ENHANCING ANIMAL PRODUCTIVITY THROUGH BIOTECHNOLOGY

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INTRODUCTION

Livestock products such as meat, milk, egg and hides account to about 25% of the total agricultural production in Africa (FAO, 1998), while animal traction and manure for fertilizer and fuel were estimated to be about half of the combined value of meat, milk and eggs. Despite these values, animal productivity per head is far below global standards with milk and milk products from cattle averaging only 13 and 306 kg/head respectively and 2.5 and 7.9 kg from small ruminants.

Productivity of the indigenous animals is hampered primarily by genetic components, shortage of feed, disease, and management factors in addition to policy and institutional problems. Economic losses due to disease is so enormous that it represents an immediate target for solution using both conventional methods and/or biotechnological tools.

The need for improvement

The human population in Nigeria is projected to grow at an annual rate of 2.2% to the year 2025. Population growth has surpassed food production and at the moment it is estimated that about one quarter of the population are already facing chronic food insecurity.

Livestock production has to improve if the ever-increasing demand for animal products and services are to be met. The genetic merit of many of the available genotypes have never been unfolded. The challenge before us is to characterize, conserve and improve the indigenous stock to a satisfactory level without the indigenous stock with possible introduction of genetic stock from outside the country where it is highly essential and feasible. The increase in supply of animal products would only be achieved from concerted efforts and improvements in both the horizontal and vertical component of production.

Potentials of Nigeria’s livestock for improvement and contribution to global livestock industry

With almost 125 of Tropical Livestock Tails of animal population in Africa available in Nigeria alone (Table 1) (i.e. 12.5 million) out of the 147 million TRLLU (ILCA, 1993), the contribution of Nigeria to the genetic resource of livestock species, breeds and strains in the world is highly significant. Although data on the numbers and their characteristics are still very limited. The different species and breeds have better survival are basically, have high degree of heat tolerance, are partially resistant to many of the prevailing diseases and possess the ability to survive long periods of feed and water shortages under hostile environments and poor management practices. These properties are basically genetic and have been acquired through natural selection over hundreds of generations, hence the indigenous livestock breeds are representatives of unique genetic traits which could be used in other parts of the world. Most populations of indigenous livestock in Africa in general and in Nigeria in particular have been subjected to little or no deliberate selection for productivity. Selection is the basic programme used both by nature and by man to enhance the animal population in any programme for livestock improvement, the first difficulty and sometimes, the greatest is the decision on the objective for reasonable period of time (sustainable).

In other words, the process of selection involves the choice or preference of certain animals to others which subsequently leads to changes in frequency of particular genes between parents and offspring generations and in this way performance might be affected.

Selection as normally practiced works only on the additive part of the genetic variation, VA, which is the chief component of resemblance between relatives. This ratio of additive to total variation VA/VV referred to as heritability ranges from low to medium to high. When the value is high, more rapid response to selection is expected whereas on the other hand when it is low, progress might be slow or there might be total lack of progress. The response to selection per generation on the other hand depends not only on the heritability but also on the selection pressure applied, which is reflected in the average superiority of the selected parents over the mean of their group and the proportion of animals selected (i.e., selection differential) Falconer, 1965).

In practice, a lot of attention is paid to make accuracy of selection as high as possible by using many records on the same individual and information about the performance of the individual’s relatives and his or her progeny.

Although this trend to substantially increase the interval between generations, a practical benefit of genetic improvement must be measured as progress per year, there must be avoidance of inbreeding in selection programmes, such that adequate number of sires in the top group within the herd should be selected. Although large numbers of breeding males (sires) will reduce genetic superiority, this has to be done to ensure long-term effectiveness of the programme.

Breeding and Improvement technologies

Intramm production of milk, meat, eggs, and animal fibres has been based on extensive records of pedigree performances which are essential for accurately identifying superior individual animals.

The science of population genetics developed in the 1930s and 1940s, by scientists in Europe and North America has since been effectively applied to achieved substantial increases in animal production and productivity in developed countries. Progress has been greatest in dairy cattle, pigs and poultry. Compared with improvement achieved 30 years ago, today’s dairy cow in Europe and the United States, and other industrialized countries produces around 5,000 kg of milk per cow per year and sometimes twice as much milk. Fat thickness has declined by almost today’s; pigs, while the broiler chicken today matures in 6 weeks instead of 3 months (NRC, 1993). By contrast, average annual milk production per cow is 5,000 kg in Africa, 610 kg in Asia and 900 kg in South Africa (Head, et al., 1992).

