WHY WE LOOK AT THINGS NOT SEEN: ANIMAL GENES AND THEIR WINKING EYES

by

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FUNAAB INAUGURAL LECTURE SERIES

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My Academic Mentors,
Friends of the University and Special Guests,
Ladies and Gentlemen.

1.0 INTRODUCTION

It is indeed a great pleasure for me to stand before you today to present the 62nd Inaugural Lecture of the Federal University of Agriculture, Abeokuta. Someone has well said that the delivery of an Inaugural Lecture, by tradition, is an academic debt that one owes as an academic when one has risen to the rank of Professor. It presents an opportunity to "blow one's trumpet" vociferously and unchallenged usually to an open, and perhaps, enthusiastic audience of gown and town. It is an opportunity to present one's academic case and score card and highlight the very important contributions that one has been enabled to make so far in one's academic and research career. I am therefore privileged and blessed to have this opportunity to take this time out.

This is the fourth Inaugural Lecture from the Department of Animal Breeding and Genetics, one of the foundation Departments of this great University. The first three Inaugural Lectures from the Department were presented by Professors O. A. Osinowo, O. A. Adebambo (Mrs.) and M. O. Ozoje. This is also the eleventh Inaugural Lecture from the College of Animal Science and Livestock Production, coming after presentations by Professors E. B. Oguntona, I. F. Adu, O. A. Osinowo, O. A. Adebambo (Mrs.), C. F. I. Onwuka, S. S. Abiola, D. Eruvbetine (Mrs.), A. B. J. Aina, O. S. Onifade and M. O. Ozoje.

2.0 ANIMAL GENES

The title of this Inaugural Lecture is **WHY WE LOOK AT THINGS NOT SEEN: ANIMAL GENES AND THEIR WINKING EYES**. The inspiration for this title was derived from the Bible in 2 Corinthians 4: 18 which reads "While we look not at the things which are seen, but at the things which are not seen; for the things which are seen are temporal, but the things which are not seen are eternal."(KJV).In the course of this Lecture, we will provide details of our research findings and reports on the sights and grasps of genes towards livestock improvement in Nigeria. Genes are the basic units of inheritance that are transmitted from parents to their offspring in all living things. Genes are not visible to the naked eye but they are detectable and they manifest their effects phenotypically in ways that can be observed or measured or assessed or evaluated. Every living organism, plant or animal, lower or higher, has genes which it transmits from generation to generation in ways that ensure the survival and preservation of the species. Genes are unique in their influence on specific characters or features or functions which are important in the classification of organisms into species, breeds and varieties.

Genes are basically located on chromosomes at points that are called loci (singular: locus). There are different types of chromosomes in animals. In man and other mammals, these are autosomes and sex chromosomes, X and Y. In birds such as domestic chickens, ducks, turkey, quails and guinea fowl, chromosomes are classified as macro-chromosomes, micro-chromosomes and sex chromosomes (Z and W). There are six (some earlier publications report eight) pairs of large macro-chromosomes and thirty-three (33) pairs of smaller micro-

chromosomes in the chicken (Smith *et al*., 2000). The chicken micro-chromosomes have been reported to be more gene-dense and gene-richer than the macro-chromosomes (McQueen *et al*., 1998; Smith *et al*., 2000) owing to the higher rate of recombination events in them relative to the macro-chromosomes. McQueen *et al*. (1998) suggested a six-fold difference in gene density between the micro-chromosomes and the macro-chromosomes and that 75 % of all chicken genes were located on the micro-chromosomes.Smith *et al*. (2000) reported a more conservative estimate of 50 %of all chicken genes being located on the micro-chromosomes.

The presence of genes on sex chromosomes leads to the expression of characters that are sex-linked. We will, in the course of this Lecture, provide details of our research findings and reports on the very important productivity traits we have mapped to be controlled by quantitative trait loci on some specific chicken macro-chromosomes, micro-chromosomes, and sex chromosomes.

The alternate forms of genes are called alleles which are borne in pairs on chromosomes. This has given rise to dominant genes and recessive genes. Dominant genes are genes the presence of which, singly or in pairs, guarantees the expression of the character or feature in question. Genes that need the dual presence in the genotype to express a character or feature are recessive genes. Pairs of genes and gene combination are called genotype and they are responsible for the overall manifestation of specific characters or features in plants and animals.

Traits that are expressed by genes and genotypes can be desirable or undesirable. In animal breeding practices and animal improvement

programmes, genes and characters that are desirable are selected for while genes and characters that are undesirable are selected against. Examples of traits or characters in man that were previously selected against consciously or unconsciously include albinism, sickle cell anaemia, haemophilia, and Down Syndrome condition. Nowadays, discriminatory selection practices in humans are being down-played in technologically advanced countries of the world due to advancement in technology, education and information dissemination. In livestock species, deleterious and undesirable genes which are usually selected against include pale-soft-exudativeness (PSE, for short), while desirable genes are those which control the expression of productivity, adaptability and livability traits.

3.0 ANIMAL PRODUCTIVITY, ADAPTABILITY AND LIVABILITY

Issues of life, any life, are summed up in these three crucial areas of relevance, influence and impact – productivity, adaptability and livability. Success or failure of businesses, careers, and executive performance are judged and evaluated on the tripodal nodes or planks of productivity, adaptability and livability.We have focused our research work on animal genetics on these three broad areas of animal productivity, adaptability and livability because of the 'winking eyes' of animal genes that are permanently focused on these traits.

Productivity entails increase, growth and multiplication. In animal husbandry, productivity has to do with growth, positive growth rate, reproductive efficiency, on the part of both the male and the female animals, pre-weaning performance, post-weaning performance, offspring thriftiness and offspring viability, which may or may not be

traceable to parental performance and nursing ability. Adaptability relates to such traits as tolerance of, or susceptibility to, environmental and climatic conditions, and ability to thrive, produce and reproduce in such conditions. Livability is basically the ability of the animal and its offspring to survive.

Talking about the environment under which animal husbandry activities are majorly carried out in Nigeria, the tropical environment has been reported to be characterised by stress factors which include high ambient temperatures, high relative humidity, high solar radiation, poor feed resources, poor water availability and poor management practices. The hot, humid climate prevailing in the tropical world is not only stressful for humans but also debilitating to his animals and the feed resources as well. These problems of feed and water availability and the poor standard of management under the traditional animal rearing and production practices compound an already bad situation for animals in their efforts to produce and reproduce. The environment is a very important component in the animal genotype–to-phenotype relationship as the environment always affects the crucial issues of animal productivity, adaptability and livability.

Today, the prevailing phenomenon of climate change is undeniable and the extreme weather conditions and variations it brings have impacted negatively on the productivity, adaptability and livability of animals as well as on animal feed resource availability, quality and diversity. Osinowo (2013) reported that global warming and climate change could lead to depressed livestock productivity because of animal exposure to extremes of weather conditions under the prevailing traditional production systems and higher disease incidence arising from increasing precipitation in other areas. IPCC (2007) defined climate

change as: a change in the state of the climate that is identifiable using statistical tests by changes in the mean and/or the variability of its properties, and that persists for an extended period, typically decades or longer. On the other hand, animal production, especially cattle production, leads to the emission of greenhouse gases such as methane, ammonia, nitrous oxides, carbon dioxide, etc to the environment and so, has been implicated as a contributory factor in global warming and the resultant climate change. It has been estimated by some researchers such as DeMichele (2018) that an adult cow releases 70 – 120 kg of methane to the atmosphere each year. With a global cattle population of 1.2 – 1.5 billion, the volume of methane released to the atmosphere remains substantial. Johnson and Johnson (1995) and Shibata and Terada (2010) reported that factors affecting methane emission in cattle include level of feed intake, type of carbohydrate in the diet, feed processing, addition of lipids in the diet, alterations in the ruminal microflora and environmental temperature. Research efforts are presently being directed towards reducing the emission of greenhouse gases by cattle and mitigating the impact of cattle production on climate change and the role of genes and genetic components in this regard cannot be over-emphasised. In the meantime, we will provide, in the course of this Lecture, reports of our findings on the effects of some animal genes that act as chaperones in getting the animal to adapt to the environmental stresses such as heat stress to which it is exposed and enable it to survive and thrive.

4.0 LIVESTOCK PRODUCTION IN NIGERIA

Different livestock species are found and / or produced in Nigeria. These include poultry species (chickens, ducks, turkey, quails, guinea fowl, ostriches, etc.), rabbits, pigs, sheep, goats, and cattle. Available

breeds are generally local with some exotic (foreign) breeds raised on some commercial and institutional farms. Local breeds of sheep are the West African dwarf, the Yankasa, the Uda and the Balami. Local goat breeds are the West African dwarf, the Red Sokoto and the Sahel, while for cattle, the Nigerian breeds include the Muturu, the White Fulani, the Sokoto Gudali, the Kuri, the Wadara, the Ambala, the Red Bororo, etc. Various animal scientists in universities and research institutes have worked to characterise and compare the productivity, adaptability and livability of these local breeds among themselves and relative to exotic breeds under different conditions.

In Nigeria, livestock production has remained largely in the hands of resource-poor farmers who generally employ traditional rearing practices of subsistence, extensive system and pastoralism, depending on the livestock species involved. Under these approaches, animals and their herders are exposed to extremes of weather conditions and a wide spectrum of environmental hazards, such as accidents, predators, pests and diseases while in search of feed and water. Modifications or variations of this general trend are seen in various parts of the country depending on the prevailing local traditions, resource endowment, and on climatic and vegetative conditions of the areas .Under natural conditions and without the input of man, forage and water availability is seasonal and cyclical and generally dependent on rainfall pattern. In the dry season, animals and their herders frequently visit perennial streams, f*adamas* and river basins where fresh fodder is usually guaranteed. In the past thirty or more years, there has been a noticeable trend towards the settlement of the pastoralists in the southern part of Nigeria where there is natural pasture and ready market, as against the previous cyclical migration. Our studies have reported on this trend and the

implications for the hosting states and villages (Oduguwa *et al*., 1995; Ikeobi, 1997). In recent times, there have been frequent clashes in different parts of the country, Nigeria, between animal herders and crop farmers when animals wander off into arable crop farm lands and devour and destroy arable crops. These frequent clashes have led to massive loss of human lives, destruction of farmlands, properties and animals. It represents a sad commentary on the primitive and prevailing state of affairs in the livestock industry sub-sector in Nigeria. It is important that efforts are put in top gear by governments at various levels, especially at the centre, to seriously address this situation and combat the menace.

Under these extensive, open range and pastoral systems of rearing the different livestock species in Nigeria, animal productivity in terms of body weight, growth rate, and reproductive efficiency is very low. Losses due to predators, accidents, pests and diseases are very high. Overgrazing of available pasture land often results in environmental degradation and soil compaction, with little or no remedial action provided, Livestock production has the potential to contribute greatly to the nation's gross domestic product (GDP) if concerted efforts are made to modernize and develop the sector beyond what it is today.

5.0 MY RESEARCH CONTRIBUTIONS

The focus of my research in the area of animal genetics through the years has been on the quantitative genetic and molecular genetic characterisation and evaluation of Nigeria's animal genetic resources, with special emphasis on the local chicken, and on the identification and mapping of the quantitative trait loci (genes) affecting broiler chicken traits such as body weight and growth at three, six and nine weeks,

abdominal fat laydown, skin fat deposition, fat distribution, and carcass traits. The population of local chickens and other livestock species in Nigeria previously put at 120 million for chickens, 30 million for goats, 22 million for sheep and 12 million for cattle (RIM, 1991)and the significant contributions being made by these animals to the food and income needs of the people, especially the rural dwellers justify this emphasis.

5.1 Quantitative Genetic Characterisation and Evaluation of Nigeria's Animal Resources

Much of our research efforts have focused on the chicken, especially the Nigerian local chicken. At the early part of my career in FUNAAB, we carried out a retrospective study which dwelt on the productive potentials and the occurrence of major genes of frizzling, naked neck, and dwarfing of the local chicken. The report of the study (Ebozoje and Ikeobi, 1995) highlighted the unique features and genetic potentials of the local chicken that could be exploited in future breeding and improvement programmes based on it being a repository of and supplier of gene complexes affecting productivity, adaptability and livability traits in the species. Working with other researchers, we have been able to genetically and comparatively characterise the local chicken with respect to productivity in terms of body weight and growth at the different stages of life, egg production, egg fertility, egg hatchability, etc and the effects of the major genes of frizzling and naked neck in both the extensive, farmer-managed flocks and intensive system. Our research and publications extend the base of knowledge available on the roles of major genes, skin and plumage pigmentation genes and plumage distribution on adaptability traits of body temperature regulation and productivity indices in a hot, humid environment such as is prevailing in

south-western Nigeria. The frequencies of the frizzling and naked neck genes in the Nigerian local chicken are very low. Ikeobi *et al*. (1996) found the frequencies of the frizzling allele, *F*, naked neck allele, *Na*, and non-dwarf allele, *Dw* in the Nigerian local chicken to be 0.06, 0.05 and 0.93 respectively while the recessive alleles (*f*, *na*, *dw*) had the frequencies of 0.94, 0.95 and 0.07 respectively.

