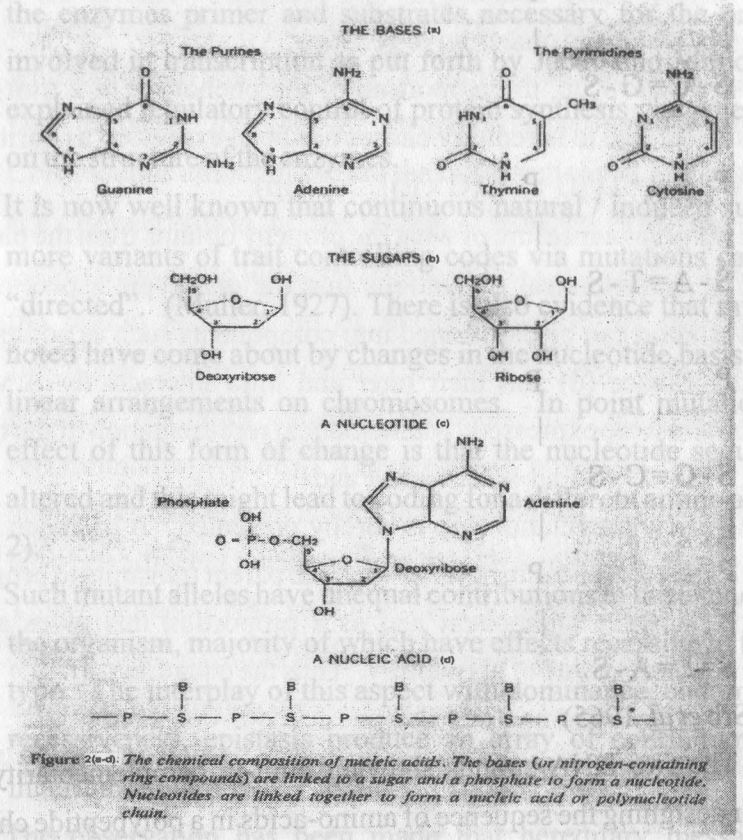


Figure 2(a-d). *The chemical composition of nucleic acids. The bases (or nitrogen-containing ring compounds) are linked to a sugar and a phosphate to form a nucleotide. Nucleotides are linked together to form a nucleic acid or polynucleotide chain.*

DNA molecule was shown by Watson, Crick and Wilkins to be composed of two polynucleotide chains anti-parallel to one another and coiled in a plectonemic spiral or helix. The chains are held together by weak hydrogen bonding between the bases on opposite chains. The bonds break during DNA replication which is semi conservative. The specificity of the gene is carried in the linear sequence of nucleotides within the DNA molecule. This sequence is shown in figure 3.

Figure 3: Portion of DNA Strand showing built-in Complementarity

```
P       P
|       |
S-C=G-S
|       |
P       P
|       |
S-A=T-S
|       |
P       P
|       |
S-G=C-S
|       |
P       P
|       |
S-T=A-S
```

(After Srb *et al.* 1965)

The two DNA strands showing built-in complementarity is the code for designing the sequence of amino-acids in a polypeptide chain of a particular protein. The gene and its polypeptide products are collinear. It is believed that the code is probably a triplet code in the protein transcription synthesis;

(3) there is a realization of the intricate nature of the two major functions of the DNA hereditary transmission (from parent to offspring) and body regulation (protein synthesis) in control of body physiological processes. In these functions, the long stride

contributions of Severo Ochoa and Konberg and several others on the enzymes primer and substrates necessary for the processes involved in transcription as put forth by Jacob and Monod, have explained regulatory control of protein synthesis via gene control on the structure of the enzymes.

(4) It is now well known that continuous natural / induced supply of more variants of trait controlling codes via mutations cannot be "directed". (Muller, 1927). There is also evidence that mutations noted have come about by changes in the nucleotide basis or their linear arrangements on chromosomes. In point mutations, the effect of this form of change is that the nucleotide sequence is altered and this might lead to coding for a different amino acid (Fig 2).

(5) Such mutant alleles have unequal contributions to the phenotype of the organism, majority of which have effects recessive to the wild type. The interplay of this aspect with dominance, codominance, recessiveness, epistasis produce an array of continuum in the inheritance of traits.

(6) The observation has been made that hereditary message gets expressed in environments and these modify the penetrance or expressivity of the trait in consideration. A modest model representation of this is by the popular genetic equation.

$P = G + E$ ..... (i)

$P = G + E + (G \times E)$ .....(ii) (where P = phenotype G = genotype, E = Environment and (G x E) = interaction of G and E).

When a population is being considered, the average performance

of the hereditary control rather than the individual gene control is feasible, more meaningful and realistic. This is the birth of population and quantitative genetics.

(7) As a follow up, the proportion of the phenotype of a trait that is attributable to hereditary causes has been expressed as heritability

$h_b = G/P = G/[G + E + (G \times E)]$..... (iii).

This gives a measure of what the progeny obtains from the parent.

(8) The mathematical derivations that the genotypic aspect of total variation can be partitioned into components such as additive (a), dominance (d) and their inter and intra interactions of various orders were expressed. Mathematical representation of the type

$G = a + d + aa + ad + aaa + add + aad +$ ..... (iv)

To show the relationship is hereby presented. It has been shown that the major contributor to what the parent transmits to progeny is the additive component and as a proportion this gives a more reliable estimate of heritability. Thus the equation

$h_n = a/P = a/[a + aa + ad + dd +$.....$+ E + (G \times E)]$ ..... (v)

The symbols h_b and h_n represent heritability broad and narrow sense respectively.

(9) further quantitative findings showed that h_n can in fact be estimated by the regression of parent on offspring performance.

(10) Invariably all the genetic findings stated above have been observed to have general applicability to all living organisms. Where exceptions were observed, these have in fact been used to further buttress the general compliance of organisms to the basic laws of Mendel. The same situation applies to quantitative characters

most of which are of economic importance in organisms.

(11) At the molecular genetics level, elegant research findings of scholars support crystal clearly the fact that the conventional gene, which hitherto was defined as an indivisible unit of heredity, is in fact divisible by way of structure, function and mutation. Conspicuous among these are the contributions of Seymor Benzer (i.e. Benzerisation of the gene). Working with the bacteria Escherichia colae in the rII region of the T_4 phage Benzer showed the region is made up of linear sequences of two separable functional sections (cistrons) of the rII gene consisting three hundred or more mutable elements that are separable by recombination (recon). The resolving power of recombination analysis in this system is such that recombination events occurring between adjacent nucleotides of the DNA molecule are detectable. This elucidated fine structure clearly buttresses the notion that point mutation results from the alteration in the base component in the nucleotide molecule.

It is in place to remark that improvement in desired characteristics, which is the ultimate objective in plant breeding has been aimed at via various means for many centuries. Initially as an art but currently more as a science with tinges of artistic inputs. To this end, very many of the beneficial traits which exhibit simple Mendelian inheritance pattern (qualitative traits) have been exhaustively investigated. Currently the exploration of the inheritance of quantitative traits (i.e. traits controlled by many genes each with small effects) is being embarked upon. Fortuitously very many of these traits are of economic importance. The traits

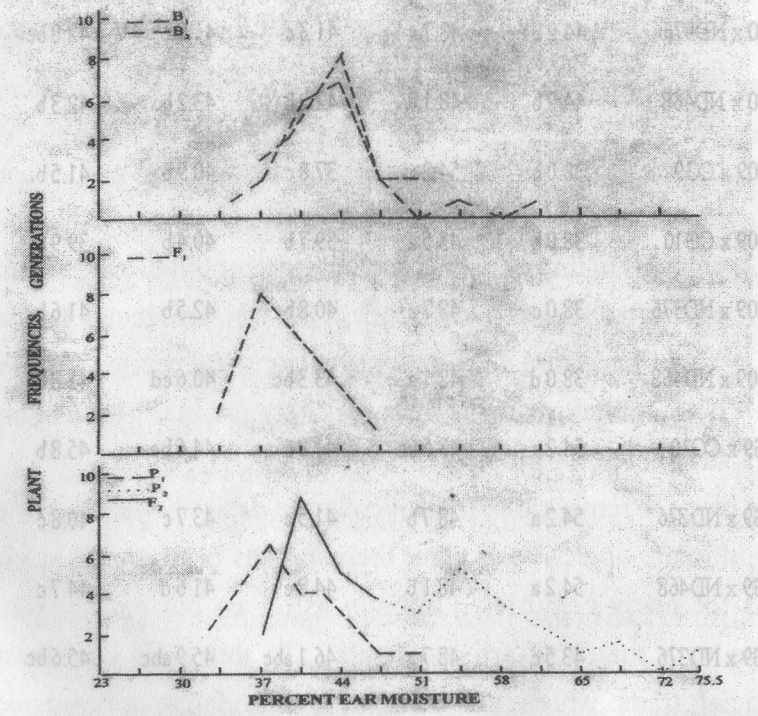
Table 2. Population means for present ear moisture at physiological maturity.

Crosses	P_1	P_2	F_1	F_2	B_1	B_2
1. A90 x A509	44.2 a*	38.0 b	38.4 b	38.8 b	41.8 a	36.7 b
2. A90 x CG9	44.2 b	54.2 a	39.9 c	41.4 bc	43.0 b	42.1 bc
3. A90 x CG10	44.2 a	43.5 a	41.9 a	44.0 a	43.8 a	44.1 a
4. A90 x ND376	44.2 b	48.7 a	41.3 c	41.0 c	42.0 bc	44.3 b
5. A90 x ND468	44.2 b	48.1 a	42.2 b	43.2 b	42.3 b	43.8 b
6. A509 x CG9	38.0 c	54.2 a	37.8 c	40.9 b	41.5 b	41.3 b
7. A509 x CG10	38.0 b	43.5 a	39.7 b	40.4 b	39.9 b	40.7 b
8. A509 x ND376	38.0 c	48.7 a	40.8 b	42.5 b	41.6 b	43.6 b
9. A509 x ND468	38.0 d	48.1 a	43.3 bc	40.6 cd	41.8 bc	44.6 b
10. CG9 x CG10	54.2 a	43.5 bc	41.8 c	44.6 bc	45.8 b	43.2 bc
11. CG9 x ND376	54.2 a	48.7 b	41.5 c	43.7 c	40.8 c	43.6 c
12. CG9 x ND468	54.2 a	48.1 b	44.8 c	41.6 d	44.7 c	46.4 bc
13. CG9 x ND376	43.5 c	48.7 a	46.1 abc	45.9 abc	45.6 bc	47.1 ab
14. Cg10 x ND468	43.5 c	48.1 a	44.6 bc	46.7 ab	44.5 bc	46.5 ab
15. ND376 x ND468	48.7 a	48.1 ab	43.3 c	45.8 bc	45.1 c	45.5 bc

*Across generations within each cross, values followed by the same letter do not differ significantly at 5% level.