Genetic improvement of local domestic stock is therefore not only a very important option but a condition for the development of the livestock sector in developing countries.

Traits and Improvement Methods

Many breeders usually want to improve every trait or at least several traits at the same time. The more the traits that are included in the selection process, the less is the progress for individual traits and vice versa. Progress could result from inclusion of too many traits. This paper emphasizes the importance of getting the objectives right and pursuing the objective to a logical conclusion.

Genetic traits

Breeds with unique physiological or other characteristics are of great interest in the global livestock development.
In the past, such breeds have provided missing links in the genetic history of livestock species through the study of blood groups, protein polymorphisms and morphological characteristics. The developing sciences of molecular engineering to identify DNA sequences that indicate transgenic animals for products used in pharmaceutical industries are still far from application in Nigeria. Yet, the current stage of livestock improvement programmes generally require population sizes that are larger than can be managed by single institution farming practices. Thus, the current stage of livestock improvement programmes must be put into place to accommodate the need of mini-cattle, large volumes of animal life, historical and precise animal data needed in livestock improvement programmes, and the ability to disseminate data and information both nationally and internationally at least within the African continent.

Genetic diversity

Genetic diversity within a livestock species is reflected in the range of types and breeds that exist and in the variation that is present within each genotype. It has been shown that differences among breeds substantially exceed those within breeds, suggesting that compensatory factors occur in their unique genetic and geographic locations. The presence of breeds with distinct characteristic attributes, and the genetic diversity at high frequencies, greatly enhances the efficiency of the improvement process. The recombination of favourable genes within major commercial stocks under intensive selection have allowed development of animals with productive capacities that greatly exceed those of their ancestors. The scope of genetic diversity within commercial stocks is still largely unexplored, and the potential for increasing productive capacities to change in response to new demands in global livestock improvement programmes, if only fed semi-productive systems that can produce enough and even surplus quantities of meat and milk, can be found in Nigeria's livestock improvement programmes.

Enhancing Productivity

Genetic improvement is one of the most effective strategies available for improving the performance of farm animals. It is relatively slow compared to some other methods such as improved feeding but it is permanent and cumulative and in most cases highly cost effective and sustainable. Genetic improvement has been used effectively in pig and poultry industries in many countries. Rules of genetic improvement depend on four main factors:

- Selection intensity achieved
- Accuracy with which genetic merit in the trait of interest is predicted
- Amount of genetic variation in the trait of interest
- Generation interval

The main opportunities for breeders to accelerate rates of improvement are through choice of the highest genetic merit predictors. Selection indices should include traits that are highly genetic merit predictors and that are not correlated with other traits. A better understanding of the relationships between traits of production and those affecting adaptation to local environments would help in the production of more sustainable breeding programmes. In most cases, the techniques to achieve these improvements are already available but need to be fine-tuned and applied more widely.

Reproductive Technologies

It is possible to achieve much higher selection intensities in species from breeds with a high reproductive rate than in those with lower reproductive rates. Similarly, shorter generation intervals can be achieved in species or breeds which exhibit sexual maturity at a younger age. Because of the biological advantage in reproductive rates, higher rates of genetic change are possible in pigs and poultry than in ruminants. In cattle on the other hand, the major trait of interest is again sex limited and can only be increased fairly late in life. This therefore prompted breeders of these species to look into new reproductive technologies that can accelerate progress in genetic improvement programmes in ruminants.

Reproductive technologies

There are two types of new technologies which can have major impact on rates of livestock improvement. These are:

- Reproductive technologies
- Molecular genetic technologies
These reproductive technologies include:
- Artificial insemination (AI)
- Multiple ovulation, embryo recovery, and embryo transfer (MOET)
- Intracytoplasmic sperm injection (ICSI)
- Embryo splitting and nuclear transfer
- Embryo and semen sexing
- Cloning (mass production of identical embryos)

Many of these techniques are not only of potential value in accelerating response to selection in breeding programmes, they have potentially a major impact in disseminating genetic improvements from elite to commercial lines of livestock industries. Although techniques for selection are usually useful in dissemination not all techniques of value in dissemination are useful in selection.

**Artificial Insemination**

This technique has been available to cattle breeders for over 50 years to enhance reproductive rates of males. The development of improved techniques for extending and freezing of cattle semen has also augmented its benefits.

AI allows much higher selection intensities among males than those possible with natural mating. Also, the desired number of progeny can be produced sooner by AI than by natural mating, hence male generation interval can be reduced.