5.1.1 *Effects of Major Genes in the Nigerian Local Chicken*

In addition, Ikeobi *et al*. (1996) reported that the frizzled local hen laid and hatched the least number of eggs per year under the open range system of management compared to the naked neck and normal feather birds under similar conditions. Our studies on the local chicken under intensive system of management resulted in similar findings (Peters *et al*., 2002). In another study, we found that the effects of major genes were significant for egg weight, favouring the frizzled chicken (8.13 % increase) and the naked neck chicken (5.85 % increase) over the normal feather local birds (Peters *et al*., 2007).

Plate 1.
Frizzle-feathered local chicken

Plate 2.
Normal-feathered local chicken

Plate 3. Naked neck local chicken

We also evaluated the semen quality traits of seven chicken genotypes including local naked neck chicken, local frizzle-feathered chicken, local normal-feather chicken, Nera Black, White Leghorn, Giriraja and an improved indigenous chicken strain, Alpha (Peters *et al*., 2008a). The White Leghorn cock had the largest ($P < 0.05$) semen volume while the naked neck cock had the least. The naked neck bird had the highest value for motile spermatozoa, while the Giriraja had the least. Simple correlation coefficients between semen volume and the other semen quality traits were generally low and positive (from 0.01 to 0.35). Local cocks had comparable results with the exotic ones and can therefore be used in chicken genetic improvement as they are contributors of rare and novel genes. In addition, large genetic variation in semen quality traits existed in the cocks which can be exploited in future breeding programmes.

Another study was carried out to compare the fertility and the hatchability of eggs of pure and crossbred chicken genotypes, from direct and reciprocal crosses (Peters *et al*., 2008b). In matings where the naked neck gene was involved, the lowest hatchability was obtained

compared to the other matings involving the other pure and crossbred genotypes. Similarly, purebred mating of the naked neck local bird resulted in high percentage of dead-in-shell confirming earlier reports of the lethal effects of the naked neck gene on chicken embryo viability and survival.

We also studied the variations in the haematological indices of the Nigerian local chickens using clinically normal naked neck, frizzle-feathered and normal-feathered chickens (Peters *et al*., 2011). Parameters evaluated included red blood cell count, white blood cell count, mean haemoglobin concentration, packed cell volume, mean corpuscular haemoglobin concentration, serum urea, glucose, albumin, cholesterol, globulin and creatinine. We found that normal feather local chickens had significantly ($P < 0.05$) higher mean values for the parameters compared to naked neck local chickens and frizzle-feathered local chickens, except for red blood cell counts, white blood cell counts, albumin, and mean haemoglobin concentration. There were also substantial genetic variations in these haematological parameters that could be used as indicator traits in future studies. The results suggest that these major genes can be incorporated into an improved local chicken strain for commercial egg production. This particular paper, published in a United Kingdom journal, *Tropical Animal Health and Production*, has received extensive citations and reviews from researchers in different parts of the world.

These and the other studies have formed the bases for the work in FUNAAB on the genetic improvement of the Nigerian local chicken for meat and egg production, reports of which have also been given in some publications. We carried out a study to evaluate the effect of

crossbreeding local chicken strains with an exotic strain on fertility, hatchability and embryo mortality (Adeleke *et al*., 2011a). The results showed that the frizzled local-sired cross gave the best fertility (98.5 %) and the best hatchability (96.8 %), compared to the other crosses involving the local normal feather chicken or the local naked neck birds. Adeleke *et al*. (2011b) also reported that growth performance traits from day-old to twenty (20) weeks of age of the frizzle-feathered, normal-feathered and naked neck local chickens were comparable, with only slight variation in the mean values. In crosses involving an exotic broiler breeder strain, normal-feather- sired cross had the best growth performance compared to the other hybrids.

Our comparative study on the eggs of four local poultry species (Ikeobi *et al*., 1999) showed that the eggs of Nigeria's local poultry species met the prevailing United States Standards for quality of industrial eggs as earlier categorised. Eggs of local chicken, local guinea fowl and local pigeon with their very high Haugh units of more 60 were in category A, while eggs of local ducks with an average Haugh unit of 41.55 fell under category B.

We extended our study on major genes in the Nigerian local chicken to tolerance to *Eimeria tenella* infection and found that the effects of major genes of frizzling and naked neck were not significant ($P > 0.05$) for tolerance for coccidiosis as chicken genotype had no significant effect on body weight, haematological parameters, faecal oocyst and lesion score (Adenaike *et al*., 2016a).

We also conducted a study to investigate the genetic variation in the carcass traits and blood parameters of local naked neck and normal-

feathered chickens and their crosses with Marshall broiler chickens (Akpan *et al*., 2018). Male chickens were consistently heavier in all the carcass traits evaluated compared to the females. The naked neck and the normal-feathered chickens had the lowest values for mean haemoglobin, white blood cell count, and red blood cell and also had the highest values for globulin.

5.1.2 *Rare Qualitative Characters in Local Chickens*

Our studies have also reported on some rare qualitative characters with underlying genetic basis in the local poultry species. These include incidence of ptilopody (feet feathering), incidence of polydactyly (presence of extra toe or toes), presence of head spurs, incidence of cresting, and comb types and the relationships between these conditions and local chicken adaptation and productivity in the local environment. Ikeobi *et al*. (1998) found that the effects of feet feathering were significant ($P < 0.05$) for breast girth and breast length and favoured the feet-feathered local chickens and for yearly egg and chick production favouring the chickens with smooth shanks.

Plate 4. A Polydactylous local chicken

Plate 5. Crested Local chicken

This showed that feet feathering appeared to directly enhance meat characters in the Nigerian local chicken while lowering egg production and hatching results in the strain. Hatching profiles were, on the average, 78.09 % for the smooth-shank group and 59.81 % for the feet-feathered chickens. Going forward, Ikeobi *et al*. (2001b) estimated the frequency of the *Fsh* allele affecting ptilopody in the Nigerian local chicken to be 0.08 while its recessive allele, *fsh*, had a frequency of 0.92 and the observed frequencies significantly ($P > 0.05$) did not fit the expected, suggesting that there has been deliberate selection against the condition in the local chicken in south-west Nigeria.

Ikeobi and Godwin (1999) reported that the penetrance of the polydactylous condition in the Nigerian local chicken was generally very low (0.446 %) in south-western Nigeria, giving rise to a frequency of 0.002 for the dominant allele, *Po*, influencing the condition. The frequency of the recessive allele, *po*, was very high (0.998) and these allelic frequencies significantly did not fit the expected values. The authors posited that these variations could be due to the role of natural selection and social preference both operating against the polydactylous local birds.

Cresting has been defined as the presence of a tuft of feathers on the top of the head of some breeds of chickens. The sizes of the tuft of feathers in the crested chicken vary from chicken to chicken. It can be very long and at times may not be easily distinguished from the uncrested condition. Hutt (1949) reported that cresting was caused by an incompletely dominant autosomal gene, *Cr*. Our study found that the incidence of the cresting condition in the Nigerian local chicken was 13.1 % while the uncrested condition occurred at a frequency of 86.1 %. Frequencies were 0.07 for *Cr* and 0.93 for the *cr*+ allele (Ipaye, 1999).

On comb types, Ikeobi *et al*. (2001b) found the *P* allele (for Pea comb) to have a frequency of 0.02 and *R* allele (for rose comb) to have a frequency of 0.01 while the recessive forms, *r* and *p*, had frequencies of 0.99 and 0.98 respectively. The single comb of genotype *rrpp* is the predominant comb type in the Nigerian local chicken (Ikeobi *et al*., 2001b), thereby highlighting the effect of natural selection in the evolution of the species. Siegel and Dudley (1963) reported that pea comb cockerels were subordinate to the single comb males when they were housed together and that the single comb cockerels won more agonistic encounters than did the pea comb cockerels.

Plate 6. Rose comb in local chicken

Plate 7. Local chicken with Pea comb

Plate 8. Local chickens with single combs

Previous studies by Ikeobi *et al*. (1998) yielded results that suggested that genes for single comb, pea comb and rose comb did not significantly ($P > 0.05$) influence body weight, linear body measurements, and egg production studied in the Nigerian local chicken. Shoffner *et al*. (1993) obtained similar results which showed that egg weight and egg production were not significantly affected by genes for pea comb and rose comb. Rose comb is widely known to be associated with low fertility in chickens.

The incidence of spurs in extensively-managed local chicken was 0.999 % (Ikeobi and Oladotun, 1998). Length of spurs were highly variable, ranging from 0.50 cm to 2.00 cm, with an average length of 1.02 cm. Spur size (length) was found to be positively associated with the body weight of the birds ($r = 0.693$). Spurs have been reported to be a secondary sex character in chickens with a strong male hormone influence (Hutt, 1949).

In a work we carried in south-west Nigeria, we found only one incidence of brachydactyly out of 2046 matured extensively-managed local chickens surveyed. Brachydactyly is a condition in which the size of the chicken's outer toe is shorter than usual. In our study (Onifade, 1999), we found that the third toe was shortened to about 0.75 cm and the condition was unilateral and not bilateral. Incidentally too, this single brachydactylous chicken manifested bilateral polydactyly.

In line with the rarity of these qualitative characters in commercial exotic flocks, we have also estimated the frequencies of the various genes influencing these conditions in the Nigerian local chicken. These reports highlight the need to conserve these rare characters for the benefit of present and future generations of humans.

5.1.3 *Studies on Pigmentation Genes*

Studies on pigmentation genes have also been carried out by our group on other animal species such as guinea fowls, local ducks, local turkeys, pigeons and goats to compare the effects on their performance. Adebambo *et al*. (1996) reported that black local ducks laid and hatched significantly ($P < 0.05$) more eggs in a year when compared to white and mottled (white/black) ones, while local ducks with white shanks laid and hatched significantly more eggs in a year relative to black-shank ducks. The same study also reported that features of importance in the performance of the local turkeys included colours of the plumage, shanks and ear lobe. Mottled local turkeys were the heaviest and also had the largest breasts (Adebambo *et al*., 1996).

We also worked on plumage and skin pigmentation in the local chicken. In one of our reports (Adebambo *et al*., 1999), we found that plumage pigmentation which is genetic in origin significantly affected body weight, breast girth, breast length and egg production in the local chicken. Shank (skin) colour also significantly affected live weight of the birds. The significant effects of plumage and skin pigmentation on productivity traits may be mediated through body temperature regulation which enhances adaptability of the species in the hot, humid environment in which they are reared.

In one of our studies (Ozoje *et al*., 1999), we reported on the occurring patterns, mode of inheritance and frequencies of plumage, skin, beak and ear lobe pigmentation genes in local ducks, local turkeys, guinea fowls and pigeons. It has also been observed that plumage, skin and ear lobe colours were useful in the selection and genetic improvement of a poultry species especially as they relate to breed identity and

intellectual property rights and registration. Gene frequencies and modes of inheritance varied greatly among these local poultry species, highlighting key and basic differences among them.

We have also previously reported (Ebozoje and Ikeobi, 1998) that reproductive performance and pre-weaning growth in West African dwarf (WAD) goats were significantly influenced by coat pigmentation. Black WAD does were found to have the largest litters at birth and at weaning and they also weaned the heaviest kids at 120 days of age.