The F_2 distribution for this trait showed a spread that more closely approached the lower moisture content of the parental lines (figure 4). Influence of environmental factors was found to be high.

Figure 4: Frequency distribution of % ear moisture in the P_1, P_2, F_1, F_2, B_1 and B_2 generations related to the cross (A509 x CG9)



Comparison of the magnitude of gene effects as suggested under similar situations by Anderson and Kempthorne (1954); Robinson *et al* (1955), Gamble, (1962) indicated that the dominance (d) and the dominance x dominance (dd) interactions constituted two out of the three greatest gene

effect contributors relative to the mean estimate, m (Table 3). With the relatively low estimates of additive gene effects, selection for high or low percent kernel moisture at physiological maturity will invariably encounter.

Table 3:

Table 3: Mean estimates of the six gene effects for the 15 maize crosses for percent ear moisture at physiological maturity.

Crosses	m	a	d	aa	ad	dd
1. A90 x A509	+38.8**	+5.1	-1.1	+1.6	+2.0	+0.5
2. A90 x CG9	+41.5**	+0.8	-4.9	+4.3	+5.9	+3.8
3. A90 x CG10	+44.0**	-0.3	-2.2	-0.3	-0.6	-3.8
4. A90 x ND376	+41.0**	-2.4	+3.3	+8.4	-0.1	-5.6
5. A90 x ND468	+43.2**	-1.5	-2.7	-0.8	+0.4	+5.3
6. A509 x CG9	+40.9**	+0.1	-6.2	+2.1	+8.2	+0.1
7. A509 x CG10	+40.4**	-0.9	-1.4	-0.4	+1.9	+0.1
8. A509 x ND376	+42.5**	-2.1	-2.1	+0.4	+3.3	-2.6
9. A509 x ND468	+40.6**	-2.8	+10.6	+10.3	+2.2	-10.3
10. CG9 x CG10	+44.6**	+2.5	-7.4	-0.4	-2.8	+3.8
11. CG9 x ND376	+43.7**	-2.7+	-16.0	-6.1	-5.5	+23.2
12. CG9 x ND468	+41.6**	-1.7	+9.4	+15.8	-4.8	-6.1
13. CG9 x ND376	+45.9**	-1.5+	+1.6	+1.7	+1.1	-2.7
14. CG10 x ND468	+46.7**	-2.0	-6.2	-5.0	+0.3	+3.9
15. ND376 x ND468	+45.8**	-0.3	-7.0	-2.1	-0.6	+4.6

** significance at 1% level

+ Estimate larger than the standard error but were not significant

minimal progress considering the variability exhibited by the parental lines involved in this study. Suffice it to say that by the estimates indicated, genetic control is majorly dominance and epistatic. Much of the observed genetic variability thus appears "tied up" or "chelated" and unavailable for genetic advance in the current study.

2.2. Ear drying rate: The six parental corn inbreds were also assessed for ear drying rate. The lines showed a variability of 3.8×10^{-3} grains moisture/gram of ear/hour at physiological maturity. Significant variability which can be attributed to genetic sources was observed by the generation components of partitioned genotypic mean square estimates for this trait. Magnitude of gene effects was highest for epistatic sources followed by dominance gene effects in most of the crosses. The pattern appeared similar to the situation obtained for the percent ear moisture at maturity indicated above. Thus for this quantitative trait as in the previous one, variability exists in its genetic control. This is however "tied up" and requires special breeding technique to make it available for genetic advance (Sanwo, 1971). The other traits (ear dry weight, grain dry weight and shelling percentage) studied in this experimentation series indicated high genotypic variability. The variance for each of these traits was however not partitioned to show the component contributions to this source of variability.

The investigations reported here in Zea mays L indicate the observation of high genetic variability for the traits under consideration. Minimal availability of this variability has limited its use in selection for better lines except other breeding tools are embarked upon.

3.0. GENETIC VARIABILITY IN SOY BEANS (Glycine, max L. Merrill)

Soybean cultivars are classified into maturity groups ranging from 00 to 10 based on the day length and degree day calculations. The 00 maturity group thrives best in areas with long days and a relatively short growing season corresponding to the northernmost fringes of soybean cultivation. The group 10 areas reflect zones with very short day length during the growing season. The intermediate maturity groupings fall between these two extremes.

An increase in latitude is usually accompanied by a decrease in temperature which raises questions as to the comparative vigour of cultivars particularly in the seedling stage under cold stress. Information on seedling vigor within and among soybean cultivars under favourably warm planting conditions and under cold stress is sparse. Above all definitive studies of variability within and among maturity groupings on seedling vigor was minimal. Investigations were thus carried out to study (a) variability in seedling vigour within and among cultivars of different maturity groups; (b) differential response of soybean cultivars to imbibitional chilling (a measure of cold tolerance); (c) the influence of seed source in seedling vigour and response to imbibitional chilling and (d) general and specific combining abilities as determined from a six parental diallel cross.

3.1. Seedling, vigour response after normal temperature imbibition:

Great variability existed among as well as within each maturity group for normal temperature germination situations. Maturity groups 00, 0, 1, 2, and 3 were statistically similar for inviable seed count Table 4). **Table 4:**Frequency distribution for % ear moisture in the P_1,P_2,F_1,F_2,B_1 and B_2 generations related to the cross (A509 X CG9)

TABLE 4.

ANALYSES OF VARIANCE FOR SOYBEANS AXIS LENGTH, FRESH WEIGHT, DRY WEIGHT, % MOISTURE, INVIABLE SEED AND HARD SEED FOR HIGH INITIAL SEED MOISTURE WARM IMBIBITION TEMPERATURE TREATMENT.

		MEAN SQUARES							
Source	Length d f	Axis length	Run d f	Fresh wt.	Dry wt. .	% moisture	Inviable seed	Hard seed d f	Hard seed
Genotype	80	158.51 **	80	2.51×10^{-2} **	1.012×10^{-4} **	4.315×10^{-1} **	6.00×10^{-1} **	21	3.8×10^{-1} **
Maturity groups (MG)	7	848.57 **	7	1.31×10^{-1} **	8.680×10^{-3} **	1.61×10^{0} **	1.97×10^{0} **	7	1.30×10^{-1} NS
Varieties (MG)	73	92.43 **	73	1.49×10^{-2} **	1.026×10^{-4} **	3.2×10^{-1} **	4.70×10^{-1} **	14	5.00×10^{-1} **
Var (MG 00)	9	92.50 **	9	1.43×10^{-2} **	1.463×10^{-2} **	5.2×10^{-1} **	5.00×10^{-2} NS		
Var (MG 0)	7	36.36 **	7	9.00×10^{-3} **	5.900×10^{-3} NS	3.2×10^{-1} **	1.50×10^{-1} NS		
Var (MG 1)	9	119.96 **	9	1.90×10^{-2} **	1.726×10^{-4} **	4.2×10^{-1} **	9.00×10^{-2} NS		
Var (MG 2)	9	94.33 *	9	1.80×10^{-2} **	1.342×10^{-4} **	5.8×10^{-1} **	9.00×10^{-2} NS		
Var (MG 3)	11	42.65 **	11	7.00×10^{-3} **	6.240×10^{-3} *	6.4×10^{-1} **	2.50×10^{-1} NS		
Var (MG 4)	10	96.30 **	10	1.0×10^{-2} **	8.090×10^{-3} **	4.0×10^{-2} NS	3.50×10^{-1} *		
Var (MG 5)	10	179.35 **	10	2.00×10^{-2} **	9.030×10^{-3} **	2.0×10^{-2} NS	8.40×10^{-1} **		
Var (MG 6)	8	62.48 **	8	1.70×10^{-2} **	7.500×10^{-3} *	4.0×10^{-2} NS	2.03×10^{0} **		
Error	5762	8.49	551	2.986×10^{-2}	3.18×10^{-3}	1.375×10^{-1}	1.543×10^{-1}	149	7.083×10^{-2}

* = Significance at 5% level

** = Significance at 1% level

NS = not significant

While table 5 showed the maturing group means for the traits, the cultivars ranges were 2.73cm 9.94cm (axis length), 0.076g to 0.353g for fresh hypocotyls axis length, 0.0044g to 0.0208g for dry hypocotyls weight, 91.95% to 95.00% for seedling moisture, 0.00% to 52% for inviable seeds and 0.00% to 19% for cultivar hard seed content. Magnitude of variance was higher among maturity groups than within the cultivars of each maturity group for axis length and dry weight (table 4). This suggests that classification into maturity grouping has simultaneously effected selection for normal germination as indexed by these traits. Axis fresh weight, inviable seed and hard seed distribution however indicated variance magnitudes that suggested that classification into maturity groupings had minimal impact on the high variability that existed within cultivars irrespective of their maturity groupings. Data pointed to the fact that for axis length, fresh weight and dry weight cultivars differences (Table 4).

Table 5:

TABLE 5: DUNCAN'S MULTIPLE RANGE TEST OF TRAITS OF SEEDLINGS IMBIBED AND GERMINATED AT 25^{0}C

			MG means			
Maturity groups	Axis length	Axis fresh weight	Axis dry weight	% moisture	Inviable seed	Hard seed
oo	8.14 a[2]	2.666 x 10 -1 a	1.646 x 10 -2 a	93.71	1.00 f	0.00 b
0	7.36 b	2.409 x 10 -1 b	1.531 x 10 -2 ab	93.81	3.13 def	0.75 ab
1	7.24 b	2.383 x 10 -1 b	1.531 x 10 -2 ab	93.79	3.00 ef	0.70 ab
2	6.16 c	2.162 x 10 -1 c	1.391 x 10 -2 bc	93.63	4.70 cde	1.30 ab
3	6.19 c	2.042 x 10 -1 c	1.331 x 10 -2 bc	93.54	6.33 bcd	1.17 ab
4	5.63 d	1.825 x 10 -1 d	1.448 x 10 -2 abc	93.73	6.36 bc	3.45 a
5	5.19 e	1.706 x 10 -1 d	1.12 x 10 -2 bc	93.46	10.73 b	1.36 ab
6	5.04 e	1.473 x 10 -1 e	9.419 x 10 -3 c	93.62	15.00 a	0.22 b

1. Duncan's test based on transformed means.
2. Means with same letters in a column are not significantly different.

.Within maturity groups 00 to 3 remained relatively negligible and then increased thereafter as maturity group increased (Table 5). These three traits however showed that axis length, fresh weight, and dry weight increased as maturity grouping decreased. Implied in this inverse relationship is the observation of poorer quality seeds coming from later maturity groups. Basnet et al. (1974) made similar observations on yield traits in soybeans.