AI contributes to more accurate evaluation of genetic merit as well as permitting large-scale progeny testing in many breeds. As a result, substantial rates of genetic improvement have been achieved in several countries through the use of AI in well-designed cattle breeding schemes.

The fact that AI in cattle is relatively cheap and simple, allowing access to very reliable proven, high genetic merit animals, means that it is currently the most effective method of disseminating genetic improvement to commercial herds especially in dairy cattle breeding schemes.

In commercial beef cows on the other hand, because of the extensive production system that makes estrus detection more difficult, the use of AI is limited. However, with the growing use of estrus synchronization in commercial beef herds, access to bulls of higher genetic merit becomes possible and use of AI more practical.

The poor conception rate with cervical inseminations of frozen semen in beef has limited the use of AI in this species. Much success had been achieved with laparoscopic intra-uterine inseminations of frozen semen, but the use of this technique is highly limiting. Any technique that can produce high conception rates and use less invasive insemination method than laparoscopy would have a major impact on both rates of genetic and dissemination of genetic improvement in sheep and goats industries.

**Multiple Ovulation Embryo Transfer (MOET)**

Over the last few decades, increasingly reliable procedure have been developed for super-ovulation, embryo recovery, and freezing and transfer of embryos in cattle (Woolham and Wilmut 1989).

In sheep, the embryo recovery and transfer techniques are only possible with laparoscopy or surgery (Dingwall and Mc Kelvey 1993, Gordon 1997).

The use of MOET has accelerated.

- Within-breed genetic improvement programmes
- International trading of genetic materials with potential advantages in economy, animal welfare and disease control
- Accelerated breed substitution by multiplication of newly introduced breeds
- Conservation of genetic material by freezing embryos from valuable animals and from rare and endangered breeds or species.

MOET offers similar benefits in selection of females as those offered by AI. In males though the benefits are smaller and are not easily disseminable. The major advantages are found in:

- Increased selection intensities for females
- Reduced generation intervals
- Accuracy of evaluating embryo donors
- Increased availability of fertile cattle progeny

Since mid 1970s, potential impacts of MOET on rates of improvement in cattle (beef and dairy) and sheep have almost doubled compared to conventional breeding schemes. However, without current MOET technique, donor females produce relatively few embryos compared with rates of semen that can be produced from AI in males. For this reason and for complex techniques involved, MOET remains for more expensive than AI and so less attractive as a means of dissemination.

**In-vitro Embryo Transfer (IVF)**

Over the last few decades, a great deal of effort has gone into developing techniques for the in-vitro maturation, fertilization and culture of eggs for farm animals as well as humans.

In vitro means in glass as opposed to the body. The aim for this research in humans is to allow certain types of infertility to be overcome (e.g. those due to blocked fallopian tubes) or to allow the use of donor men or eggs in cases of complete infertility of one partner.

The main aim of developing this technique in farm animals is to allow the use of thousands of eggs present in the ovaries of female animals at birth, most of which never develop to point of ovulation (Gordon 1974, Gordon and Lu, 1990, Wilmut, et al., 1992).

In U.K. and New Zealand (1990) studied the performance of companies established for collection of eggs from slaughtered beef heifers in abattoirs, they discovered that despite the ready supply of ovaries only few transferable embryos are possible per cow. Also most of transferred embryos resulted in very low calves and only 10% survive.

**Semen and Embryo Sexing**

Semen sexing has been the holy grail of reproductive technologies for decades. Using real or apparent physical differences between X and Y bearing sperm chromosomes as the basis for separation, the procedure exploits differences in mass, surface charge, antigenic properties and buoyant density of X and Y bearing sperm but success rate and repeatability have usually been very low (Cram and Johnson, 1975, White 1989).

In the last few years a more reliable technique for semen sexing using the fact that X and Y bearing sperm chromosomes differ slightly in their DNA content was developed. Using the technique called “Flow cytometry”, the differences in size can be detected. The techniques staining sperm with fluorescent stain and using differences in fluorescence when the cells pass through a laser
Molecular genetic technologies

To date, most selection in livestock has been practiced with little or no knowledge of what is happening at the DNA level. Selection has been on the effect of the genes rather than directly on the genes themselves. Some traits are controlled by single genes and have a large effect on the phenotype. However, for most traits of economic importance, the performance is affected by the genotype at many different loci; they are influenced by the environment, so the link between the gene and the phenotype is further complicated. While their relatives to estimate the additive effect of all loci affecting the trait and at the same time removing environmental influence they are good at predicting the average genetic merit of records of their own. Under the new development techniques, molecular technologies are already having impact or may have impact in the future.