Plate 9:
***B_locus* Black West African dwarf goat (Horned, Right wattled, Unbearded)**

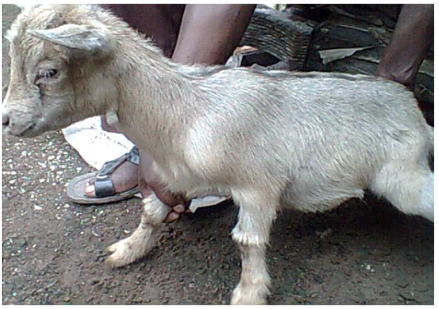

Plate 10: *A_locus* Tanned West African dwarf goat

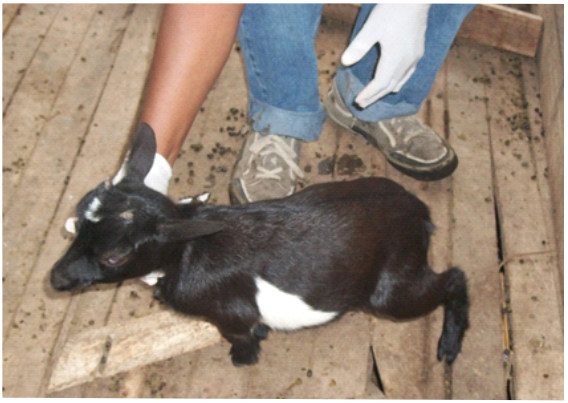

Plate 11: West African dwarf goat (*S_locus* Black with white markings)

Plate 12: *B_locus* Brown West African dwarf goat (Bearded, Left wattled)

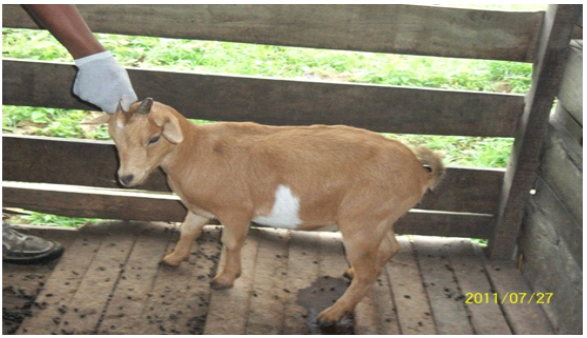

Plate 13: *S_locus* Brown West African dwarf goat with white markings

Plate 14: *A_locus* Grey West African dwarf goat

Plate 15: *A_locus* Blackmask West African dwarf goat (Unwattled)

Plate 16: *A_locus* Mahogany West African dwarf goat

Plate 17: *A_locus* Bezoar West African dwarf goat

Plate 18: *A_locus* Lightbelly West African dwarf goat

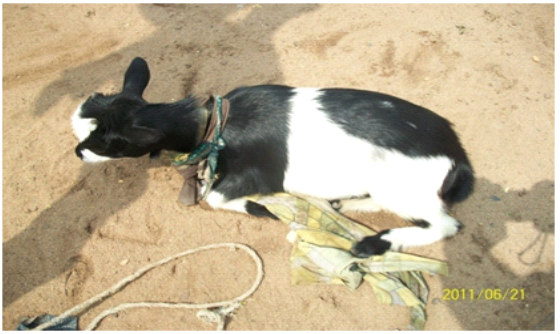

Plate 19: *A_locus* Swissmarking West African dwarf goat

Plate 20: *A_locus* Badgerface West African dwarf goat

In addition, mortality was higher among white / tan goats which suggested that coat pigmentation played a crucial role in the survival and adaptation of the WAD goat in the hot, humid conditions prevailing in southern Nigeria. We later extended our study on the effects of coat pigmentation genes to sheep and found that the West African dwarf sheep with brown coat colour (*Bb*) and badger face (A^b) were able to withstand heat stress better relative to black (*BB*) or white/tan (A^{wt}) ones (Decampos *et al*., 2013).

5.1.4 *Direct Genetic Effects, Maternal Effects and Parameter Estimates*

As part of the work on genetic evaluation, we have estimated some direct genetic and maternal effects and parameters for poultry (including local chickens), pigs and rabbits. These parameters are important in crossbreeding and selection programmes for animal improvement as some follow-up studies have shown.

Our research efforts yielded results that showed that genetic correlations for growth traits and carcass traits ranged from low to high (Ikeobi and Peters, 1996a, b), suggesting discriminatory approaches in seeking to improve several traits in meat-type chickens. Ikeobi (1998) reported high heritability estimates for body weight (0.71) and egg weight (0.42) and low heritability estimates for egg production (0.16). Intake of feed and feed conversion ratio with very high environmental components of variance had very low heritabilities (0.09 and 0.06 respectively). Egg production also showed positive genetic correlation with feed intake, feed efficiency and egg shell thickness. We also later reported that both broad sense and narrow sense heritabilities for body weight in chickens were very high, ranging from 0.75 to 0.90 (Adebambo *et al*., 2008a), and that the estimates decreased with advancing age of the chicken (Adebambo *et al*., 2009).

Using diallel analyses involving the local chicken and some exotic chicken strains, we found that both additive and dominance gene effects were important in feed efficiency. Feed efficiencies were low for the normal feather local cocks (0.12) and normal feather local hens (0.14) compared to an exotic hen, Anak Titan (0. 22) (Adebambo *et al*., 2008b). The results of the diallel analyses to test for general and specific combining abilities of breeds of chickens showed that additive genetic and maternal effects were important ($P < 0.01$) for economically-important productivity traits while dominance effects were important for the survival traits (Adebambo *et al*., 2010, 2011, 2012). We obtained similar results on the combining ability of growth traits in rabbits (Adenaike *et al*., 2013a). Significant reciprocal cross differences for body weight in crosses between an Indian chicken strain and the Nigerian improved chicken were also reported by us (Amusan *et al*., 2013).

We also evaluated the reproductive performance of three Nigerian indigenous chicken strains and their crosses with Marshall (Bassey *et al*., 2016). The local strains were the normal-feathered, the frizzle-feathered, and the naked neck. Heritability values for first egg production traits were 0.37 for normal-feathered chicken, 0.16 for the naked neck strain and 0.66 for the frizzle-feathered chickens. Heritability values for the Haugh Unit were 0.14, 0.07 and 0.08 for the normal-feathered, the naked neck and the frizzle-feathered strains respectively. Our results further showed that the crossbreds generally performed better than the indigenous purebreds in terms of egg production (Bassey *et al*., 2016).

Working with both local and exotic turkeys, we found that toms had significantly ($P < 0.05$) higher body weights relative to turkey hens and that local turkeys had higher feed efficiency than the exotic ones (Ilori *et al*., 2010). In line with our findings in this study on turkeys, Ikeobi *et al*. (1995) had earlier reported significant sexual dimorphism in two strains of commercial broiler chickens. We also assessed some physiological indices in turkeys and found that the effect of genotype was significant for heat tolerance traits with the highest mean values for rectal temperature, pulse rate and heat stress index observed for exotic turkeys (Ilori *et al*., 2012). The significantly higher H/L ratio of the exotic turkeys was an indication of heat stress in the genotype.

In another study, we used multifactorial discriminant analysis to evaluate the morphological and physiological traits in indigenous, exotic and crossbred turkeys (Yakubu *et al*., 2012). Sexual dimorphism was observed in some morphological traits with the toms having significantly ($P < 0.05$) higher body weight, body length, thigh length, and keel length compared to the female turkeys. Step-wise discriminant

analysis revealed that body weight, thigh length and heat stress index were the most discriminating variables for separating the turkey genotypes.

The farrowing records of Large White and Landrace breeds of pigs and their crosses were studied to evaluate the direct genetic and additive maternal effects on swine litter performance in south-western Nigeria. Direct genetic effects were reported to be important for pre-weaning piglet weight and survival (Ikeobi, 1993) and for pre-weaning litter size and weight (Ikeobi, 1990; Ikeobi and Ngere, 1994). Additive maternal effects were also important for piglet weight at 21 days of age (Ikeobi, 1999), favouring the crossbreds with Landrace dams.

These reports are important because while the sire usually makes only a genetic contribution to their offspring through their gametic transmissions at mating, the dam usually brings in both the genetic contribution through the gene transmissions and the maternal contributions in terms of suckling, nursing and *in utero* and rearing interactions with the offspring. Ikeobi and Ngere (1993) reported remarkable differences among exotic sows in nursing ability due to age. They found that the optimal nursing age for sows was 38 months in a hot, humid environment. Going further, Ikeobi and Ngere (1996) obtained results that suggested that pre-weaning interactions among swine littermates were crucial to the individuality of the piglets as expressed in their pre-weaning weights and survival to weaning. In addition, we found that percent heterosis was low in the swine first crossbred litters and generally increased in the backcross litters and that the results generally depended on the extent of dissimilarity between the parents (Ikeobi, 1994). Our subsequent study reported important

maternal effects for average birth and weaning weights in rabbits (Aina *et al*., 1998).

We also evaluated three Nigerian goat breeds (West African dwarf, Red Sokoto and the Sahel) for their morphological characteristics and heat tolerance traits (Wheto *et al*., 2015). Results showed substantial genetic variation among the breeds which can be exploited for genetic improvement in terms of animal survival and productivity.

5.1.5 *Studies on Modelling and Prediction of Growth and Disease Resistance*

Our study used three non-linear models, Gompertz, Monomolecular and Richards, to fit weight – age data for seven chicken genotypes, four of which were local chicken genotypes. All three models underestimated the asymptotic mature weight of the chicken but the Gompertz function gave a better estimate compared to the other two (Peters *et al*., 2005). The results suggest that more than one growth model will be required to best describe the growth curve and maturing patterns of various chicken genotypes. In another study (Peters *et al*., 2006), we used linear, exponential and polynomial models in the prediction of live body weight from linear body measurements in pure local and pure exotic chickens and their crossbreds in south-west Nigeria. A combination of shank length and breast girth tended to provide a better prediction of live body weight of chickens when compared to breast girth alone.

In another study (Adenaike *et al*., 2017), we compared five growth functions: the Brody function, the Gompertz function, the Logistic function, the von Bertalanffy function and the Richards function, to describe the growth rate and growth pattern of normal-feathered local

chickens, the naked neck local chickens and the Marshal chickens. The Gompertz, the von Bertalanffy and the Logistic functions fitted the growth patterns of all three chicken genotypes very well and the R^2 values were all above 99.89 %. Based on all comparison criteria, the Logistic model gave the best fit for the body weight – age relationship for the chicken genotypes. Brody function and Richards functions proved unhelpful in fitting the growth data of the genotypes in this study, going by the parameter estimates, p values and the convergence criteria.

We evaluated the relationships among body weight and morpho-structural parameters to predict the body weight of chickens from their orthogonal body shape characters using principal component analysis and also to morphologically classify chicken genotypes using multivariate discriminant procedure (Ajayi *et al*., 2011a). Chicken genotypes were the local normal-feathered chickens, the local frizzle-feathered chickens, the local naked neck chickens and Anak Titan exotic chickens. Breast girth, keel length, thigh length, shank length and wing length were the most discriminating variables to separate the chicken genotypes. About 22.7 % of the normal-feathered chickens were wrongly classified as naked neck chickens, while 33.0 % of the naked neck chickens were wrongly classified as normal-feathered chickens. The results suggested a high rate of gene flow between the normal-feathered local chickens and the naked neck local chickens in the study area. Working with only normal-feathered and frizzle-feathered local chickens, Ajayi *et al*. (2011b) reported that step-wise discriminant analysis revealed that keel length, shank length, and body length were the most discriminating variables in separating the frizzle-feathered and the normal-feathered local chickens.

We have also compared the use of principal component regression and the original interrelated linear measurements in predicting the body weight of five strains of locally adapted chickens (Adenaike *et al*., 2016b). We obtained results that showed that the use of independent orthogonal indices PC1, PC2, and PC3 was more appropriate in predicting the body weight of chickens compared to the use of the original interrelated linear measurements. Similar results were obtained and reported when we used a Bayesian approach in combination with principal component analysis in predicting the body weight of the Nigerian indigenous normal-feathered chickens from linear measurements (Sonubi *et al*., 2017).

We also carried out a study to compare the Gompertz and Logistic growth functions in describing the body weight changes over time and to predict the growth curve parameters of the Nigerian indigenous normal-feather chickens using Bayesian Gompertz and Logistic models (Iyiola *et al*., 2017). The Gompertz model gave the better fit for the body weight – age relationships for the normal-feather local chicken. However, the Logistic function was equally good in predicting the growth curve parameters of these chickens. Based on our studies with the local chicken, we recommend the use of Bayesian weighted multiple regression model in fitting linear body measurements of local chickens in the prediction of body weight as it fitted better than unweighted multiple regression model (Adenaike *et al*., 2019a).

A study was conducted by us on the prediction of the body weight of mature extensively-managed West African dwarf and Red Sokoto goats using their orthogonal shape characters under principal component analysis. Four linear body measurements were taken and these were

body length, heart girth, height at withers and neck length (Okpeku *et al*., 2011). Principal component-based regression models accounted for 89 % and 96 % as well as 81 % and 91 % of the variance in doe weight and buck weight of WAD and RS goats respectively.

We applied the principal component regression method to predict the body weight of the West African dwarf sheep (Bello-Ibiyemi *et al*., 2016). The PCA based on regression models revealed that the body weight of indigenous sheep was best predicted using heart girth, and a combination of rump height and height at withers. Decampos *et al*. (2014) had earlier obtained similar results for indigenous sheep using only a simple principal component analytical procedure and concluded that PC1 and PC2 could be used to predict the body weight of indigenous sheep with better results than when the original inter-related linear body measurements were used.