The significant phenotypic variability observed among and within maturity groups has some genetic basis. This variation can be explained in terms of natural and conscious artificial selection both of which have systematically altered the frequency of relevant genes towards better seedling vigour performance as cultivars became adapted to early maturity (cooler) zones.

3.2. Seedling vigour response after imbibitional chilling injury:

3.2.1.Absolute values: Axis length, fresh weight of axis and inviable seeds showed high variability between and within maturity groups. The magnitude of variability within maturity groups did not show ascending or descending pattern with increase or decrease in maturity group for any trait (Table 6).

TABLE 6:
ANALYSIS OF VARIANCE FOR SOY BEAN AXIS LENGTH, FRESH WEIGHT, DRY WEIGHT,% MOISTURE, INVIABLE SEED AND HARD SEED FOR LOW INITIAL SEED MOISTURECOLD IMBIBITIONAL TEMPERATURE TREATMENT.

Source	Length df	Axis length	Run df	Fresh wt.	Dry wt.	% moisture	Inviable seed	seed df	Hard seed
Genotype	80	45.79**	80	8.00 × 10–3**	1.49 × 10–5**	4.5 × 10–1	3.36**	44	8.96 × 10–1**
Maturity groups (MG)	7	166.25**	7	3.60 × 10–2**	1.91 × 10–5**	2.6 × 10–1	17.49**	7	1.01 × 10–1**
Varieties (MG)	73	34.24**	73	5.00 × 10–3**	1.45 × 10–5**	4.4 × 10–1	4.4 × 10–1**	37	8.74 × 10–1**
Var (MG 00)	9	60.09**	9	6.00 × 10–2**	1.46 × 10–5**	4.3 × 10–1	4.3 × 10–1**		
Var (MG 0)	7	77.01**	7	9.00 × 10–2**	1.39 × 10–5**	2.5 × 10–1	2.5 × 10–1**		
Var (MG 1)	9	48.00**	9	7.00 × 10–3**	2.51 × 10–5**	3.7 × 10–1	3.7 × 10–1**		
Var (MG 2)	9	15.47**	9	4.00 × 10–3**	1.98 × 10–5**	4.9 × 10–1	4.9 × 10–1**		
Var (MG 3)	11	39.50**	11	5.00 × 10–3**	7.4 × 10–6NS	4.2 × 10–1	4.2 × 10–1**		
Var (MG 4)	10	3.99NS	10	1.00 × 10–3**	3.5 × 10–6NS	5.0 × 10–1	5.0 × 10–1**		
Var (MG 5)	10	28.85**	10	5.00 × 10–3**	2.29 × 10–5**	4.3 × 10–1	4.3 × 10–1**		
Var (MG 6)	8	10.69**	8	3.00 × 10–3**	9.6× 10–6NS	5.8 × 10–1	5.8 × 10–1**		
Error	3937	3.78	551	7.164 × 10–4	6.84 × 10–6	1.78 × 10–1	1.78 × 10–1	310	1.46 × 10–1

* = Significance at 5% level

* = Significance at 1% level

NS = Significance

While table 7 gives the maturity group means (MG) for these traits MG ranges are from 1.68cm to 3.35cm for axis length, 4.53×10^{-2} to 9.64×10^{-2}g for fresh weight, 3.85×10^{-3} to 6.33×10^{-3}g for dry weight, 90.21% to 93.36% for axis moisture content, 10.00% to 55.45% for inviable seed and 0.40% to 9.27% for hard seed. Observation ranges were 0.522 0.77cm, 1.30×10^{-2} 1.77×10^{-1}g, 2.31×10^{-3} 1.14×10^{-2} 85.99% - 95.55%, 1.00% to 96% and 0.00% to 32.00% for the respective traits as stated for the maturity

groups above. Traits showed the same trend as was observed for seedling vigour traits under normal temperature imbibition.

TABLE 7.

DUNCAN'S[1] MULTIPLE RANGE TEST OF 6 TRAITS OF LOW MOISTURE SEEDS IMBIBED AT 5°C AND GERMINATED AT 25°C

	MG means					
Maturity groups	Axis length	Fresh weight	Dry weight	% moisture	% Inviable seed	% Hard seed
oo	2.59 c[2]	7.0×10^{-2} b	5.85×10^{-3} ab	91.35	10.00 e	0.40 c
0	3.07 b	8.9×10^{-2} a	$5,62 \times 10^{-3}$ bc	93.36	16.75 d	1.50 c
1	3.35 a	9.64×10^{-2} a	6.33×10^{-3} a	93.26	12.60 e	3.40 bc
2	2.14 d	6.28×10^{-2} c	5.43×10^{-3} bc	91.27	33.00 c	6.90 ab
3	2.32 d	6.40×10^{-2} c	5.11×10^{-3} bc	91.85	30.50 c	8.50 a
4	1.68 f	4.55×10^{-2} d	4.25×10^{-3} c	90.38	55.45 a	9.27 a
5	1.78 ef	4.80×10^{-2} d	4.21×10^{-3} c	90.32	49.82 b	5.09 ab
6	1.85 de	4.53×10^{-2} d	3.85×10^{-3} c	90.21	53.22 a	2.00 c

1 Duncan's test based on transformed means.

2 Means with same letters in a column are not significantly different.

This similarity in warm and cold imbibitional response was supported by reports from Sayed and John (1973) in tomato while Segeta *et al* (1966) reported a contrary trend in cucumbers. In terms of magnitude of variability, cold imbibition germination gave more reduced ranges for all the traits than normal imbition except for hard seed where it was reversed (Table 6). This same pattern also was found in the mean values of the traits (Tables 5 & 7).

It would appear, from the observed results, that high initial seed moisture high temperature imbibition and low initial seed moisture-low temperature imbibition follow parallel trends across maturity groups in their effects on seedling vigour. There were high amounts of variability among maturity groups as well as between cultivars within each maturity group, although the mean response for desirable aspects of seedling vigour decreased as maturity group increased. A relative advantage for seedling vigour is in place for the tropical soybean breeder who imports germplasm from areas of early maturity group over the temperate zone breeder in a reverse importation situation. This advantage is not much since variability within each maturity group is reasonably large.

3.2.2. **Relative Values**: Cold tolerance as assessed by this criterion showed high variation between and within maturity groups for axis length, fresh and dry axis weights, inviable seed and hard seed. Magnitude of variation within maturity groups did not show any trend except for hard seed where groups 2 & 3 gave the highest variations (table 8).

TABLE 8. ANALYSES OF VARIANCE FOR SOYBEANS AXIS LENGTH, FRESHWEIGHT,DRY WEIGHT, % MOISTURE, INVIABLE SEED AND HARD SEED FOR IMBIBITIONAL CHILLING INJURY TREATMENT BASED ON RELATIVE VALUES.

Source	Length d f	Axis length	Run d f	Fresh wt.	Dry wt.	% moisture	Inviable seed	Hard seed d f	Hard seed
Genotype	80	1.00×10^{-1} **	80	1.00×10^{-1} **	6.0×10^{-2} **	1.5×10^{-1}	36.52 **	21	2.60 **
Maturity groups (MG)	7	2.10×10^{-1} **	7	1.90×10^{-1} **	1.2×10^{-1} **	1.4×10^{-1}	149.57 **	7	4.65 **
Varieties (MG)	73	9.00×10^{-2} **	73	9.00×10^{-2} **	6.0×10^{-2} **	1.5×10^{-1}	25.68 **	14	2.40 **
Var (MG 00)	9	8.00×10^{-2} **	9	6.00×10^{-2} **	3.0×10^{-2} NS	1.6×10^{-1}	3.09 NS		0.09 NS
Var (MG 0)	7	1.30×10^{-1} **	7	1.00×10^{-1} **	3.0×10^{-2} NS	1.0×10^{-1}	11.10 **		0.32 NS
Var (MG 1)	9	1.00×10^{-1} **	9	8.00×10^{-2} **	5.0×10^{-2} NS	1.4×10^{-1}	7.62 *		2.66 **
Var (MG 2)	9	5.90×10^{-2} NS	9	7.00×10^{-2} **	9.0×10^{-2} **	1.8×10^{-1}	35.38 **		4.29 **
Var (MG 3)	11	6.20×10^{-2} NS	11	5.00×10^{-2} **	4.0×10^{-2} NS	1.7×10^{-1}	25.25 **		5.19 **
Var (MG 4)	10	9.00×10^{-2} **	10	1.2×10^{-1} **	9.0×10^{-2} **	1.6×10^{-1}	47.83 **		2.50 **
Var (MG 5)	10	1.1×10^{-1} **	10	1.3×10^{-1} **	8.0×10^{-2} **	1.3×10^{-1}	56.61 **		2.25 **
Var (MG 6)	8	1.3×10^{-1} **	8	1.2×10^{-1} **	6.0×10^{-2} **	1.8×10^{-1}	8.50 *		0.66 NS
Error	551	3.27×10^{-2}	551	3.0436×10^{-2}	3.55×10^{-2}	5.98×10^{-2}	4.0036	149	0.8111

* = Significance at 5% level

** = Significance at 1% level

NS = not significant

The means of the relative values for the traits presented in table 9 for MG comparison lead to the inference that the observed variability between and within the groups did not show a pattern suggestive of natural or unconscious artificial selection for any of the traits with increasing or decreasing maturity groups.

TABLE 9: DUNCAN'S MULTIPLE RANGE TEST OF RELATIVE VALUES FOR TRAITS OF IMBIBITIONALLY CHILLED SOYBEAN SEEDINGS.

Maturity groups	Axis length	Fresh weight	Dry weight	% moisture	C-E inviable seed	C-E hard seed
00	0.323 cd [2]	0.268 c	0.359 c	0.975	0.922 d	0.052 e
0	0.421 ab	0.368 ab	0.364 c	0.995	1.344 d	0.078 ed
1	0.467 a	0.405 a	0.419 a	0.994	0.813 d	0.275 cde
2	0.352 cd	0.299 c	0.403 a	0.975	2.541 c	0.568 abc
3	0.373 bc	0.311 bc	0.389 ab	0.982	2.348 c	0.685 a
4	0.311 d	0.268 c	0.384 ab	0.945	4.413 a	0.501 ab
5	0.342 cd	0.283 c	0.394 a	0.966	3.580 b	0.375 bcd
6	0.365 bcd	0.309 bc	0.429 a	0.963	3.708 b	0.181 de

1. Duncan's test based on transformed means.
2. Means with same letter in a column not significantly different.

C = Mean seed count from warm imbibition treatment.
E = Mean seed count from warm imbibition treatment.

Investigation into location effect showed that the environment of seed production per se could influence the performances of the seeds during germination with regards to axis length, fresh and dried axis weights and moisture content of the seedlings but not the proportion of inviable and/or
hard seed lots. Results also showed that genotypes responded differently when seeds were produced under different environments. Basnet *et al.* (1974) and Fehr and Probst (1971) substantiated these findings. Wilcox *et al* (1974) and Mack and Ivarson (1972) showed that location effect on seedlings vigor is exerted during grain filling and seed maturation.

3.3. INHERITANCE STUDIES ON SEEDLING VIGOUR

3.3.1. Under high initial moisture warm temperature imbibition: High genotypic variation was observed for all traits except percent moisture. General combining ability (gca) which measures the additive genetic effects and specific combining ability (sca) a measure of non-additive genetic effects were observed to be very high for axis length and dry weight.

TABLE 10. ANALYSIS OF VARIANCE AND ESTIMATES OF COMPONENT GCA, SCA, AND RECIPROCAL FOR TRAITS OF SEEDS IMBIBED AT 25°C

Source	df	length	Run df	Fresh weight	Dry weight	% moisture	Inviable seeds
Genotype	35	157.5443**	35	2.3773×10^{-2}**	9.840×10^{-5}**	1.0442×10^{-3} NS	0.3988**
Error	1919	9.2398	178	4.9356×10^{-3}	1.757×10^{-5}	7.6246×10^{-4}	0.1786
gca	5	2.3307**	5	1.6×10^{-3} NS	2.255×10^{-5}**	1.441×10^{-4} NS	1.37×10^{-2} NS
sca	15	1.9870**	15	4.4×10^{-3}**	1.592×10^{-5}**	4.493×10^{-5} NS	2.12×10^{-2} NS
recipro.	15	2.5897**	15	2.6×10^{-3}**	1.304×10^{-5}**	8.07×10^{-5} NS	6.73×10^{-2}**
Me [1]	1919	0.1684	178	8.2156×10^{-4}	2.924×10^{-6}	1.269×10^{-4}	2.97×10^{-2}

* = Significance at 5% level
* = Significance at 1% level
NS = Significant

Gca was low for fresh weight and inviable seeds. Gca and Sca were not important for percent moisture (Table 10). Ratios of the gca:sca were found to be 1.5:1 in all traits where the former was greater. This pattern and higher proportions of sca control are characteristic of genetic systems in which more complex breeding methods than mere mass selection are needed to make progress. This pattern also indicates previous selection on the parental experimental materials either consciously or unknowingly for the traits under consideration (Griffing 1956; Sprague and Tatum, 1942). Low heritability values are thus estimated. Heterosis was high for all traits except percent moisture.

3.3.1. **Inheritance under Imbibitional Chilling**:

3.3.1.1. Absolute values: Genotypic values were important for gca, sca and reciprocal components of genotypic variance for all traits except for percent moisture and inviable seeds (Table 11).

Table 11: ANALYSIS OF VARIANCE AND ESTIMATES OF COMPONENTS OF GCA, SCA AND RECIPROCALS FOR TRAITS OF SEEDS IMBIBED AT 5°C

Source	Indiv. Df	Length C	Run df	MEAN Fresh wt. C	SQUARES Dry wt. C	% Moisture	Inviable seeds
Genotype	35	39.5483 **	35	1.3928×10^{-2} **	3.424×10^{-5} **	1.9713×10^{-2} **	1.633**
Error	954	6.1729	178	3.2156×10^{-3}	8.16×10^{-6}	1.0433×10^{-2}	0.420
gca	5	2.3025 **	5	4.297×10^{-3} **	1.501×10^{-5} **	8.201×10^{-4} NS	2.91×10^{-2} NS
sca	15	2.4916 **	15	2.142×10^{-3} **	5.489×10^{-6} **	1.433×10^{-3} NS	3.73×10^{-2} NS
recipro.	15	1.1255 **	15	2.595×10^{-3} **	4.333×10^{-6} **	2.105×10^{-4} NS	7.53×10^{-2} NS
Me[1]	1919	0.2231	178	5.353×10^{-4}	1.358×10^{-6}	1.737×10^{-3}	6.991×10^{-2}

* = Significance at 5% level
** = Significance at 1% level
NS = not significant

Based on the ratio of gca to sca, a breeding scheme using mass selection could offer some progress for fresh weight and dry weight traits while recurrent selection would produce good results for these two as well as axis length (Griffing, 1956). The cultivar, Traverse, was identified as being superior in tolerance to imbibitional chilling and in its ability to transmit this complex trait to its progenies. This was closely followed by Hawkeye while the rest were low. Sca estimates for all crosses were high and predominantly negative thus indicating a net depressing effect of dominance and epistatic gene action in cross combinations. The effect of heterosis was overwhelming in all traits except for percent moisture.

3.3.2.2. Relative values: Assessment on this basis indicated high genotypic variance. The gca component of genotypic variance was important for all traits except relative moisture content. Sca component was only high for relative axis length and relative inviable seed content (Table 12).

TABLE 12: ANALYSIS OF VARIANCE AND ESTIMATES OF COMPONENT GCA, SCA AND RECIPROCAL COMPONENTS OF GENOTIPIC VARIANCE FOR TRAITS OF RELATIVE VALUES.

Source	Df	Ratio (length)	Mean	SQUARES Relative Fr. Wt.	Relative Dry wt.	Relative % H_2O	Relative Inviable seeds
Genotype	35	1.8988×10^{-1} **		2.0087×10^{-1} **	1.0886×10^{-1} **	1.5752×10^{-3} **	22.6899**
Error	178	5.3507×10^{-2}		5.9719×10^{-2}	3.4872×10^{-3}	8.3518×10^{-4}	6.0170
gca	5	6.2×10^{-2} **		6.13×10^{-2} **	5.15×10^{-2} **	3.67×10^{-5} NS	5.4611 **
sca	15	1.72×10^{-2} *		1.55×10^{-2} NS	7.30×10^{-3} NS	6.273×10^{-5} NS	25.065 **
recipro.	15	1.31×10^{-2} NS		1.03×10^{-2} NS	1.34×10^{-2} *	1.083×10^{-5} NS	3.120 **
Me[1]	178	8.91×10^{-3}		9.941×10^{-3}	5.805×10^{-3}	1.390×10^{-4}	1.0016

* = Significance at 5% level
** = Significance at 1% level
NS = not significant

While some breeding progress was shown as achievable via mass selection method for most of the traits, high sca value for inviable seeds suggests that recurrent selection would have to be employed for selection against inviable seeds to make breeding progress. This pattern however is much confounded with the observed high heterotic effects in all traits except moisture content. Experimentation showed that the gca reserves have not been depleted by selection and could still be exploited.

4.0. GENETIC VARIABILITY IN CASHEW

During cashew improvement investigations at the Cocoa Research Institute, fifteen fruit, apple and nut traits were each studied from 25 trees over a four week period (Sanwo, 1980b). Results showed that tremendous variability existed between and within trees for the 15 traits studied. The variability was evenly distributed within each harvest although the fourth week's harvest tended to be more variable. Tree means for each trait varied highly. For example fruit weight had tree means ranging from 28.29 ± 1.24 to 119.56 ± 3.47 grams; fruit length: 5.31 ± 0.05 to 11.82 ± 0.14cm, apple fresh weight: 25.02 ± 1.20 to 112.78 ± 3.41 grams; apple dry weight 1.13 ± 0.09 to 4.46 ± 0.14 grams; nut weight: 3.19 ± 0.06 to 8.31 ± 1.54 grams; nut length: 2.32 ± 0.02 to 3.43 ± 0.02cm; kernel weight: 0.63 ± 0.03 to 1.73 ± 0.03 grams and kernel length 1.36 ± 0.29 to 2.36 ± 0.04cm.

The high between tree variations when compared with within tree variations indicate genetic basis for inheritance of these traits. The variability observed within trees and the high tree x harvest week interaction effects for character trait suggest multiple factor inheritance pattern for the studied traits. While fruit and kernel correlations were generally high, fruit width was noted as giving the best selection criterion and it additionally afforded ease of field use for good kernel identification of trees with good quality kernels. The study further showed that if nuts from various trees have been bulked before selection was initiated (i.e. post harvest), then nut length gave the best indicator for trees with desirable economic and fruit quality traits. Thus fruit width (for pre-harvest) and nut length (for post harvest conditions) are useful indicators of trees with desirable and harvestable cashew fruit traits, each under a different circumstance. Due to the fact that fruit and nut traits are from the

maternal generation and the economic kernel traits are in the filial generation, this form of selection cannot predict/indicate more than 50% genetic representation (i.e. maternal tree selection).

Tree selection in a 142 hectare cashew plantation over a three-year period indicated that repeatability estimates for total nut count, total nut weight and average nut weight were significant but low in magnitude (Sanwo, 1980a). These are suggestive of low heritability narrow sense estimates for the same traits even if there was adequate genotypic variation in the control of the traits under study. This inference notwithstanding, mass selection was suggested as being capable of having an impact on improvement in our locally available germplasm which has very diverse sources of origin (Togun, 1977) and can still be ranked as a "land variety".

A survey by Sanwo (1978b) on cashew plantations in Nigeria indicated the presence of sufficient diverse variability in tree yields among local plantations to justify the selections of high yielding trees as a means of improving cashew yield per hectare by planting improved materials. The existence of cashew materials in various parts of the country, whose importation histories indicate diverse sources of origin, lends support to the existence of locally available high variability for this crop. Survey observations buttressed the existence of fruit and agronomic trait divergence in the cashew crop within Nigeria. Much of the variability is enhanced by the predominantly outcrossing nature of the crop.

5.0. GENETIC VARIABILITY IN COLA

The experiences acquired researching in Cola (*Cola nitida* (Vent.) Schott. End). indicate that large amounts of benefits are derivable from the acquisition of a large genetic variability in the crop. *C. nitida* (Vent. Schott. Endl.), indigenous to West Africa and South Western Nigeria in particular, has adequate untapped wide genetic base for improvement via breeding.