We have also developed sex-specific statistical tools that can successfully predict and differentiate *Eimeria*-infected and uninfected local chickens (Adenaike *et al*., 2018a). Using our two models, more than 90 % of infected chickens could be successfully distinguished from the uninfected group, using four variables (packed cell volume, white blood cell count, lymphocytes and body weight gain at day 3) for male chickens, and three variables (PCV, RBC, and body weight gain at day 3) for female chickens. It is recommended that our two models below could be used in diagnosing and predicting chickens infected with *Eimeria* through routine blood tests and estimates of body weight gain especially where key facilities and personnel are lacking.

Y = -742.46 + 389.26PCV – 14.77WBC – 0.63 BWG3 + 527.17LYMP (for males)

$Y = -140.35 + 162.609PCV + 55.62RBC + 20.50BWG3$ (for females).

We have also compared the effectiveness of different chick sexing methods using the local chicken and found that vent sexing method was low in accuracy (61.54 %) relative to the feather sexing method which was more reliable (87.69 %) for the local chicken (Adenaike *et al.,* 2016c).

Working with locally-adapted turkeys, we have also developed a regression model for the estimation of body weight from linear body measurements using path analysis (Adenaike *et al*., 2018b). The significant morphometric differences between the male turkey and the female turkey have necessitated this approach. Path analysis showed that body length only had a positive and significant influence on the body weight of the male turkey. Keel length had the highest direct and significant influence on the body weight of the female turkey followed by the body length. Therefore, the body weight of locally adapted turkeys could be assessed using prediction tools like body length for males and keel length and body length for females.

In another study (Sanni *et al*., 2013), we leveraged our understanding of the polymerase chain reaction techniques to attempt a molecular diagnosis of subclinical *Trypanosoma vivax* infection in three breeds (West African dwarf, Red Sokoto, and Sahel) of extensively-managed goats in three geographical zones in Nigeria. Using this technique, we found subclinical infection rates (SCIR) of 71.0 %, 75.9 %, and 55.6 % for WAD goats, RS goats and SH goats respectively, with an average SCIR value of 71.7 %. Statistical analyses showed that *T. vivax* infection was significant for goat respiratory rate and was associated with high serum creatinine levels. Logistic regression analysis further

showed that respiratory rate was the most important predictor of the presence of *T. vivax* infection in extensively-managed goats in Nigeria.

We have further reported that the best prediction equation for goat body weight with R^2 of 0.84 was obtained when body length, height at withers and chest depth were included in the model for Kalahari Red goat (Sanni *et al*., 2018). Step-wise discriminant analysis revealed that height at withers, chest depth, and body length were the most discriminating variables for morphologically separating these four breeds of goats: Kalahari Red, Red Sokoto, Sahel and West African dwarf.

The milking potentials of the West African Dwarf (WAD) goats have been investigated by several workers, some of whom we collaborated with. Goat milk has been found to have several beneficial properties which are useful to man. In one of such studies (Williams *et al*., 2012), we found that the milk yield and the dry matter intake of WAD does increased with milking frequency. Our study concluded that twice daily milking of WAD goats (at 6.00 am and at 6.00 pm) in Abeokuta gave optimal milk yield compared to once daily milking at 6.00 am only and thrice daily milking at 6.00 am, 2.00 pm and at 10.00pm.

5.2 Identification and Mapping of Quantitative Trait Loci (QTL) for Broiler Chicken Traits

Recent trends in livestock genetic research have dwelt on the application of new technologies such as the deoxyribonucleic acid (DNA) marker technology on animal improvement. Under the classical and conventional methods of animal genetic improvement, the progress made is usually slow and potentially involves many generations of breeding and selection. The detection and mapping of quantitative trait

loci (genes) on chromosomes constitute a key process in hastening the genetic improvement of animal performance as the major genetic basis influencing the animal species is highlighted much sooner.

Using an array of 101 microsatellite markers and an F_2 population made up of 466 individuals from 30 different families resulting from a broiler line – layer line cross, we detected and mapped quantitative trait loci (QTL) controlling growth up to three, six, and nine weeks of age, abdominal fat deposition, skin fat deposition, fat distribution, and meat yield, muscling and muscle distribution in chickens. Within-family regression analyses using the 101 microsatellite markers were done based on genome-wide significance thresholds. Our research efforts have yielded widely-acclaimed scientific reports on the QTLs affecting three of the most important productivity trait groups in chickens – growth, fat deposition and distribution, and meat yield.

5.2.1 *QTL For Chicken Growth*

The quantitative trait locus with the largest single additive genetic effect for growth in broiler birds was found in our study on chicken chromosome 4, and the effect of substituting one copy of the gene was an increase in weight of 249 grams in the bird (Sewalem *et al*., 2002; Ikeobi *et al*., 2002). Our study found evidence of statistically significant QTLs on chromosomes 1, 2, 4, 7, and 8 affecting chicken body weight at two of the three ages studied and one statistically significant QTL on chromosome 13 affecting chicken weight at all three ages (three, six and nine weeks of age). The QTLs on chromosome 2, 4, and 8 for chicken body weight at six and nine weeks of age were undetected at three weeks of age (Table 1).

Table 1. Significant QTLs for Chicken Weight at 3, 6, and 9 weeks of age

Body weight	Chr	F	Position cM	Additive effect, g (SE)	Dominance effect, g (SE)	% variance
At 3 weeks	1	8.5^	145	11 (3.7)	-13 (5.2)	3.7
	1	8.1*	481	25 (6.4)	-10 (14.6)	3.2
	7	10.1**	58	37 (8.3)	30 (25.6)	3.9
	13	10.4**	6	24 (5.3)	-7 (10.1)	4.3
	Z	11.2**	127	16 (3.6)	-9 (4.9)	4.7
At 6 weeks						
	1	8.5*	160	54 (13.2)	6 (23.6)	3.5
	1	8.9*	466	83 (19.7)	-7 (55.2)	3.7
	2	10.3**	302	58 (13.4)	-20 (20.5)	3.8
	4	12.3**	165	137 (27.7)	18 (91.6)	5.1
	7	8.6*	60	107 (26.0)	-10 (78.9)	3.3
	8	9.4*	68	102 (23.6)	-68 (65.5)	3.7
	13	11.1**	23	70 (16.9)	52 (32.6)	4.4
	Z	6.7+	127			
At 9 weeks	1	9.2*	404	76 (21.6)	87 (35.2)	3.9
	2	10.7**	302	79 (19.2)	-57 (29.4)	4.1
	4	18.2**	177	249 (41.4)	42 (138.1)	7.6
	8	8.2*	34	186 (48.2)	73 (183.8)	3.4
	13	8.7*	15	106 (26.1)	12 (52.5)	3.6
	27	9.7*	0	86 (19.5)	-11 (27.1)	4.0

•Significant (5%); ** Significant (1%); + Suggestive Source: Sewalem *et al.* (2002)

Our study identified a significant QTL for chicken body weight at three weeks of age on the Z chromosome which was only suggestive at six weeks of age and was undetected at nine weeks of age. These results suggest that differing set of genes are likely to be involved in the different stages of growth in the chicken. They also suggest that these genes influence the development of the digestive organs or skeletal growth of the chicken and that the subsequent growth of muscle tissue leading to body weight gain is also affected by a different set of genes.

The results we obtained for chicken growth QTL on chromosome 1 agrees with the report of Tatsuda and Fujinaka (2001) on QTL for

chicken body weight at sixteen weeks of age. The very large differences in weight between the parental lines used in the original cross (layers and broilers) increased the chance of detecting greater number of statistically significant QTLs in our studies relative to previous results of other workers (van Kaam *et al*., 1998, 1999; Tatsuda and Fujinaka, 2001; Sewalem *et al*., 2002).

5.2.2 *QTLs For Fat Deposition in The Chicken*

Abdominal and subcutaneous fat deposition in poultry birds has been of great interest to scientists and researchers of different disciplines through the years owing to the health and nutritional implications both for the species and for the consuming humans. We also studied fat deposition in the chicken and the results have crucial implications on the animal product consumption pattern of the average Nigerian. The average weight of chicken skin with underlying fat at nine weeks of age (94 grams) was far greater than the mean abdominal fat weight at same age (51 grams).

Table 2. Sex Differences in carcass, abdominal fat and skin fat weights.

Trait	Male	Female
Number	216	226
Carcass weight (g)	2223.9^{a}	1734.1^{b}
Abdominal fat weight (g)	51.66	50.17
Skin fat weight (g)	102.50^{a}	86.20^{b}

Means in the same row bearing different superscripts are significantly different

There were also highly significant ($P < 0.001$) and remarkable differences between the two sexes in the deposition of skin fat at nine weeks of age (Table 2) while sex differences for abdominal fat

deposition were not appreciable. In our study, we also found a positive and highly significant correlation of 0.667 ($P < 0.001$) between carcass weight and skin fat weight. Similarly, the Pearson correlation of carcass weight and abdominal fat weight was 0.431 ($P < 0.001$). These results suggest that the longer birds are kept and fed to increase their carcass weights, the more the birds will accumulate both skin fat and abdominal fat. Physical removal of the chicken skin and the underlying fat before cooking or roasting or grilling is therefore suggested to improve the quality of the meat and to minimise the intake of fat by lovers of chicken meat. The crucial role of eateries, caterers, food vendors and domestic cooks in ensuring and promoting this important aspect of food safety for the populace cannot be over-emphasised.

Table 3. Quantitative Trait Loci (QTL) affecting fatness in chickens

Fat trait	Chr	F	Position cM	Additive effect (SE)	Dominance effect (SE)	% variance
Abdominal	1	8.14*	126	-0.23 (0.07)	0.20 (0.10)	3.00
Fat	3	8.16*	40	0.18 (0.09)	0.51 (0.15)	3.26
	5	10.89**	50	0.32 (0.08)	0.27 (0.11)	4.25
	7	11.50**	39	0.72 (0.15)	-0.29 (0.48)	4.51
	28	9.25*	17	-0.34 (0.10)	0.43 (0.17)	3.84
Skin fat	3	9.05*	170	0.44 (0.11)	0.30 (0.24)	4.05
	7	8.36*	78	0.44 (0.11)	0.13 (0.25)	3.19
	13	8.51*	35	0.34 (0.09)	-0.14 (0.14)	3.59
	28	8.36*	0	-0.28 (0.08)	0.23 (0.10)	3.64
Fat distribution	5	8.58*	51	0.30 (0.08)	0.22 (0.11)	3.64
	7	11.08**	36	0.66 (0.15)	-0.70 (0.45)	4.40

•Significant (5%);** Significant (1%); Source: Ikeobi *et al*. (2001a)

Our study (Ikeobi *et al*., 2001a, Ikeobi *et al*., 2002) found that both skin fat deposition and abdominal fat deposition in chickens had different QTLs and chromosomal linkage groups associated with them. We found evidence of statistically significant QTLs for fat traits on chromosomes 1, 3, 5, 7, 13, 15 and 28 and suggestive linkages for fat traits on chromosomes 2, 4, 6, 9 and Z. We also found evidence for two positions on chromosome 3 affecting abdominal fat deposition and skin fat deposition respectively at different ends of the chromosome. There is therefore the need to give specific selection attention to both abdominal fat deposition and skin fat deposition in the efforts to improve the overall quality of chicken meat. We found the largest additive QTL on chromosome 7 for abdominal fat deposition in the chicken (Table 3) and it accounted for more than 20 % of the mean weight of abdominal fat.

5.2.3 *Comparative Fat QTL Mapping Results*

Based on the genome-wide significant QTLs detected for skin fat deposition, abdominal fat deposition and fat distribution in the chicken, Ikeobi *et al*. (2001a) reported on the comparative mapping results for mice and humans and found interesting homology relationships to QTLs in mice and humans (Table 4). In addition, our comparative mapping studies revealed some candidate genes with likely impact on the fat traits and thus corroborate the homologous results on obesity in mice and humans (Ikeobi *et al*., 2001a). The effects of the QTL for abdominal fat deposition on chromosome 1 were low (Table 3) and comparative mapping identified some candidate genes responsible for many traits in the species. An example is the *sox2* gene responsible for high growth in the mouse.

Our results on chicken chromosome 3 suggest two possible loci important for fat traits in chickens, one located at 40 cM controlling abdominal fat deposition and the other located at 170 cM affecting skin fat laydown. The dominance portion was high for abdominal fatness suggesting differences in gene action for the two fat traits on chromosome 3. The abdominal fat locus on chromosome 3 is homologous to human loci 2p21 and 19p13.1 and mouse chromosomes 9 and 17 with previously-identified QTLs as Qlw9 responsible for live weight at nine weeks and LSL for serum leptin levels. Serum leptin level has been implicated in the regulation of body fat (Comuzzie *et al*. 1997). They also noted that a major gene for obesity, *POMC* for proopiomelanocortin maps to the same region.