An attempt was made at exploring the "virgin" *C. nitida* grove in the Shagamu area (Sanwo, 1998; Sanwo and Odulaja, 1986). The area was partitioned into A, B. C. and D zones of which the zone C was studied. Yield traits were initially studied for five years. Selections were then observed for another three years. This investigation showed that of the three yield traits studied, number of nuts produced per tree per annum

exhibited the highest variability. This was followed by nut weight. Number of nuts per pod was minimally variable (Table 13).

TABLE: 13 CUMMULATIVE ANNUAL PERFORMANCES OVER 8 YEARS.

	MEAN POD	MEAN NUT	AVERAGE NUT	NUTS/POD
TREE NO.	PRODUCTION	PRODUCTION	WEIGHT (g)	
Li 164	536	3877	30	7
Li 147	151	1339	19	9
Or 70	136	1228	13	9
Sh 7	128	959	13	8
Li 145	100	884	25	9
Li 154	87	848	24	10
Or 65	106	793	5	8
Or 61	101	791	12	9
Or 81	87	769	13	9
Sh 38	75	656		9
Or 63	76	652	10	9
Or 97	53	650	9	10
Or 72	64	628	8	10
Mean	132	1083	15	9
Cv%	94.67	80.14	51.08	10.57

The study also revealed that the inherent potentiality for consistent annual nut production per tree and stability in nut number in production, even among averagely high nut yielding trees, were under independent genetic control and had high variability among individual trees. While some selected trees combined high nut production with either of the other two traits, only one tree, Li 164, combined the three traits naturally (Figure 5).

Figure 5:

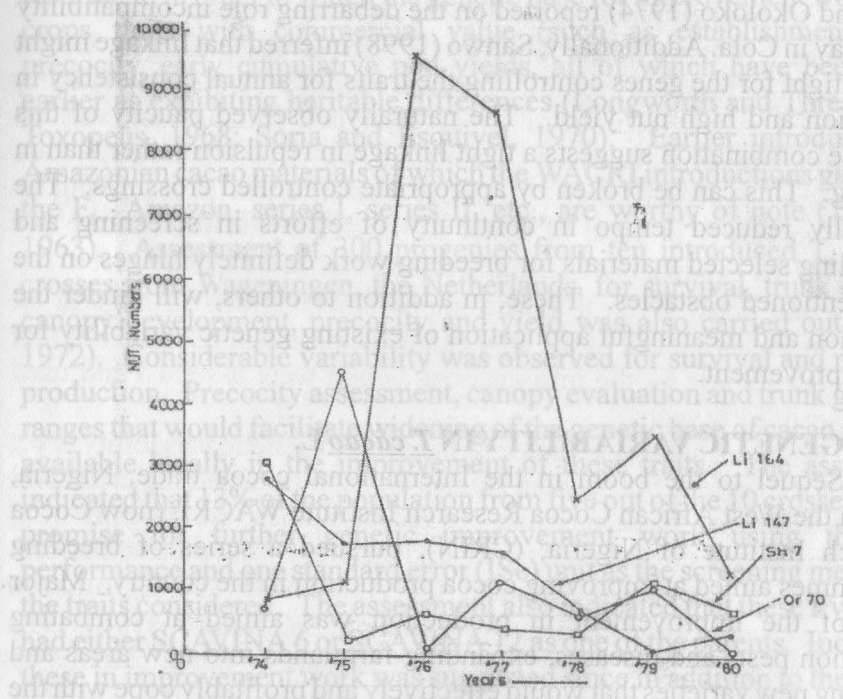


Fig.5: Annual yield pattern of 4 C. nitida trees

This finding lends support to the possibility of combining all these traits in one tree via breeding. The production pattern of the trees studied clearly support the possibility of improvement via selection in the Cola grove of desirable trees and the subsequent combination of the traits in a single tree. It is sad to note that the pursuit of exploration of high yielding and desirable materials in the Shagamu grove has been abandoned despite its obvious promise for success. High staff turnover, inadequate research financing and the long gestation nature of tree crops are reasons for the abandonment. Suffice it then to infer that abundant and minimally explored genetic variability exists within the country for improvement work in C. nitida production. For very many years, there has been little or no improvement in Kola yield (Russel, 1955; Eijnatten and Quarcoo,

1968; Quarcoo, 1972; Afolami and Egbe, 1984). What then could possibly be the hindrance in Kola yield improvement? Jacob (1973), Jacob and Okoloko (1974) reported on the debarring role incompatibility could play in Cola. Additionally, Sanwo (1998) inferred that linkage might be very tight for the genes controlling the traits for annual consistency in production and high nut yield. The naturally observed paucity of this desirable combination suggests a tight linkage in repulsion rather than in coupling. This can be broken by appropriate controlled crossings. The drastically reduced tempo in continuity of efforts in screening and assembling selected materials for breeding work definitely hinges on the aforementioned obstacles. These, in addition to others, will hinder the realisation and meaningful application of existing genetic variability for Cola improvement.

6.0 GENETIC VARIABILITY IN *T. cacao* L.

Sequel to the boom in the International cocoa trade, Nigeria, through the West African Cocoa Research Institute WACRI, (now Cocoa Research Institute of Nigeria, (CRIN), pursued a series of breeding programmes aimed at improving cocoa production in the country. Major thrust of the improvement in production was aimed at combating production pests and diseases, expanding farmlands into new areas and providing new varieties that would effectively and profitably cope with the production challenges ahead .Later, a very important complex quantitative character, establishment ability, was identified (Toxopeus 1963). The hitherto very promising Amelonado variety from which the selection, N38, was very productive and popular, could not cope with the needs in newly opened marginally suitable T. cacao lands. Also the rapid invasion of cocoa farm lands by the deadly cocoa swollen shoot virus (CSSV), for which there was no cure, led to the shifting of the country's cocoa production base from around Ibadan to the forest farmlands in Ondo Province (now Ondo State). The Ibadan CSSV infested area "was named area of mass infection" (AMI). Need to evolve varieties, with suitable establishment ability in the Ondo area, and other edaphically optimum but less climatologically suitable lands in the humid forest zones of southern Nigeria, was focused upon. The narrow genetic base of Amelonado

variety appeared inadequate for genetic improvement solely based on locally available germplasm. Importation of germplasm by CRIN was resorted to in order to widen the genetic base for improvement work on the crops traits with commercial value (such as establishment ability, precocity, early cumulative pod yields, all of which have been shown earlier as exhibiting heritable differences (Longworth and Thresh, 1963; Toxopeus, 1968; Soria and Esquivel, 1970). Earlier introductions of Amazonian cacao materials of which the WACRI introductions gave rise to the F_3 Amazon, series I, series II, etc., are worthy of note (Toxopeus, 1963). Assessment of 300 progenies from ten introduced T. cacao L. crosses from Wageningen, the Netherlands, for survival, trunk diameter, canopy development, precocity and yield was also carried out (Sanwo, 1972). Considerable variability was observed for survival and mean pod production. Precocity assessment, canopy evaluation and trunk girth gave ranges that would facilitate widening of the genetic base of cacao materials available locally in the improvement of these traits. The assessments indicated that 13% of the population from five out of the 10 crosses showed promise for further genetic improvement work using the mean performance and one standard error (ISe) unit as the screening measure for the traits considered. The assessment also indicated that these five crosses had either SCAVINA 6 or SCAVINA 12 as one of the parents. Inclusion of these in improvement work was suggested since in addition to the promise they showed in the current assessment locally, Soria and Esquivel (1967) had reported the strains had promise in transmitting a high level of resistance of *Phytophthora palmivora* to their progenies. The strains have also been reported as being high pod yielders (Bartley, 1967). The selections were incorporated into subsequent breeding work (Sanwo, 1988).

Under the research banner of WACRI, mass importation of Cacao germplasm materials had earlier been effected to provide rehabilitation materials. Old Amelomado plantations were to be rehabilitated with promising vigorous seedlings from the Amazon (Toxopeus, 1963). Assessment of the performances of the second generation seedlings of these introductions of crosses culminated in the release of the F_3 Amazon variety (Toxopeus, 1964). Sanwo and Ojo (1980) later assessed the yield

components in the F_3 Amazon variety of cocoa. In the initial assessment, the ten pod components were observed to have high variability and hence indicative of greater potential of the F_3 Amazon variety in breeding programmes. Putting these findings to use in the Nigerian Cocoa improvement, effort was promptly pursued within a very short breeding span crosses and selections of T. cacao types suitable for various ecological niches were released (Atanda, 1973). The releases included WACRI series I, WACRI series II, CRIN establishment Elites giving an average superiority in yield of about 224kg dry cocoa per hectare per annum over the F_3 Amazon (Ojo, Sanwo and Esan, 1980). Suffice it to say that the great boost given to cocoa improvement efforts in Nigeria all became fruitful as a result of the very extensive broadening of the original narrow genetic base by the introductions which were assessed and used over a span of forty years.

The extent of the magnitude of the infused genetic variability is yet to be fully exploited. Subsequent studies on the introduced materials still continue to suggest more promise. In recent studies, the progeny of *T. cacao* introductions were found to respond differently but more superiorly to various soil coppers levels than the Amelonado and F_3 Amazon population (Sanwo and Obatolu, 1996; Obatolu and Sanwo, 1996). The variability in seedling response was along previously noted patterns by researchers on these introductions (Atanda, Sanwo and Jacob, 1975); namely that the materials whose origins were traceable to the Nanay and Parinari tributaries of the Amazon river exhibited such vigor that favoured their commercial establishment in Nigeria and West Africa in general. Trials in which such assessment were made have clearly indicated the versatility in variability, a high proportion of which is genetic and hence transmissible.

The importation of cocoa germplasm into Nigeria perhaps was at peak with the 1967 Trinidad introductions. These involved progeny of selected crosses of *T. cacao* strains from the "witches broom" (*Marasmus perniciosus*) resistance farm ("Marper farm") in Trinidad. Marper farm was planted with a collection of selections from the cacao expeditions into the Amazon basin led by Pound in search of Witches Broom resistant materials (Pound, 1938). As at today, this germplasm importation is by far

the largest cacao introductions ever carried out by CRIN. The materials were planted at four locations at the Gambari Experimental Station (GES) i.e. the headquarters location of CRIN in the plots Onipe 1/1, Onipe 2/1, Onipe 2/2 and Onipe 2/3. In addition, some of the materials (not necessarily duplications) were planted at Ikom substation, Uhonmora substation, and at Ibule and Alade plots of the CRIN Owena substation. The materials were progenies of crosses which comprised predominantly of intra-Nanay and intra-Parinari hybrids totally numbering close to 20,000 seedlings at planting in 1967 and 1968 (Sanwo, 1978).