The QTL effects for fat laydown on chromosome 5 were of additive origin and showed pleiotropy as it also affected fat distribution in the chicken (Table 3). The QTL obtained in our studies on chromosome 7 suggests a possible pleiotropic effect on abdominal fat deposition and fat distribution in the chicken as the two positions are very close to one another (Table 3), requiring resolution through fine mapping. The QTL effects on both traits were also high, indicating a major locus affecting adiposity. Taylor and Philips (1996) identified a QTL for adiposity in the homologous mouse locus 1-19. A QTL was also found in our study on chromosome 7 determining skin fat deposition. Candidate genes and QTLs in this region that may be related to obesity include the *BBS5* (Bardet-Biedl Syndrome 5), Obq2 and Obq3.

Table 4. Fat QTLs in Chickens and their Homologues in mice and humans

Chicken Chr	QTL position (cM)	Fat trait affected	Mouse Chr	Human Chr	QTLs (Candidate genes)	Homologous References
1	126	Abdominal fat	6,10,12	6,8,12	MGF, IGF1, many	Pomp (1997) DeBry & Seldin (1996)
3	40	Abdominal fat	9, 10	2p21, 19p13.1,	Qlw9, LSL, POMC	Comuzzie *et al* . (1997)
	170	Skin fat		6q12-q25	Obq4,Bw6g, Qlw4,IGF2R	
5	50	Abd. fat, fat distribution	2,17,19	11p15.5-q13	BBS1,Qfa1, Obq3,Tub, IGF2,ABCC8	Warden *et al*. (1997) Coleman & Eicher (1990)
7	36 –39	Skin fat, a bd. fat, fat distribution	1	2q31-q37	BBS5,Obq2, Obq3, HDLBP	Taylor & Philips (1996), DeBry & Seldin (1996)
13	35	Skin fat	13, 18	5q23-q35	Qlw18,Pfa3, GRL, ADRB2	Large *et al*. (1997)
28	17	Abdominal fat	8, 10, 17	19p13.3-p12	Qlw9, FH	Pomp (1997)
	0	Skin fat			LDLR, INSR	DeBry & Seldin (1996)

IGF2: Insulin-like growth factor 2; IGF2R: Insulin-like growth factor 2 receptor; Qlw9: QTL for 2.4% late weight gain; LSL: Serum leptin levels; POMC: Proopiomelanocortin; Obq4: Obesity QTL for 6.1% adiposity; BBS1 or 5: Bardet-Biedl Syndrome, type 1 or 5; Qfa1: QTL (Lepr) for 5.4% weight; Obq3: Obesity QTL for 7% adiposity, ABCC8: ATP-binding Cassette sub-family C member 8; TUB: Mouse Tubby; Obq2: percentage fat pads at 16 weeks; Qlw18: QTL for 3.0% late weight gain; Pfa3: QTL for percentage fat pads at 12 weeks; GRL: Glucocorticoid receptor; ADRB2: beta-2 – adrenergic receptor; INSR: Insulin Receptor;; LDLR: low density lipoprotein; FH: Familial Hypercholesterolemia; HDLBP: High density lipoprotein- binding protein.

Source: Ikeobi *et al*. (2001a)

The skin fat QTL on chromosome 13 is in a region homologous to human loci 5q23-q35 and mouse chromosomes 13 and 18 with obesity QTLs, Qlw18 and Pfa3. The QTLs on chromosome 28 controlling

visceral fat and skin fat coincide with the location for the gene, INSR (insulin receptor) and LDLR (low-density lipoprotein receptor) (Table 4), which are major receptors controlling fat metabolism in animals. Candidate genes and QTLs in this region include QLw9 and FH (Familial Hypercholesterolemia) both having major roles in obesity.

In addition, these candidate genes highlight the probable role that the chicken can play in helping to understand the genetic basis for obesity and other fat-related health conditions in humans and how to combat them. In a world that is increasingly conscious and highly discerning of the quality and constitution of its food and meat intake, these results are important as they indicate the pathway to a fast, efficient, and reliable improvement in chicken meat quality. In which case, direct attention can be focused on the implicated chromosomal regions through the application of fine mapping techniques and the techniques of marker-assisted selection (MAS) and / or marker-assisted introgression (MAI). The gene effects showed that the additive effects of the broiler allele were mostly positive, suggesting that selection against fat laydown in the broiler chicken may benefit from the detected fat QTLs through marker-assisted selection.

5.2.4 *QTLs For Meat Yield and Muscling in The Chicken*

Table 5. Significant QTLs for Meat Yield and Muscling in the Chicken

Trait	Chr	F	Position cM	Additive effect, g (SE)	Dominance effect (SE)	% variance
Carcass Yield	4	8.6*	154	105 (25.7)	-34.4 (74.6)	3.6
Breast muscle Yield	8	9.9*	0	13.5 (3.1)	-9.3 (7.3)	4.0
Thigh Yield	1	11.1**	82	7.2 (1.8)	-11.7 (4.3)	4.6
	4	8.1*	0	4.2 (1.1)	1.7 (1.6)	3.2
Thigh m. yield	1	9.1*	136	3.0 (0.9)	-3.5 (1.5)	3.7
Drum Yield	4	8.0*	231	3.4 (0.9)	2.0 (1.3)	3.2
	5	8.6*	15	-2.6 (1.2)	6.3 (1.8)	3.8
	7	10.1**	41	-4.3 (2.3)	28.6 (7.1)	4.3
	13	11.1**	28	-0.9 (1.3)	-10.7 (2.4)	4.6
	Z	8.1*	106	-4.7 (1.2)	1.6 (2.0)	3.4
Drum muscle Yield	6	10.2**	29	-3.1 (0.7)	1.6 (1.2)	4.2
	7	8.1*	45	-2.0 (1.6)	19.3 (5.1)	3.4
	13	11.0**	27	0.2 (0.9)	-7.8 (1.7)	5.0
Wing Yield	4	8.2*	231	2.8 (0.7)	0.3 (1.0)	3.6
	7	11.3**	26	-2.5 (1.3)	15.1 (3.5)	5.1
	27	8.7*	0	3.7 (0.9)	0.2 (1.2)	3.5

•Significant (5%); ** Significant (1%); Source: Ikeobi *et al*. (2004)

Our studies also detected several statistically significant quantitative trait loci on twelve chromosomal linkage groups (chromosomes 1 to 9, 13, 27 and Z) for eleven muscling and meat yield traits in chickens. We also obtained statistically significant dominance effects for many of the QTLs and several of these (Table 5) were of relatively large effects (Ikeobi *et al*., 2004).

The magnitude of each quantitative trait locus represented 3.2 to 5.7 % of the residual phenotypic variation and the additive effects accounted for 0.2 to 0.8 phenotypic standard deviations. Ikeobi *et al*. (2004) also detected and reported a QTL on chicken chromosome 8 which is of great economic importance as it enhanced relative breast muscle yield in chickens by almost 5 %. Our studies also identified a QTL on chicken chromosome 4 which possesses a relatively large effect for carcass yield (Ikeobi *et al*., 2004), for body weight (Sewalem *et al*., 2002) and also for body weight, egg weight and feed intake Tuiskula-Havisto *et al*., 2002).

5.2.5 The Rich QTL Content of the Chicken Z Chromosome For Body Weight, Fat Deposition and Meat and Muscle Yield

The chicken Z chromosome was found to harbour a quantitative trait locus which affected live body weight at three weeks of age and which also suggestively affected live weight at six weeks of age. The effects of this QTL disappeared at nine weeks of age. A new QTL significantly manifested its effect at nine weeks of age but at the opposite end of the chromosome relative to the earlier QTL (Sewalem *et al*., 2002). The earlier QTL at the distal end of the Z chromosome (127cM) was found to have a pleiotropic effect on abdominal fat deposition in chicken (Ikeobi *et al*., 2002). Ikeobi *et al*. (2004) also found a QTL on chicken Z chromosome affecting drum yield and drum and thigh muscle yield and also suggestively affecting wing yield in the chicken. It would therefore appear that the body weight, abdominal fat deposition and drum and thigh muscle yield in the chicken are partially sex-linked.

These remarkable results on the identification and mapping of quantitative trait loci for growth at 3, 6 and 9 weeks of age, abdominal fat deposition, skin fat deposition, fat distribution, carcass yield, meat

yield and muscling in chickens have commanded a great deal of interest from several scientists and have also received extensive and positive reviews and citations by several researchers such as Hocking *et al*. (2002), Hocking (2005) and Abasht *et al*. (2007).

5.3 Genetic Diversity and Association Studies

The development of new technologies, some of them DNA-based, has enabled the integration of these technologies with the classical animal breeding and genetics research. In this respect, we have studied more closely and at the molecular level, several genes implicated in livestock productivity, adaptability and livability, especially for indigenous animal genetic resources. Reports of our findings have been published in several journals in Nigeria and outside Nigeria. In addition, the sequences of some of the genes arising from our work have been accepted and deposited in the GenBank for ease of reference by other scientists and comparison with sequences of other animal breeds and species. This represents a major scientific contribution in our work as these globally-available resources will assist in studying evolutionary trends and relationships among animal breeds and species with respect to these genes. Summary of such accepted and deposited sequences and their accession numbers are presented in Table 6. Gene polymorphisms detected in our studies and their possible effects on animal performance are summarised in Table 7 (for chickens), in Table 8 (for small ruminant animals) and in Table 9 (for cattle).

Table 6: Deposited Gene Sequences at GenBank and Accession Numbers

Gene	Gene Notation	Species	GenBank Accession Numbers
Tumour Necrotic Factor Receptor Super family 1A	*TNFRSF1A*	Chicken (local and exotic)	KY494915 – KY494922
Zyxin	*Zyxin*	Chicken (local and exotic)	KY560190 – KY560196
Insulin-like growth factor 1	*IGF1*	Chicken	MK416185
Toll-like Receptor 4	*TLR4*	Chicken	MN745543 – MN745548
Toll-like Receptor 2	TLR2	Cattle	KY778741 – KY778746
Heat Shock Protein 90	HSP90	Cattle	MN334701 – MN334742 MN329663 – MN329670

We carried out a study on the preliminary screening of the genetic lineage of three different strains of the Nigerian local chicken using blood proteins as markers and the three strains were compared with an exotic strain. The local strains were the normal feather (*nana, ff)* local chickens, the naked neck (*Na-, ff*) local chickens and the frizzled (*nana, F-*) local chickens. Three blood proteins, globulin, albumin and transferrin, were screened in these strains. The report (Adeleke *et al*., 2011c) which was published in a globally-acclaimed FAO journal, *Animal Genetic Resources*, showed that these chicken strains were clearly separate from each other, having a mean genetic similarity of 55 % and that the naked neck local chicken was the most diverged.

We extended this methodology to screen the serum proteins in West African dwarf (WAD) goats and in Red Sokoto (RS) goats (Ogunfuye *et al*., 2016). Two globulin types (AA and BB) and three albumin types

(AA, AB, and BB) were identified in our study. Our study revealed that high serum protein polymorphism existed among the WAD goats while low serum protein polymorphism existed among the RS goats.

In one of our studies (Oni *et al*., 2016), we compared the effectiveness of the random amplified polymorphic deoxyribonucleic acid (RAPD) and microsatellite markers with three local and two exotic chicken populations in Ogun and Ondo States in Nigeria. The local chicken populations were the frizzle-feathered, the naked neck and the normal-feathered. Our results showed that the microsatellite markers gave a more accurate cluster than the RAPD markers, suggesting a superiority of the microsatellite markers in probing and eliciting the genetic background of both local and exotic chicken populations.

We used ten (10) morphological traits and fifteen (15) microsatellite markers to characterize 402 sheep from four Nigerian breeds: West African dwarf, Yankasa, Uda and Balami and found that the Yankasa and the Balami were the most genetically closely-related pair while the West African dwarf and the Balami were the farthest apart (Agaviezor *et al*., 2012a). Yankasa sheep had a very high number of alleles. This may be one of the reasons for the breed's adaptability to more agro-ecological zones in Nigeria compared to the other three sheep breeds.

In a companion study, we investigated the genetic diversity of the four Nigerian indigenous sheep breeds using mitochondrial D-loop sequences (Agaviezor *etal*., 2012b). Ninety-six (96) haplotypes were observed with a mean haplotype diversity of 0.899 ± 0.148. Uda sheep had the highest gene diversity and the West African dwarf breed had the lowest. The highest number of polymorphic sites was found in the

Yankasa breed (201) and the lowest in the Uda (96). These differences need to be conserved to maintain the genetic distinctiveness of the sheep breeds.