For various reasons only the introductions at the Uhonmora CRIN substation had been preliminarily assessed (Atanda, Sanwo and Jacob, 1975). A substantial proportion of these introductions have been totally lost due to one operational hindrance or the other (Sanwo, 1978).

An attempt was made to assess the relative flowering potential and spread of the intra-Nanay and intra-Parinari crosses at one of the CRIN headquarters plots. The one year data collected showed no regular pattern (Sanwo, Kuti and Osundolire, 1973). This investigation was not further pursued due to rapid staff turnover.

Immediate replenishment of lost crosses in re-importation was deferred due to quarantine regulations and the lack of adequate phytosanitary facilities to handle importations of the magnitude of the 1967 consignment. More recently, importation (at least one set) have again resumed at CRIN in collaboration with the Black Pod resistance research team (Badaru, 2003).

Compared with what the situation was in the mid-twentieth century, the Nigerian cocoa industry now, has substantially expanded genetic base for improvement and a rich genetic pool from which to evaluate, recombine, assess and select promising strains once the machinery is in place and it is allowed to function.

Based on the earlier research findings of Toxopeus (1963) and Atanda (1972) that the determination of establishment ability of novel cacao materials gave reliable indications of the yielding potentialities of the materials, the 14 crosses highlighted as having desirable combinations of growth and yield factors (Atanda, Sanwo and Jacob, 1975) were combined into controlled meaningfully double crosses and assessed. Four

different ecological zones were used. Some selections of a 3-way cross earlier made (Sanwo, 1972), a proven pollen source, Pa 35, and a black pod tolerant strain were included in the trial. F_3 Amazon was included as a control variety. The double crosses, except for one, all showed superiority to F_3 Amazon. Within the superior ones, variability for establishment ability was clustered reflecting narrow genetic base in constituting the double crosses. Due to this, bulking of selected double crosses was recommended as planting material (Sanwo, 1988).

7.0 GENETIC VARIABILITY IN *Solanum gilo* R.

With a change in job to Ogun State University (OSU) (now Olabisi Onabanjo University (OOU)), Ago-Iwoye, the dictates and financial support on CRIN mandate crops dwindled and their research could no longer be actively and physically pursued as in the past. *Solanum gilo* Radii ("Igba"), which is one of the research neglected crops in the diet of West Africans, was focused upon, research wise. *S. gilo* R. germplasm collections from the Northern and Southern parts of Nigeria numbering up to seven distinct types were planted at the Ikenne substation of the Institute of Agricultural Research and Training (IAR & T) for agronomic assessments in the wet humid tropics. Strain identification was based on immature fruit trait characteristics. Collaborative research with a nematologist and a phytopathologist from the state led to the finding that the assessed strains had varied susceptibility to *Meliodogyne incognita* attack. One strain, which tasted particularly bitter, was very tolerant of nematode attack (Afolami, Sanwo and Adebayo, 1988). The initial relocation of the College of Agricultural Sciences to Aiyetoro and vice versa, coupled with inadequate technical support staff and inadequate financing resulted in improper storage and loss of viability of seeds. Subsequent revitalization of research efforts on this crop has revealed that strains normally cultivated in the "fadama" areas of the derived savannah and savannah zones (Zaria) of Nigeria exhibited luxuriant growth and a fruiting season spread of 5 6 months in the humid tropical forest locality of Ago-Iwoye, Ogun State. These introductions into the South humid tropics gave the best yield performance at 10,000 plants/ha when compared with 15000 and 20000 plants/ha population densities on

application of NPK fertilizer. For the best planting densities, extrapolated fruit yield of over 111.4 tons/ha were estimated from the experimental plots (Sanwo, 1996). Further findings supporting the feasibility of commercial production of these derived savannah introductions in the south humid tropics were additionally reported (Oloruntoba and Sanwo 2000; Oloruntoba and Sanwo, 2002). S. gilo R. can also be suitably intercropped with early maize where the maize crop will be harvested at the milk dough (fresh) stage.

In one of the germplasm plots at Ikenne, the year 1999 witnessed an overwhelming increase in the number of strains based on fruit characteristics (Sanwo, 1999 unpublished). This provides substantiation for the natural occurrence of intra and interstrain hybridizations in the previous year and subsequent manifestation of segregation and thus highly enriched genetic variability in the field in 1999. It is in place to affirm that relatively easy gene exchange occurs between these various cultivars of S. gilo irrespective of initial location of origin i.e. sympatry is yet to be attained between the various cultivars/strains. Omidiji (1981) substantiates this inference.

8.0 GENERAL OBSERVATIONS

The picture presented and encountered in each of the four crops upon which considerable years of research have been spent is that genetic variability now locally exists naturally or has been amassed in pursuit of whatever improvement targets were initially set. Genetic improvement in crops however is much dependent on the successful manipulation (i.e. identifying, fixing, recombining, selecting and assessing promising strains/genomic parts available) of the variability to obtain desirable lines. From the onset of Mendelism, improvement efforts to obtain desirably optimum types from both parents have been based on equal gamete contribution subject to the phenomena of dominance, recessiveness, espistatic interactions, multiple allelic situation and environmental effects. Qualitative traits express these clearly. It has also been demonstrated that quantitative characters (i.e. traits controlled by multiple loci but each with small effect) also obey these rules. A high proportion of breeding/improvement efforts which involve recombination still adopts

this methodology with necessary modifications if and where necessary.

8.1 Obvious constraints in genetic improvement efforts

In many cases, progress in improvement or lack of it has been reported. Various reasons have been adduced for the latter situation. Some of these include:

(i) lack of political will to substantiate efforts in improvement research formulation;
(ii) budgetary/financial constraints
(iii) gross inadequacy of the right type of expertise (i.e. manpower) both professional and technical for improvement work;
(iv) lack of job satisfaction in itself and in relation to other professions in compensation for longer meaningful research gestation periods measured in experimentation terms;
(v) the nature and functioning of the hereditary material itself and
(vi) many others.

Bottlenecks (i) to (iv) highlighted above are of immense importance and need be addressed seriously for continuous success in improvement research/work. A careful global view of these factors will show that the impact of any of them and their interactions inter alia are surmountable. The level at which any nation responds to its commitment bears strong relevance to its success in its genetic improvement and manipulation activities. If the global advancement pace is to be taken as a yardstick then it is crystal clear that judging from what obtains in Nigeria currently, only lip service is being paid to improvement research /work. The situation is very true of national tertiary education development and sustenance in the country.

The structure and properties of the DNA (the hereditary material) which have earlier been discussed is again worthy of note here. During DNA replication, crossovers resulting in recombinant types in the hereditary material occur only between gene loci.

Figure 6:

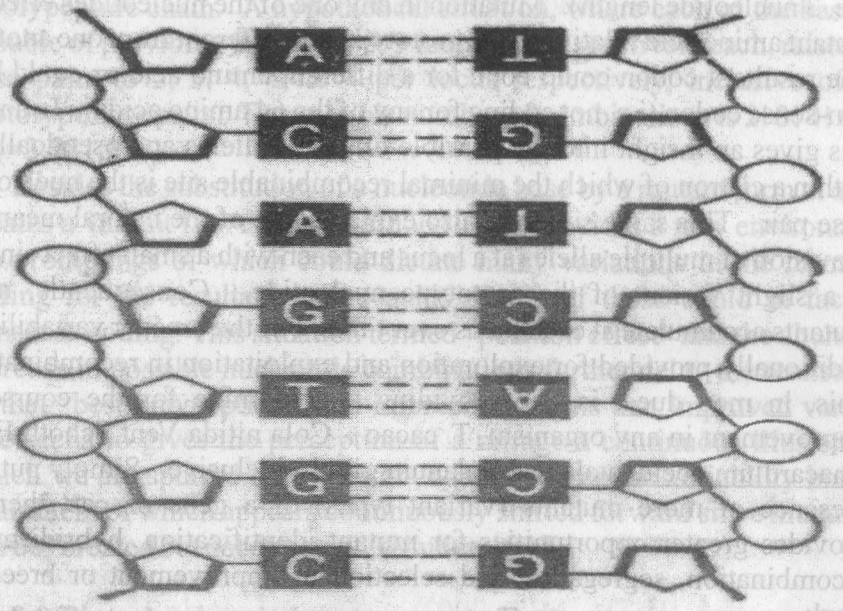


Fig. 6: The physical structure of a model DNA showing the double helical nature in diagrammatic form. (Circles=phosphates ;pentagons=deoxyribose and squares=bases with broken lines indicating hydrogen bonds). (After Crick, 1954).

This ensures precision and minimizes "mistakes" in the resulting recombinants. The linear arrangements of these "beadlike" structures are in concordance with this situation. Explanation of the double helical structure of the DNA now provides an indisputable linear structure with a phosphate backbone to which nucleotides are attached by hydrogen bonding (Watson and Crick, 1953). Further proof of linearity and the divisibility of the conventional gene (Benzer, 1947) by way of function (cistron), recombination (recon) and mutation (muton) indicates that there

could be recombination within the cistron and that mutation could occur even at the nucleotide base level. Benzer further demonstrated that the genetic coding for an amino acid could be minimally a three letter code (i.e. 3 nucleotide length). Mutation in any one of the nucleotides effects a mutant amino acid relative to the prototype but different from one another. The resultant codon could code for a different amino acid or could be a non-sense codon (i.e. not coding for any of the 64 amino acids). In a way, this gives an insight into the possible origin of alleles and pseudoalleles within a cistron of which the minimal recombinable site is the nucleotide base pair. This same situation also explains one of the natural means of provision of multiple alleles at a locus and each with a small effect since it is a slight variant of the prototype nucleotide. Consequently, more mutants accumulate at each locus over time. For the breeder variability is additionally provided for exploration and exploitation in recombination. This, in meo duce, is like providing a gold mine for the course of improvement in any organism, T. cacao ., Cola nitida Vent Schott. Endl, Anacardium occidentale and Solanum gilo L. inclusive. Simply put, the presence of more mutants (variant types) of a gene or part thereof) provides greater opportunities for mutant identification, hybridization, recombination, segregation and selection in improvement or breeding work.