We extended this study to the three Nigerian goat breeds (West African dwarf, Red Sokoto and Sahel) in which we investigated the mitochondrial DNA hypervariable region I (HVRI) and compared with Kenyan and Asian breeds of goats (Okpeku *et al*., 2016). It has been reported that the hypervariable region I was highly polymorphic and was useful in studying genetic diversity in many animal species (Zhao *et al*., 2014). Our results on genetic relatedness and evolutionary relationships showed a complex gene flow among Nigerian goat breeds and also revealed the Kenyan local goat as an intermediate breed between the Nigerian and Asian goat breeds.

We also assessed the association between growth hormone gene polymorphism and body weight and carcass characteristics of the improved Nigerian indigenous chickens using Polymerase Chain Reaction - Restriction Fragment Length Polymorphism (PCR - RFLP) Techniques. Effects of growth hormone (GH) gene polymorphism were significant for body weight, bled weight, eviscerated weight and breast weight. There were significant sex–GH gene polymorphism interaction effects on carcass traits of chickens (Wheto *et al*., 2016).

We carried out a sequence analysis of the insulin-like growth (IGF) 1 gene in five mammalian species which revealed the presence of five (5) haplotypes in pigs, two (2) in cattle, four (4) in water buffalo and one (1) in horse (Akinfenwa *et al*., 2011). Results showed that there was abundant polymorphism in the *IGF1* gene in mammals and that it can be

used as a potential marker in association and evolutionary studies. Insulin-like growth factor 1 has been reported to stimulate systemic body growth and to regulate cell growth and development. We extended this sequence analysis study to four poultry species (chicken, turkey, duck and goose) and found that the IGF1 gene was highly conserved in the four poultry species (Obetoh *et al*., 2011). Perhaps, in line with this report, we later found that the effects of insulin-like growth factor 1 (IGF1) gene polymorphism were not significant for any of the chicken carcass traits studied (Wheto *et al*., 2017).

In another study, we used three restriction enzymes, *MspI*, *BseRI* and *TaqI*, to individually digest the PCR products of the major histocompatibility complex (MHC) B-LßII gene in three strains of the local chicken (frizzle-feathered, the naked neck and the normal-feathered). While we obtained no cutting sites for the *MspI* and *BseRI* enzymes, the *TaqI* enzyme exhibited monomorphic pattern with genotype AA and at a frequency of 1.0, perhaps, suggesting the fixation of the naturally selected AA genotype of the B-Lß II gene in the Nigerian local chicken strains (Akpan *et al*., 2019).

An earlier report by our group, using *MspI* restriction enzyme to digest the PCR products of the tumour necrotic factor receptor super family (*TNFRSF*) 1 A gene in the Nigerian indigenous naked neck chicken (Adenaike *et al*., 2018c), found the prevalence of the homozygous genotype AA with an allelic frequency of 0.796 while the homozygous genotype BB had an allelic frequency of 0.204. These differences could be of great significance in association studies on the effects of the polymorphism in the gene on chicken performance traits.

Going further, our analyses of the tumour necrotic factor receptor super family (*TNFRSF*) 1 A and the zyxin genes in three local chicken strains (frizzle-feathered, the naked neck and the normal-feathered) and one exotic chicken strain (Nera Black), showed high nucleotide divergence and high haplotype diversity which, along with the evolutionary relationships, suggested historically restricted gene flow among the chicken genotypes studied (Adenaike *et al*., 2019b). There existed genetic differences in the *TNFRSF1A* and zyxin genes among the four genotypes of chickens studied with significant genetic diversity at both loci. The naked neck local chicken manifested the highest level of genetic diversity at the zyxin locus while the Nera Black showed the highest genetic diversity at the *TNFRSF1A* locus. This study derives its importance from the crucial roles played by both the *TNFRSF1A* and the *zyxin* genes as immune genes and in protecting birds against coccidiosis (Hong *et al*., 2009). Rezaei (2006) reported that the tumour necrotic factor receptor superfamily 1A was a multifunctional cytokine that facilitated the induction of cytokine secretion, promoting host defence against intra-cellular pathogens and the activation of leucocytes. On the other hand, Moon *et al*. (2006) reported that zyxin functioned to encode proteins that were useful in wound healing and tumour metastasis. Our group also reported 6 SNPs in the heat shock protein (*HSP*) *90AA1* gene in two exotic layer strains of chickens reared in Nigeria for commercial egg production but association studies showed no significant effect on heat tolerance traits evaluated (Irivboje *et al*., 2020).

Table 7: Summary of Polymorphisms in Chicken Genes and Associated Effects

S/N	Gene	Gene Notation	Animal Species	Polymorphism Type	Effects on Performance	Reference
1.	Growth hormone	GH	Chicken	RFLP	Body weight, bled weight, breast weight	Wheto *et al*. (2016)
2.	Insulin-like growth factor 1	IGF 1	Chicken	RFLP	–	Wheto *et al*. (2017)
3.	*TNFRSF1A*	*TNFRSF1A*	Chicken (Na-)	RFLP	–	Adenaike *et al*. (2018c)
4.	*TNFRSF1A*	*TNFRSF1A*	Chicken	SNP	–	Adenaike *et al*. (2019b)
5.	Zyxin	Zyxin	Chicken	SNP	–	Adenaike *et al*. (2019b)
6.	B-Lß II	B-Lß II	Chicken	RFLP	–	Akpan *et al*. (2019)
7.	HSP90AA1	*HSP90AA1*	Chicken	6 SNPs	–	Irivboje *et al*. (2020)

TNFRSF1A: Tumour Necrotic factor Receptor Super family 1A; *HSP90AA1*: Heat shock Protein 90AA1

Table 8: Summary of Polymorphisms in Small Ruminant Animal Genes and Associated Effects.

S/N	Gene	Gene	Animal Species	PolymorphismType	Effects on Performance	Reference
1.	G6B	G6B	Sheep	8 SNPs	-	Amusan (2012)
2.	BAT2	BAT2	Sheep	9 SNPs	-	Amusan (2012)
3.	ApoM	ApoM	Sheep	5 SNPs	-	Amusan (2012)
4.	Toll-like receptor 1	TLR1	Goat	5 SNPs	-	Wheto (2012)
5.	Toll-like Receptor 2	TLR2	Goat	5 SNPs	-	Wheto (2012)
6.	Toll-like Receptor 3	TLR3	Goat	19 SNPs	-	Wheto (2012)
7.	Toll-like Receptor 5	TLR5	Goat	0 SNP	-	Wheto (2012)
8.	Myostatin	*MSTN*	Goat (RS)	6 SNPs	Body length	Sanni *et al.* (2019)
9.	Melano-philin	MLPH	Goat	1 SNP & RFLP	-	Adefenwa *et al.* (2013)
10.	Tenascin XB	TNXB	Sheep	1 SNP & RFLP	Body weight, fore cannon bone length, pulse rate, skin temperature	Ajayi *et al.* (2013)

We have investigated the colour genes in Nigerian goats and detected a novel polymorphism in the melanophilin gene in the three Nigerian breeds of goats which had no associated effect with coat colour as there was very low differentiation within and among goat breeds in the g.469C > G locus (Adefenwa *et al*., 2013). This polymorphism in the melanophilin gene is the first in any breed of goat and also first in Nigerian indigenous goat breeds.

Our work on the exons 1 and 3 of the myostatin gene in the Red Sokoto goat breed focused on the amplification, sequencing and bioinformatic analyses of the sequences. Goat morphological traits analysed included body weight, height at withers, body length and chest depth. Five non-synonymous single nucleotide polymorphisms were detected in exon 1 three of which had non-neutral effects on protein function. One non-synonymous SNP was detected in exon 3 and was found to have a possible neutral effect on protein function. A variant at the exon 1 region was significantly associated with body length of Red Sokoto goats which were extensively-managed (Sanni *et al*., 2019). Myostatin is a member of the transforming growth factor-ß superfamily and is involved in growth and muscle development of animals (Yu *et al*., 2007). Earlier in 2016, we had reported interesting homology and evolutionary relationships of the myostatin gene in goats and other mammals (Sanni *et al*., 2016).

In one of our studies on Nigerian sheep breeds (Ajayi *et al*., 2013), we detected a novel *TaqI* polymorphism in a 454 bp fragment of the tenascin-XB (*TNXB*) gene with obvious changes in protein function. The SNP genotype had significant effect on body weight and on fore cannon bone length of sheep and was significantly associated with

pulse rate and skin temperature (Table 8). These effects may be due to the reported role of the tenascin-XB gene in connective tissue maturation in both heart and skeletal muscles (Matsumoto *et al*., 1994). In one of our previous studies on Nigerian sheep breeds, Amusan (2012) reported eight, nine and five non-synonymous mutations in ovine *G6B* gene, *BAT2* gene and *ApoM* gene respectively, highlighting rich genetic diversity among Nigerian sheep breeds at these various loci.

Table 9: Summary of Polymorphisms in Cattle Genes and Associated Effects.

S/N	Gene	Gene	Animal Species	Polymorphism Type	Effects on Performance	Reference
1.	Toll-like Receptor 1	TLR1	Cattle	7 SNPs	WBC, RBC PCV eosinophil	Agbalaya *et al*. (2018)
2.	Toll-like Receptor 2	TLR2	Cattle	9 SNPs	WBC, PCV	Agbalaya *et al*. (2018)
3.	Toll-like Receptor 3	TLR3	Cattle	9 SNPs	WBC, PCV	Agbalaya (2016)
4.	Toll-like Receptor 5	TLR5	Cattle	10 SNPs	WBC, PCV	Agbalaya (2016)
5.	Leptin	Leptin	Cattle	RFLP	-	Ogunnwa *et al.* (2019)
6.	Heat shock protein 70	HSP70	Cattle	21 SNPs	-	Onasanya *et al.* (2019)
7	Heat shock protein 90	HSP90	Cattle	4 SNPs	Body temperature, rectal temperature, respiratory rate, heat tolerance coefficient.	Onasanya *et al.* (2020) a, b.
8.	HSP90AB1	HSP90 AB1	Cattle	20 SNPs	-	Decampos (2018)

Working with a Nigerian cattle breed, White Fulani and a temperate breed, Angus, our study identified a previously-uncharacterised gene called ODF-1 owing to the presence of an intact alpha crystalline domain (Ajayi, 2014). Although this gene has been reported in humans, our study was the first in cattle. In addition, RNA sequence analyses of the skin transcriptome identified two hundred and twenty-five (255) differentially-expressed genes between the tropically-adapted White Fulani cattle and the temperate Angus cattle (Ajayi, 2014).

We also investigated the role of toll-like receptor (*TLR*) 1 and 2 gene polymorphisms on trypanosomosis traits of Muturu and White Fulani breeds of cattle challenged with *Trypanosoma vivax* in Nigeria. Sixteen (16) single nucleotide polymorphisms (SNP) were detected, 7 in *TLR 1* gene, and 9 in *TLR 2* gene (Agbalaya *et al*., 2018). The traits that were mostly associated with the SNPs in *TLR 1* and *2* were white blood cell count (WBC) and packed cell volume (PCV). The study concluded that 12 SNPs in Muturu and White Fulani breeds of cattle were associated with WBC, 7 with PCV, 3 with red blood cell count (RBC), 2 with eosinophils, and none with monocytes. It is important to note that these significant relationships can be exploited in the efforts to control trypanosomosis and other diseases in cattle in Nigeria. It has been reported that TLR2 recognised a variety of molecules such as glycosyl-phosphatidyl-inositol from trypanosome species, zymosan from yeast, peptidoglycan and lipoiteochoic acid derived from gram-positive bacteria (Takeda and Akira, 2005).

The PCR-RFLP technique was employed in the screening for polymorphisms in the leptin gene in three of the cattle breeds found in Nigeria, the White Fulani (WF), the Kuri and the N'dama. Two restriction enzymes, *MspI* and *HindIII* were used. The evolutionary relationship among the three cattle breeds showed a separate clustering of the WF as a group, while the Kuri and the N'dama formed a separate cluster (Ogunnwa *et al*., 2019). This divergence may be attributable to the zebu nature of the WF while the separate cluster for both the Kuri and the N'dama suggests their taurine descent. The three cattle breeds studied (Kuri, N'dama and White Fulani) were all in Hardy-Weinberg equilibrium at the leptin locus, suggesting that the effects of evolutionary forces were balanced in the three breed populations. Leptin is important in maintaining the energy balance in animals as it controls intake of feed and expenditure of energy, in addition to regulating reproductive functions and immune responses (Kulig and Kmie, 2009).

We have also carried out some sequence analyses on the kappa casein gene which is an important gene affecting milk coagulation and milk protein content and found that haplotype diversity was 1.00 in goats, horse and sheep, indicating abundant genetic diversity of the kappa casein gene in those species (Adenaike *et al*., 2013b). Very high polymorphisms of amino acids were also observed among the animal species than within species suggesting functional differences in the casein protein and divergence. We also found six non-synonymous mutations in goats, seven in sheep, four in cattle, four in horses and three in rabbits in the kappa casein gene locus while a close relationship was observed between goats and sheep in the evolutionary tree. Similar results had earlier been obtained for the alpha 1 casein gene in goats,

sheep and cattle and this high genetic variation can be exploited in the effort to improve on the quality of milk and milk products for human consumption (Adenaike *et al*., 2011).

We have also reported on the polymorphisms obtained in the White Fulani interferon alpha gene which were very high (Irivboje *et al*., 2016). The number of haplotypes was 14 in the White Fulani cattle and 9 in the Sokoto Gudali cattle.

We also carried out sequence analyses on the major histocompatibility complex (MHC) Class I, Class II, and Class III genes in both ruminant and monogastric animals (Bolatito *et al*., 2018). Polymorphisms identified in the MHC impact on how the individual animal responds to its environment and the pathogens. Our report showed that there were high haplotype diversity in the Class I, Class II, and Class III genes for both the ruminant and the monogastric groups. MHC Class II and Class III genes revealed high nucleotide diversity in both ruminant and monogastric animals while the MHC Class I genes showed low nucleotide diversity. We also found that these evolutionary changes deviated significantly from Hardy-Weinberg equilibrium. An earlier study by us (Adenuga *et al*., 2012) had investigated the genetic variations in the MHC DRB I and DRB II genes in six animal species (sheep, goat, cattle, pig, horse and buffalo) through sequence analyses. There was high polymorphism in the ovine DRB I gene as the highest number of single nucleotide polymorphisms were found in sheep DRB I gene.

We conducted a study to assess the presence of single nucleotide polymorphisms (SNPs) in the heat shock protein (*HSP*) 90 gene in four

Nigerian Zebu cattle breeds: Ambala breed (Plate 21) White Fulani breed (Plate 22), Sokoto Gudali breed (Plate 23), and Red Bororo breed (Plate 24). High resolution melting assays were used to identify a total of eleven (11) genetic variants, five of which were major variants present in over 70 % of the animals sampled while six were minor variants seen in only 2 of the 4 breeds studied and in only 29.1 % of the animals (Onasanya *et al.*, 2020a). Using these genetic variations, we noted important shared homology and remarkable common ancestral lineage among the four breeds of cattle evaluated. The SNPs earlier detected were used to evaluate the basis for heat tolerance in the cattle breeds (Onasanya *et al*., 2020b).The heat shock protein 90 gene has been reported to be a member of the molecular chaperone sub-families that are involved in thermo-regulation in animals (Onasanya *et al*., 2017), providing cellular protection, carrying out protein synthesis and ensuring animal adaptation.

Plate 21. Ambala cattle

Plate 22. White Fulani cattle

Plate 23. Sokoto Gudali cattle

Plate 24. Red Bororo cattle

Heat tolerance traits measured in the four breeds of cattle were body temperature (BT), rectal temperature (RT), respiratory rate (RR), and heat tolerance coefficient (HTC). Four SNPs were identified as shown in Table 10. Our results showed that the heterozygous SNP genotypes had significantly ($P < 0.0001$) lower values for BT, RT, RR, and for HTC compared to the homozygous SNP genotypes at all the four positions and suggest that animals with heterozygous SNP genotypes in exon 3 of *HSP 90* gene may be tolerant to heat stress.

Table 10: *HSP 90* gene polymorphisms in Four Nigerian Zebu Cattle Breeds.

Position	SNP Variants	Type of Variants	Amino acid change	Cattle Breed
116	T → G	Transversion	Threonine → Histidine	Red Bororo
220	G → C	Transversion	Arginine → Serine	Sokoto Gudali
346	G → A	Transition	Serine → Leucine	Ambala
390	G → A	Transition	Aspartate → Tyrosine	White Fulani

Source: Onasanya *et al*. (2020b)

Our sequence data in an earlier study (Onasanya *et al*., 2019) revealed 21 SNP loci in the coding region of exon 1 of HSP70 gene: 5 in White Fulani (WF) cattle breed, 3 in Ambala (AM) cattle, 2 in Sokoto Gudali (SG) cattle and 11 in Red Bororo (RB) cattle (Tables 11 and 12). This shows the high variability in this region of exon 1 of HSP 70 gene and is in agreement with the report of Singh *et al*. (2006) that the HSP70 gene was the most genetically variable among the HSP sub-family genes with conferred advantage for tolerance to a wide range of stressful environmental and thermal assaults.

Table 11: Single Nucleotide Polymorphisms (SNPs) in the coding region of exon 1 of HSP70 gene in four Nigerian Zebu cattle breeds.

Breed	Number of a nimals Studied	Number of animals with SNPs	Number of SNPs	Distribution of SNPs
WF	25	19	5	A7del, C145T, C154G, G220A, G220T
AM	23	16	3	C154T, G220T, C244T
SG	21	10	2	C184T, T198A
RB	21	21	11	C154G, A78T, G157A, G106C, C154T, G196A, T198A, C224T, G199A, G220Y, T245A
Total	90	66	21	

Source: Onasanya *et al*. (2019)

Table 12: Nature of SNPs in the coding region of exon 1 of HSP70 gene in four Nigerian Zebu cattle breeds.

S/N	Breed	SNP	Nature of SNP
1.	White Fulani	A7del	Indel
2.	White Fulani	C145T	Transition
3.	White Fulani	C154G	Transversion
4.	White Fulani	G220A	Transition
5.	White Fulani	G220T	Transversion
6.	Ambala	C154T	Transition
7.	Ambala	G220T	Transversion
8.	Ambala	C244T	Transition
9.	Sokoto Gudali	C184T	Transition
10.	Sokoto Gudali	T198A	Transversion
11.	Red Bororo	C154G	Transversion
12.	Red Bororo	A78T	Transversion
13.	Red Bororo	G157A	Transition
14.	Red Bororo	G106C	Transversion
15.	Red Bororo	C154T	Transition
16.	Red Bororo	G199A	Transition
17.	Red Bororo	G196A	Transition
18.	Red Bororo	T198A	Transversion
19.	Red Bororo	C224T	Transition
20.	Red Bororo	G220T	Transversion
21.	Red Bororo	T245A	Transversion

Source: Onasanya *et al.* (2019)

5.4 DIVERGENT SELECTION FOR ANTIBODY TITRE

We also started a divergent selection study on the Nigerian indigenous chicken using sheep red blood cells (SRBC). The indigenous chickens comprised the frizzled-feathered, the normal-feathered, and the naked neck chickens/ The foundation stock were sourced from six states in the south-western part of Nigeria so as to ensure as wide genetic background as possible.. Sheep red blood cells were used to categorise the chickens into high antibody titre and low antibody titre groups.

The results of the divergence in the second generation were as follows: frizzle-feathered (7.27 ± 0.39), normal-feather (8.24 ± 0.26), and naked neck (9.05 ± 0.40). Results were also obtained for PCR-RFLP of B-L*ß* II gene using the following restriction enzymes: *BseRI, MspI*, and *TaqI*. However, all the enzymes showed monomorphic banding patterns. This has been reported in one of our papers (Akpan *et al*., 2019).

The divergent selection for the second generation also included serum lysozyme concentration and the results were not different among the genotypes of the indigenous chickens. These findings reflect clearly that the indigenous chicken genotypes have equal chance of survival in the tropical environment.

5.4.1 *Expression of the B-Lß II gene at cytolytic and latent immune response stages in Nigerian indigenous chickens.*

Table 13 shows the separated means of the CT values based on the tissue type (spleen and thymus), titre group (high, low or control) and sex (male or female). Considering the tissue, the B-Lß II gene expression at cytolytic stage was higher in the spleen than in the

thymus. So also the chickens with the high antibody titre had higher expression than those with the lower antibody titre or in the control group. In the same vein, the expression in the male chickens at the cytolytic stage was higher than in the female chickens.

Table 13: Effects of Tissue, Genotype, Titre Group and Sex on B-Lß II Gene Expression at the Cytolytic and Latent Stages.

Source	Category	C_T Mean ± SD (Cytolytic)	C_T Mean ± SD (Latent)
Tissue	Spleen	30.02 ± 2.03^a	25.92 ± 1.41^a
	Thymus	20.61 ± 0.92^b	18.29 ± 1.71^b
Titre	High	31.15 ± 1.58^a	26.71 ± 1.26^a
	Low	25.88 ± 1.46^b	21.10 ± 0.77^b
	Control	18.58 ± 1.45^c	18.58 ± 0.79^c
Sex	Male	27.96 ± 2.09^a	24.30 ± 0.82^a
	Female	22.23 ± 1.81^b	20.01 ± 0.54^b
Genotype	Naked Neck	24.36 ± 1.21	21.07 ± 0.61
	Frizzle-feather	23.67 ± 0.91	20.28 ± 0.72
	Normal-feather	23.87 ± 1.13	20.84 ± 0.81

abc Means in the same column within variable grouping bearing different superscripts are significantly different; SD: Standard deviation,
C_T : Cycle threshold.

Considering the expression at the latent phase in the Nigerian indigenous chicken, the spleen still had high latent expression than the thymus, while the high antibody titre birds had significantly higher expression than the low titre birds and the male chickens had higher expression than the female ones (Bello-Ibiyemi, 2017).

At both the cytolytic and the latent stages of immune response to SRBC antigen, B-Lß II gene expression in the spleen was comparatively greater than in the thymus and the height of the transcriptional activity was associated with the cytolytic stage. Also, according to the antibody categorisation (high or low), birds of high titre at both the cytolytic and latent responses had the highest mRNA expression. Effect of genotype (major gene) on B-Lß II gene expression was not significant at any of the stages.at eight weeks of age. During avian infections, the category of high immune response birds would likely perform better than the low immune response group in terms of tolerance to the infection.

The third generation individuals from the divergent selection were challenged with attenuated Newcastle Disease vaccine (NDV). From the results obtained, only the normal-feather birds from the low titre group had a very low titre. The immune response trait for the third generation was in association with interleukin 6 and 10 genes. Immune response to Newcastle Disease Vaccine was significantly ($P < 0.05$) affected by chicken genotype-antibody titre level group and sex (Table 14). Frizzle-feather High Titre group and Normal-feather High Titre chicks were significantly different from normal-feather Low Titre group chicks (4.57 ± 0.41). It is obvious from the results that the normal-feather low titre birds should not be included in any breeding programme aimed at developing or enhancing the immune response profile of the Nigerian indigenous chickens. The female chicks responded significantly better than the male ones.

Table 14: Effect of genotype-antibody titre and sex on the immune response in Newcastle Disease Vaccine after vaccination on the 14th day in Nigerian indigenous chickens.

Genotype-Antibody Titre	N	Immune Response (GMT)
Frizzle-feather High	19	6.95 ± 0.30^{a}
Frizzle-feather Low	12	6.75 ± 0.39^{a}
Normal-feather High	17	6.94 ± 0.47^{a}
Normal-feather Low	21	4.57 ± 0.41^{b}
Naked Neck High	3	6.67 ± 0.88^{a}
Naked Neck Low	4	6.65 ± 0.63^{a}
Sex		
Female	43	6.70 ± 0.22^{a}
Male	33	5.59 ± 0.40^{b}

Means in the same column within variable grouping bearing different superscripts are significantly different; N: Number of observations. GMT: Geometric mean titre.

Going further, we found that the association of interleukin 10 (IL 10) gene polymorphism affected immune response to Newcastle Disease Vaccine (NDV). The immune response of the Nigerian indigenous chickens to NDV showed that IL10 genotype AA chickens had significantly higher response than IL10 genotype AB (Table 15). The dominance of AA and the AB genotypes was an indication of the polymorphic pattern and presence of homozygous and heterozygous genotypes found in the interleukin 10 (IL10) gene using *PSTI* restriction enzyme.

Table 15: .Association of IL10 Gene Polymorphism with body weight and immune response.

IL 10 Genotype	Body weight	Immune Response
AA	69.13 ± 15.41	6.08 ± 0.44^{a}
AB	69.98 ± 15.43	5.87 ± 0.44^{b}

Means in the same column bearing different superscripts are significantly different

5.4.2 *Assessment of antibody response of F_4 progeny of divergently selected Nigerian local chickens to Newcastle disease vaccine*

Using the fourth generation (F_4) chicks from the divergent selection study, we evaluated the serum haemagglutination inhibition (HI) antibody titres to Newcastle disease virus vaccine. The chicks were so vaccinated at six weeks of age and the antibody response were evaluated a week after. Sex of chicks had no significant effect ($P > 0.05$) on the HI titre seven days after Newcastle disease vaccine administration (Adenaike *et al*., 2019c). Genetic line and genetic line by sex interaction significantly ($P < 0.05$) influenced antibody titre values post-vaccination favouring the birds from the high antibody titre chicken lines in both the main effect and the interaction effects (Tables 16 and 17). The study showed that the divergently selected chicken lines would retain their immune titres when actually challenged with Newcastle disease. In which case, it is recommended that high antibody titre chickens be used for breeding programmes since they will be less susceptible to virulence of the Newcastle disease virus.