As a response to environmental changes, natural selection gradually searches for fitness for a particular population. This it does by perfecting the combination of optimum gene complexes for the organisms in the population. The situation might not be singular. There could exist a range of organisms with gene complexes all of which present optimum or near optimum fitness for survival. A situation of genetic polymorphism for that species or population thus obtains. In these complexes the population of organisms representing the species carries some less than optimum mutant genes in the heterozygotes. Each mutant is selected for or against in combination within the population. For situations of mutants conferring lower fitness, frequency in the gene pool is lowered. Total elimination from the genepool is however rare. The situation is thus precipitated where increases in genetic variability in a population provides additional hereditary materials for manipulation. The net impact of such

increases is that it further widens the permutable combinations from which selections, natural or artificial, can be made e.g. assume that a portion of DNA containing 6 base pairs is responsible for directing the production of a polypeptide chain. A hypothetical situation, where each of the bases is capable of providing 1, 2, 3, 3,3 & 3 mutations respectively each, raises the base pairs to 2, 3, 4, 4,4& 4 per locus respectively, inclusive of the prototype base pairs. The possible number of combinations is 2! 3! 4! 4! 4! 4! (=3,981,312).

Besides the substitution of a nucleotide base by a mutant form at a site creates a variant DNA neighbourhood. This provides a new environment the promptings of which could dictate many variations in the forms of coding for the resultant amino acids. Some of these could in fact be nonsense coding. This situation termed "position effect" and the abundant increase in possible nucleotide combinations further delay the realisation of that "best polypeptide", and in breeding terms that improved variety. The scenario gives the perception of a mirage-a continuous illusion for which we are spurred on by the abundance of genetic variability but the attainment of which appears continuously shifted forward since mutations can be "created but not directed", (Muller, 1927).

9.0 Biotechnology in Improvement efforts:

This presentation on genetic variability in the current context appears incomplete without a reflection on the inputs of biotechnology into improvement. This great tool has been broadly defined as any technique that uses living organisms or parts thereof to make or modify a product, improve plants or animals or develop micro-organisms for specific use (John, 1998). In its very current application, the involvement of tissue culture and DNA manipulation (genetic engineering) for various improvement objectives constitute the aspect that bears most relevance to crop and animal improvement. Earlier before the birth of modern biotechnology, the application of biochemical control to diseases, biological control and processes such as fermentation constituted biotechnology.

In its most current understanding, biotechnology requires

(i) Trained expertise in biotechnology proper and related disciplines

to effect collaboration in a multidisciplinary approach;

(ii) Research laboratories equipped with these expensive intricate gadgets to conduct research;

(iii) Adequate funding for sustainability;

(iv) Uninterrupted recurrent materials replenishment;

(v) Collaborative work with biotechnology laboratories of excellence within the West African subregion, the Africa region and in developed countries where biotechnology is well advanced;

(vi) Involvement of both private and public sectors in policy and execution of biotechnology; and

(vii) Biosafety and intellectual property guiding laws.

In some developed countries of the world most of the biotechnology involvements as it affects agriculture has centred primarily around crop improvement via resistance to herbicides and pesticides to improve yield. At the USDA ARS cacao research meeting in Miami, Florida in January 2002, the main focus was on collaboration on research to develop disease resistant cacao cultivars. Miami Research Centre was engaged in the development of molecular marker projects for resistant strain identification (USDA-ARS, 2002). Wageningen in the Netherlands reported the development of a very expensive software "Join map" that will correctly handle mapping in an F_1 population from two heterozygous parents. Another software map QTL will also do QTL mapping in F_1 populations from heterozygous parents. The latter is the only software that handles the type of populations commonly encountered in cacao. The universal application of these markers to known clones in the cacao world with regards to witches broom resistance (*M. perniciosus*) is still being investigated in Miami. Supportive improvement breeding work is being suggested to be undertaken around Equador where high variability of germplasm exists naturally. A biotechnology detection kit for phytosanitary use to detect *Phythophtora* species, *C. pernisiosa*; *M. roreri* and CSSV is being developed at the Reading University in the UK for its reliability against the diverse strains of pathogens. Researches on biotechnological approach from South American and European

improvement programme to make it viable.

With the limited work that has been done, great promise for world food security in future has been shown. With the involvement of biotechnology, great risks of scepticism and rejection of genetically modified organisms (GMOs) is now prevalent even in the developed countries. From the stand point of genetic variability and its manipulation, molecular geneticists have used biotechnology to map a gene to a particular locus on the chromosome, excise it and transfer it to another cell to evolve a new GMO with desirable combination. For example, some success has been reported in transferring some genes of resistance to the Bt-maize (GMO). This is however not without the attending problems that are now surfacing.

Expectations in achievement via biotechnology are great, only limited scope has yet been fully accomplished even in the developed world.

With increasing genetic variability (natural or by recombination), there is a wider scope for rapid transfer of identified desirable genes with further perfection in biotechnology tools of genetic engineering. One major area to which attention should perhaps be given is the aftermath of the phenomenon of "Position effect" after gene transfer. This of course is among other bottlenecks that mandatorily dictate that all GMOs require biosafety approval and patency before release for marketing. This agent is again a process which further adds to the time to get to the promised land of release of improved freely acceptable and safe materials via biotechnology.

10.0 SUGGESTED STRATEGIES FOR THE FUTURE

10.1 The Globe: As has been clearly documented in most articles since the conventionally active manipulation of genetic variability, nature will continue to bestow on all organisms slow but assured increases in the provision of mutations. These provide a reservoir for meeting the populations needs of the future by natural or artificial means, subject to the demands for survival and fitness in a continuously changing environment. Suggestions for optimum utilization of these opportunities lie in the judicious combination of the current conventional methods of management of existing genetic variability. Ng and Ng (2000) gave very

clear approach to this. They distinctly inferred that genetic conservation and manipulation via biotechnology have high future prospects. The progresses so far reported are indicative of the more intensification of efforts in perfecting the involvement of biotechnology as a tool in improvement work. Until this is perfected, the conventional approach remains very highly relevant and should be properly sustained.

Genetics and breeding researches touch too directly on the survival and subsistence of the human race that the ability to utilize any tool to access genetic variability should be viewed as a fundamental right rather than a privilege of an endowed sector of the universe. Any attempt not to make this a generally available facility has inherent in it the attributes of global slavery resurfacing via a two prong outlet: (i) the denial of the less privileged (developing / under-developed) nations of their rights to determine what to eat and use for their survival; (ii) the possibility of indirectly refusing the under-privileged nations access to germplasm pool for research manipulation by storing the gene pool in a format not available to them. Either way, global slavery of a kind is precipitated. One would then wonder what the world has gained from the tremendous efforts, wars and loss of lives put into the abolition of the West Africa-to-America slave trade a few centuries (16^{th} 18^{th} centuries) back.

It becomes very apparent that the United Nations through its International Organisation on Human Rights has a very asserting role to play in ascertaining that germplasm of organisms are freely available to all nations via the conventional method. In the alternative, if and when biotechnology tool is perfected for genetic manipulation, the expertise and instrumentation should be made globally available to both developed and under-developed nations as a right. This latter suggestion is definitely going to involve high costs but it is not impossible.

10.2 The African Continent: For long enough time have African member countries decried colonisation and neocolonisation. Some policies and organisations to resist the adverse effects of these undesirable influences are in place. The African Union (AU) is very conspicuous in this regard. A practical intensification of germplasm exchange especially for research purposes is very desirous. National competition in the

production of economic crops poses a major obstacle to the liberalisation of germplasm exchange. Suffice it to add that under the present request for more global understanding and collaboration, need exists for intra continent liberalisation for the manipulation of genetic variability.

Al-Hassan's (2000) survey indicated that unstable electricity, inadequate funding and lack of equipment were parts of the major constraints to the development of biotechnology research in the countries assessed. The undertaking by AU or its parallel bodies in Africa to provide these cardinal needs in at least five centres one located in the North, South, East, West and Central Africa to specifically meet the biotechnology needs of the continent is mandatory. These centres will function collaboratively with other related science fields and liaise adequately with the developed world. The centres will be run and sustained on a budget funded by the continent rather than the nations or sub regions in which they are domicile.

10.3 The West African Sub Region: In the past, some relatively more liberal exchange of genetic materials and thus variability was in place within the sub-region. Ironically, this was at best when most of the countries involved were under English or French rule. With independence of most of these states, exchange of genetic materials inter se has dwindled. The major reason is competition and protection of national patency. The provision of the West Africa sub-region gene banks (crops and animals) should not be nation-specific. Rather it should have a West Africa sub region focus which provides free accessibility to all member nations in the sub region. Also in the provision and financing of the sub region biotechnology expertise, the centres should be product or product-combination specific irrespective of the nation of domicile. Staff recruitment should be targeted at individual specialisations in core subject matter areas rather than combined specialisations. Collaborative research approach of unique core specialists will more likely provide in-depth investigation results than will be otherwise obtained from part specialisation in one discipline/part in biotechnology set up. Unbroken sustainability of the gene banks and biotechnology is a focal point in the successful operation of this set up.

10.4 The Nation, Nigeria: With regards to germplasm conservation, Nigeria has a research set up based on various crops and animals in its research institutes. The research institutes which, some decades ago, were actively functional, are now moribund and in pitiable stages of research decadence. They have to be revamped. The germplasm arms of these institutes require effective reactivation where they have been inactive or initiation where they never existed. Perhaps it is pertinent at this point to stress that lip services of governments in the past to these endeavours can only worsen the current situation if it is not reversed. There is need to keep afloat the conventional methods of keeping our germplasm intact and possibly acquiring more for the nation's use. The institututional frame work is already in place. The unbreached recurrent upkeep is vital to research sustainability.

Alhassan (2000) reported that of all the 17 nations surveyed for biotechnology, Nigeria was the worst in terms of power supply. This is an inevitable resource facility, not only for biotechnology, but for all our facets of life. The epileptic power supply and current fluctuations is as old to Nigeria as all the governments after independence put together. What then is Nigeria's problem that is constantly eluding solution in the provision of stable and constant electricity? Is it leadership, planning, expertise, greed, deceit or share incompetence? Or is this nation to assume that by its leadership, past and present, the supply of constant and reliable electricity will continue to elude it like the hopes for water from a desert mirage? The unshaken truth about scientific research especially biotechnology, is that if a continuous reliable and non-fluctuating electrical power supply is not available, no reliable or reputable research can be undertaken. Nigeria has the might and financial resources that can be properly channelled to provide it with the appropriate power supply it needs. I strongly uphold the basic fact that when the governments, at the State and Federal levels, are determined to provide this facility properly, it will be done. Standby generators are no lasting solution for national regular electricity supply.