Table 16: Effect of Sex and genetic line on the antibody titres at seven weeks of age of F_4 chicks challenged with Newcastle disease vaccine.

Parameters	Sub-class	HI Titre ± SE
Sex	Male	6.45 ± 0.81
	Female	7.13 ± 0.62
Genetic line	High antibody titre line	7.59 ± 0.45^{a}
	Low antibody titre line	4.72 ± 0.31^{b}

HI: haemagglutination inhibition; SE: Standard error. Means in the same column bearing different superscripts within parameter are significantly different ($P < 0.05$). Source: Adenaike *et al.* (2019c).

Table 17: Effect of genetic line by sex interaction on the antibody titres at 7 weeks of age of F_4 chicks challenged with Newcastle disease vaccine.

Genetic line/sex	HI Titre ± SE
Female HTL chicks	8.04 ± 2.02^{a}
Male HTL chicks	7.25 ± 0.48^{a}
Female LTL chicks	4.21 ± 0.47^{b}
Male LTL chicks	4.26 ± 1.20^{b}

HI: haemagglutination inhibition; SE: Standard error. HTL: high titre line; LTL: low titre line; Means in the same column bearing different superscripts are significantly different ($P < 0.05$). Source: Adenaike *et al*. (2019c).

5.4.3 *Assessment of immune response to attenuated Salmonella of F_4 progeny of divergently selected Nigerian local chickens*

We also carried out a study to assess the immune response (in this case, haematological parameters) of the F_4 progeny of divergently selected Nigerian local chickens in response to attenuated *Salmonella*. *Salmonella* infection has over the years been a major cause of mortality

in chickens and this disease can be transmitted to humans through egg and chicken consumption. The prevention and control of this disease can be better handled through genetic approach which can be a lasting solution compared to the repeated use of antibiotics and vaccines which usually increases cost of production. In this regard, two distinct chicken lines of the local chicken were maintained over several generations on the basis of antibody titre levels (high or low) and the birds were also categorised as normal feather, naked neck and frizzle feather. The F_4 chicks from each titre line, sex and major gene were challenged with attenuated *Salmonella* at eight weeks of age and haematological parameters were assessed both prior (day before) and after this challenge (day 1, 8, 15, and 22). These parameters were packed cell volume, red blood cell count, haemoglobin concentration, white blood cell count, heterophils, lymphocytes, monocytes, eosinophil, basophil, and heterophils-lymphocytes ratio. Sex had no significant ($P > 0.05$) effect on any parameter. Genotype – antibody titre had significant ($P < 0.05$) effect on PCV, Hb and RBC favouring the high antibody titre local naked neck birds. Sex by genotype-antibody titre interaction had a significant ($P < 0.05$) effect on PCV, Hb and RBC, favouring the male high antibody titre naked neck birds (Opoola *et al.*, 2020). The other parameters did not differ significantly among the groups. The male high antibody titre naked neck chickens were the least affected by attenuated *Salmonella*, while the female low antibody titre normal feather chickens were the most affected.

The research on divergent selection is still on-going. We are presently working on the sixth generation to concretise the findings.

Plate 25: High titre frizzle cock

Plate 26: Low titre frizzle cock

Plate 27: High titre normal feather cock

Plate 28: Low titre normal feather cock

Plate 29: High titre naked neck cock

Plate 30: Low titre naked neck cock

Plate 31: High titre normal feather hen

Plate 32: Low titre normal feather hen

Plate 33: High titre frizzle hen

Plate 34: Low titre frizzle hen

Plate 35: High titre naked neck hen

Plate 36: Low titre naked neck hen

Plate 37: Control male chickens

Plate 38: Control female chickens

Plate 39: Control female chickens

6.0 SUMMARY

Apart from our research on the mapping of quantitative trait loci for performance traits and the various works done on other livestock species as reported earlier in this Lecture, our work on the Nigerian local chicken can be summarized under the following major headings:

1. The effects of the major genes of frizzling and naked neck.
2. Feather pigmentation and characterisation of effects on performance.
3. Skin pigmentation and characterisation of effects on performance.
4. Rare morphostructural features and their occurrence in the local chicken.
5. Gene frequencies for the various conditions in the local chicken.
6. Genetic differences in the adaptability and heat tolerance traits in the local chicken.
7. Growth performance of the local chicken up to 20 weeks of age.
8. Modelling and Prediction of growth in the local chicken as affected by genetic differences.
9. Semen characteristics of the local chicken as affected by major genes.
10. Fertility and hatchability of local chicken eggs as affected by major genes.
11. Egg production indices in the local chicken under various conditions and in comparison with exotic chicken strains.
12. Genetic parameter estimates (heritabiliies, repeatabilities and genetic correlations of key productivity, adaptability and livability traits in the local chicken.
13. Haematological parameters of the local chicken as affected by major genes.

14. Disease tolerance and resistance studies in the local chicken as affected by major genes.
15. Autosexing studies on the local chicken.
16. Crossbreeding results on the local chicken.
17. Diallel crosses and combining ability of strains of the local chicken.
18. Blood protein polymorphisms in the local chicken.
19. Divergent selection over several generations in the local chicken and key performance indices.
20. Genetic Improvement results in the local chicken.
21. Carcass traits of the local chicken as affected by major genes.
22. PCR-RFLP polymorphisms and associated traits in the local chicken.
23. SNPs and associated traits in the local chicken.
24. Genetic diversity in the local chicken assessed using microsatellite markers.
25. Genetic diversity in the local chicken assessed using Random Amplified Polymorphic DNA(RAPD) markers.
26. Gene expression studies in the local chicken.
27. Sequences of some genes of the local chicken in the GenBank complete with accession numbers.

Apart from providing crucial avenues for students' training and research at Bachelor, Master and Doctoral degree levels over the years, these research efforts and findings constitute a huge volume of reports in literature on the genetic evaluation, characterisation and selection of the local chicken with respect to productivity, adaptability and

livability as influenced by several genes we have worked with and their polymorphisms. They also clearly belie the erroneous and previous characterisation of the Nigerian local chicken as nondescript.

7.0 SUCCESSES REGISTERED BY THE DEPARTMENT OF ANIMAL BREEDING AND GENETICS, FUNAAB, ABEOKUTA OVER THE YEARS

It is important to highlight the very outstanding successes registered by the Department of Animal Breeding and Genetics over the years. These include:

1. Poultry Selection and Improvement
2. Special recognition as a reference point in Nigeria on work on the local chicken. Scientists and researchers come from afar to obtain foundation stock on local chickens for their own research.
3. The Department as the first in Nigeria on Animal Breeding and Genetics.
4. The Department has the richest assemblage of animal breeders and geneticists among all universities and institutions in Nigeria.
5. The Department produces the highest number of PhD degrees in Animal Breeding and Genetics each year compared to any other university in Nigeria. **Permit me to humbly state my modest contributions in this regard. To date, I have supervised to successful completion a total of 24 PhD students (13 as Major Supervisor and 11 as Co-Supervisor), 41 Master students (28 as Major Supervisor and 13 as Co-Supervisor) and more than 150 final-year undergraduate students. By the grace of God, two of my former PhD students are professors today.** In addition, one of my former M. Agric students is an Associate Professor in an American university today.

6. Successful integration of molecular genetic approach in the teaching and research in animal breeding and genetics.
7. Attraction of patronage of our Postgraduate programmes from graduates of other universities in Nigeria.

8.0 SUGGESTIONS

1. There is the need for the conservation of our indigenous animal genetic resources in Nigeria. It is recommended that a Centre for the Conservation of Indigenous Animal Genetic Resources be established. This Centre should be separate from NACGRAB to avoid conflict on crop conservation. The genetic basis of the rare conditions in the Nigerian local chicken earlier discussed in this Lecture and the need to conserve them for the benefit of this and future generations clearly justify this recommendation.
2. There is also the need for the establishment of Multiplication Centres for the Indigenous Animal Genetic resources with emphasis on genetic purity and breed distinctiveness.
3. There is also the need for a full, comprehensive and up-to-date livestock census in Nigeria We cannot continue to rely on outdated data on animal populations in Nigeria.
4. There is the need for increased funding by relevant agencies for research in universities.
5. Eateries, caterers, food vendors and domestic consumers should always physically remove the chicken skin and underlying fat before cooking, roasting, or grilling so as to enhance the quality of chicken meat and minimize the intake of chicken fat by consumers.

6. Our work has also provided research evidence that chickens can serve as model in our concerted efforts to dissect the genetic basis of adiposity and obesity and associated conditions in humans.
7. We commend the government for the establishment of a distinct Department of Animal Husbandry Services at the federal level to co-ordinate the formulation and implementation of policies geared towards the development of the animal agriculture sub-sector in Nigeria. It is however important that more well-qualified and appropriate personnel are appointed to man this and other key areas of the food animal sub-sector of the Nigerian economy.
8. The creation of new research institutes to handle research on specific animal species is long overdue to ensure that targeted attention is focused on each animal species and to improve their contributions to the food and nutritional needs of Nigerians.
9. There is also the need for a lasting solution to the incessant cattle herders – crop farmers' clashes in different parts of the country and an end to the carnage and displacement of persons that have been the results of such clashes. The country cannot afford to leave this matter without a lasting solution.

9.0 APPRECIATION

I would like to pay homage to the current Vice-Chancellor of this University, Prof. Felix Kolawole Salako, for assiduously working to provide the enabling environment under which our University has continued to thrive and excel. I also would like to thank all former Vice-Chancellors of the University for their immense contributions to the development of FUNAAB. They are Prof. N. O. Adedipe, Emeritus Prof. J. A. Okojie, Late Emeritus Prof. I. F. Adu, Prof. Ishola Adamson, Prof. O. O. Balogun, Prof. O. B. Oyewole and Prof. O. A. Enikuomehin.

I pray that the good Lord will continue to bless the living with good health and long life in Jesus' name.

I would also like to appreciate this great University for the wonderful opportunities it has bestowed upon me over the years to live my dreams. Apart from my core responsibilities as lecturer in teaching, research and community service, I have had the privilege of serving this great University at various times as Coordinator of Department, Acting Head of Department, Head of Department, Dean, Student Affairs, Dean, College of Animal Science and Livestock Production (two terms), member, University Senate (since 1990), member, Governing Council (for four years), University Orator (since 2004), Chairman of at least 38 statutory or special committees, and member of at least 103 statutory or special committees.

Permit me to use this opportunity to appreciate my academic supervisors: Prof. J. O. Akinokun (at Ife) and Late Prof. L. O. Ngere (at Ibadan). They are two of the foremost and finest animal breeders and geneticists Nigeria has ever known. I drank from their highly-esteemed and cherished fountains and my life has never been the same again. I am also grateful to Prof. J. A. Oluyemi and Prof. G. N. Egbunike, who as Heads of Department recommended me to be Teaching Assistant in the Department of Animal Science, University of Ibadan, Ibadan and kept me at it for three years.

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Finally, on this occasion, I would like to tell about a journey I made across the Niger some years ago. In September 1977, I boarded one of the luxury buses at Onitsha on my way to Ile-Ife in quest of the proverbial golden fleece. I had with me just a suitcase and a small bag, with just about everything I had in those days in them. I got to Ile-Ife and God turned my life around with an undeniable and unmistakable spiritual regeneration experience along the way. He saw me through the inimitable and the giant-humbling Great Ife! without a carry-over which was unusual in those days. Today, I want to thank God for His blessings upon my life. Next, I went to Ibadan against all odds, thinking that Ibadan was going to be a much friendlier place, a walk-over, if you like. Well, inspite of the great odds I faced at Ibadan, God saw me through successfully. Today, I want to thank God for His blessings upon my life. After Ibadan, I came to Abeokuta and God has seen me 'through all the changing scenes of life' up to this moment in time with uncountable blessings I could never have imagined. Today, I want to thank God for His blessings upon my life. He is worthy of all praises. This is my song of appreciation to the Almighty God:

Then sings my soul, my Saviour God to Thee,
How great Thou art, How great Thou art;
Then sings my soul, my Saviour God to Thee,
How great Thou art, How great Thou art.

Thank you for your kind attention. May God bless you all.

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