Recently, the Federal government launched its programme on biotechnology and collaboration both at home and in the United States of America. The collaborative nature with the developed world could be a

right step. It is however premised on a faulty footing. If the United States of America had not developed its power supply to a reliable stage, it would not delve into biotechnological research. The lesson here is crystal clear Nigeria, as a baby, must first learn to crawl, stand-up before attempting to run. Total failure is imminent to the proposed biotechnological research if the nations electricity supply remains abundantly epileptic. If Nigeria is indeed interested in scientific development, the most successful approach is that it should first put in place a stable, reliable non-fluctuating electricity power supply. Next, it should revamp the science laboratories in its tertiary and commodity research institutions to modern functioning status. This status will have to be sustained continuously via the provision of adequate funds for the capital and recurrent research needs of the laboratories.

An area of pertinence to viable and fruitful germplasm (genetic variability) conservation and utilisation in vivo is the having in place of well trained research experts in the various specialisations and disciplines. Currently, Nigeria has a substantial number of research experts trained both at home and abroad. But for a handful of these that have the rare opportunities of very recent overseas active research laboratory exposures in the United Kingdom, the USA, Canada and Europe, the equipment and laboratory working facilities available in Nigeria are, for the most parts, obsolete or approaching obsolete status. For scientific disciplines that require concurrence in precision in collaborative work with the developed world, archaic facilities can only produce less precise and second rated results. It therefore follows that until Nigeria is prepared to update and support scientific laboratory-inclined research to global competitive status, it is adviceable that post graduate training especially at the doctoral levels be allowed to be predominantly carried out in places where modern research facilities abound. Additionally, continuous placement of research scientists on more overseas laboratory study periods is highly advocated.

Hope is however not totally lost. With the Commodity Research Institutes and the Tertiary Institutions currently present in the country, there appears to be an adequate number of scientific research units for a take off. There is no need to start new "national science laboratories" of any sort. Revamp the existing ones to acceptably functional and modern status. This will definitely be cost effective. In addition, develop research

policies that will make researches oriented towards meaningful national objectives. This will allow researchers to work on specific commodities that are of interest to the nation at specific commodity research centres. The current situation whereby some experts conduct research on personal preference rather than one with relevance to national interest should be minimised. Besides, the suggested policy on research commodity guideline will bring about more judicious fund allocation to needed researches since more required materials and collaborators are already in place. Concerted inter disciplinary teamwork will be more enhanced.

Perhaps, it is vital to point out here that a great advantage lies in decentralisation rather than over concentration of these research facilities. Currently, the Federal capital territory has a relatively stable power supply. The tendency will be to concentrate research facilities in the Abuja territory. This is not what is here suggested. Relatively stable power supply could be channelled to any part of the country where the research centres and laboratories are located. Other facilities could be harnessed to these locations if they are already existing there.

11.0 Conclusion: Every species of living organisms is endowed with a hereditary survival mechanism. This is entrenched in the genes which in all eukaryotes is coded in the DNA. For each gene, nature provides variants (mutants) which may provide substitutes for prototypes to confer best fitness when changes in the environment occur. For a population, the variants and prototype provide genetic variability. Over time, the understanding of the hereditary materials and its nature has provided some basis for the manipulation and exploitation of genetic material. With further understanding of the DNA and its properties and with the application of the new tool biotechnology to it, a very wide and dimensionless reserve of genetic variability appears to have been uncovered. The advantage to this discovery is the availability of more alternatives to counter any novel situation that will make the existing prototype less fit. The reservation is the great expansion of multiple choices in genetic combination from which to determine a combination that will surpass the prototype in fitness. Biotechnology currently is active in minimising the enormity of genetic juggling required. Its application at

a more universal level still awaits the perfection of the tool and the provision of solutions to the teething problems encountered in its use. Meanwhile, nature continues in its benevolence to endow species with additional genetic variability at its own pace.

Thank you.

12.0 ACKNOWLEGDEMENTS

Priority must be given to whom it is due. I will start my appreciations by thanking God, the Almighty; for sparing my life to attain this age and stage of my career. He showed his protection over me in very many instances from infancy when all hopes were lost. The blessings on me are abundant. Rendering these testimonies will qualify for another inaugural lecture. At the end of this lecture, I will implore you all to join me in expressing profound gratitude.

To my parents, late Pa John M. O. Abraham Sanwo and late Mrs. E. A. Abraham Sanwo, I say a big thank you for all you did to prepare me for my journey of life before you departed this world, 24 years and 10 years ago respectively. Rest in peace in the bosom of the Almighty (Amen). I also seize this opportunity to express gratitude to my departed uncles, aunts, cousins and bossom friends and academic colleagues who contributed consciously to the successes in my life and career. Amongst many, I wish to mention Pa. Joseph Sanwo (Uncle), Pa. Joseph Adefuye, Pa Olowo-Ofayoku, Mama Victoria Adenaike, Mama Rosaline Onamusi, Mama Adegbemi, Pa Cosmos Adefuye, Brother Augustine Sanwo (all uncles and aunties); Mama Catherine Sanwo, Mama Shoga, Pa P. Shoga (step mothers and fathers); Sister Maggie Bello (cousin), Egbon Ganiyu Muili (a confidant), Dr. Obatolu (a colleague) and many others who had contributed to my getting this far in life. You all have gone, but the records are crystal clear that your various contributions have been instrumental to my achievements today. May your souls all rest in peace.

I use this occasion to express sincere gratitude to the institutions where I trained. The so styled "bush school" which produces eminent men of value to the Nigerian society nation. Long live St. Anthony's Grammar School,Esure, Ijebu-Imushin. May your contributions to society continue

to increase. The first and the greatest University of the nation nurtured me to B.Sc. Agriculture level. It is with pride that I dove my hat to the Faculty of Agriculture of the University of Ibadan and its devoted lecturers e.g. the calibre of Prof. V. A. Oyenuga, Modebe, late Ajibola Taylor, late Chedda, late Esuruoso, late Oluwasanmi, Profs. Adegboye, Adeyemi, Hill,Steinberg and Bowdin. These great academicians devoted all their tenure to ascertain that the 1968 crop of Agric. graduates got the best. My set and especially myself are exceptionally proud of you all and what you imparted to us. I say thank you.

The University of Guelph, Canada, where I got the first direct dosage of the breeding profession stands high amongst its mates and in the production of top brass Plant Breeders. Within 24 months, the crop of committed lecturers in the Crop Science Department were able to groom this inherently capable but initially and environmentally handicapped Master's student to world acceptable standards. I will recall Profs. Kasha, Reingberg Kannenberg, Gamble, Berth Christie, Terry Daynard amongst many others as being very helpful in moulding me up professionally. I thank all of you.

Far above Cayuga waters stands a globally acclaimed and recognised Institution of Learning Cornell University. In its department of Plant Breeding and Biometry I completed my doctoral apprenticeship in this noble plant breeding profession. Passing through this institution with daily interactions with world figures in plant breeding gave me the confidence to profess the rigor, the intrigues, the persistence and the commitment of crop improvement to this day amidst very trying obstacles. In particular, I will want to specially thank Prof. L. V. Crowder (my fatherly supervisor), Profs. R. Mclntyre and H. D. Thurston (members of my doctoral degree committee), Dr. H. Munger, Dr. Plaisterd, Obendorf, late Dr. Srb, Dr. Pearson and a host of many others who gave the appropriate doses in their various courses to ascertain academic and professional independence and basic improvision strategies for operation on return to Africa. I cannot thank you enough for all you did. I am certain that the Lord Almighty will reward you abundantly. Amen.

My research working life was predominantly at the Cocoa Research Institute (CRIN) where I encountered very collaborative senior

and junior colleagues. No doubt my lecture would have shown that I was able to undertake the long gestation investigations with patience partly because the Institute and the staff members presented an enabling environment for work. It is in place to recall the following names which in my own exposure relate to Cocoa: Prof. L. K. Opeke, Dr. Omotosho, Dr. Toxopeus, Dr. V. J. Jacob, Dr. O.A. Atanda, Dr. E. B. Esan, late Dr. Adegbola and late Dr. Obatolu, Messrs Odeboju and Olugbemi, Dr. & Dr. Mrs. Afolami, Dr. Adebayo, Prof. Ajobo, Prof. A. A. Ojo, etc. to mention a few. I thank you all and may God continue to bless you. Amen.

Olabisi Onabanjo University, formerly OSU is a young university with promise. Though currently under-financed, this institution has a staff compliment over the years that provide challenges. I have been with it since inception. The opportunity offered me to rise to the current level is very much appreciated. To this end, I express gratitude to all its Vice Chancellors without exception for exemplary leadership in various trying situations. I specially thank Prof. Layi Ogunkoya during whose leadership I was PFQed, and profound thanks also to Prof. Afolabi Soyode in whose term my professorship materialised.

OOU has provided me with the opportunity to interact with some very special people Mama Laide Soyinka, a wonderful senior sister and counsellor, the academic staff of the College of Agricultural Sciences, OOU, and of course the very fearless ASUU-OOU front at both the Congress and the Exco levels. Your support at very trying times are very appreciated. All the non-academic staff of the university and especially at the CAS with whom we now unitedly are engaged in our relocation activity to the Colleges promised land, I thank all of you for all the support.

It might perhaps sound strange but here it comes. Except for the 2½ years when I was away in Liberia on UN mission, all the students of the Agricultural College have at different measures imbibed what I have to offer in class. I thank you all; I was strict and you complained. Today, the fact that we do not have a long trail of reference students lined up by Baba Sanwo's courses is indeed an evidence that you all adjusted and passed. I thank you all for the patience and perseverance. Perhaps worthy of very unique mention is the 2000 Agric. Student set under the class Major, Mr.

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At various stages of my life, I have been branded as a difficult, rigid, strict, non-sentimental and/or too harsh person. These could be true to some extent. Amidst all these, however, someone has opted to share all her life with me and give very soothing effects to my life. "Kenken", I very much value all you have done in the past and the role you are currently playing. It is in place to emphasise that where others found it difficult to proceed, you have wonderfully forged ahead and progressively made impact. You have ushered many happy events into my life. I sincerely thank you and look ahead to more happy years ahead. Finally, I thank members of this great audience who have come to grace this lecture with

your presence.

At the beginning of my appreciation list, I started by expressing gratitude to God for His abundant gifts and blessings. The thought keep recurring in me that I cannot thank Him enough. Perhaps, taking a lead from the 140th song of David might further express my gratitude. Even with this, I realise that I croak. I therefore will enjoin the audience in singing this first stanza and chorus to the Creator of the Universe in continued expression of appreciation.

"What can I say unto the Lord? 2ce
All I have to say is thank you Lord
Thank you Lord, thank you Lord
All I have to say is thank you Lord".

Thank you all and God bless.

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