The existence and gross structure of chromosomes has been known since the early 1900s, the chemical structure of DNA and its role in inheritance came into effect in 1953. However, it is only relatively recently that advances in molecular and cell biology allowed the identification and location of individual functional genes and the sequence of the DNA on chromosomes. These in essence provide molecular tools to assist conventional selection procedures and allow gene transfer.

These recent advances include:

DNA sequencing

Nucleic acid sequencing has also been used to address virtually any systematic problems in population genetics, although it is not the most efficient or cost-effective. When two organisms are distantly related, the conserved (constant) sequence region which exhibits extensive sequence homology is used whereas when closely related, the variable region which displays different sequences are used. Once again, because genetic differences between breeds are low as detected in cattle, direct sequencing is an unlikely candidate for population analysis. In order to resolve the level of variation needed to distinguish breeds, the stretches of DNA to be sequenced would be prohibitively long. It will be labour intensive, involve use of expensive equipment, enzymes, reagents and radio-active labelling.

Discovery of restriction enzymes

These are enzymes produced by bacteria which are capable of cutting up sequences of DNA. They act as molecular scissors to protect the bacterium from attacking viral or foreign DNA (Nisholans 1980, Osde 1982). Different restriction enzymes recognize different sequences of 4 to 6 bases pairs in DNA. They make their cuts wherever they come across these sequence of bases in a strand of DNA.

For example, one commonly used restriction enzyme recognizes the sequence GAATTC. Treating or digesting identical sequences of DNA with the same enzyme produces identical sets of fragments each of a specific size. Conversely, treating different sequences of DNA with same enzyme produces sets of fragments of different sizes. Hence the enzyme are useful in detecting similarities and differences in the DNA sequences of different organisms.

For example, if animal A has 3 restriction sites

\[ A \underbrace{\text{V}}_{5kb} \underbrace{\text{V}}_{2kb} \underbrace{\text{V}}_{5kb} \]

hence the enzyme is able to cut 2kb and 5kb pairs long sequences

And an animal B with only 2 restriction sites

\[ B \underbrace{\text{V}}_{7kb} \underbrace{\text{V}}_{5kb} \]

Hence in one at 7kb pairs fragments

A third animal or an animal with these sites

\[ \underbrace{\text{V}}_{5kb} \underbrace{\text{V}}_{2kb} \]

i.e. two restriction sites on one strand and two sites on the other strand will have the 3 fragments
Detection of fragment sizes.  

**Electrophoresis**  
Fragments of different lengths (resulting from digestion with enzymes) can be separated or detected by applying samples of the fragments to a mixed sized gel and applying electric current. This technique is called Electrophoresis.  
The fragments move across the gel at different rates depending on their size. Large fragments move slowly, small fragments move faster. The gel is then stained or treated in a variety of ways to show up a series of bands each band representing DNA fragments of a particular size. Where different samples, i.e. DNA from different animals are run side-by-side on the same gel it is easy to tell whether or not the samples contain DNA fragments of a similar length.

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**Protein Electrophoresis**  
Here, a protein solution is electrophoresed through a gel with an enzyme specific reaction that highlights the locus whose allele migrates due to electric charge caused. Although this is widely in use, it has limitations in that relatively low levels of polymorphism are found at protein level resulting in lower taxonomic level for the population.

To multiply sequences of DNA rapidly.
There are two methods used for rapid multiplication of DNA:
- One: Cloning DNA
- Two: PCR reaction

**Cloning**
This is the method used in living cells. For example, mammalian DNA fragments which are to be multiplied can be incorporated into the DNA from a vector such as plasmids. Plasmids are small self-replicating circle of double stranded DNA which exists independently in some bacterial cells. Incorporation of the DNA is achieved by treating the vector DNA with the same restriction enzyme used to create the fragment of the mammalian DNA. Essentially, this means that the mammalian DNA fits into the gap left in the vector DNA. The DNA is introduced into rapidly reproducing host cell where they are produced along with the host cell. After many cycles of replication many copies of the original DNA fragments can be extracted from the host cells. The fragment can be produced when the fragment are introduced into Yeast Artificial Chromosomes - YACs.

**Polymorphic Chain Reaction (PCR)**

The PCR reaction is the procedure by which DNA is multiplied in a test tube rather than in living cells. It is called Polymorphic Chain Reaction (PCR). Polymorphisms are enzymes involved in the normal replication of DNA in the cell. In the laboratory, the DNA sequences are multiplied by adding a heat-stable version of this enzyme together with two primers (short fragments of DNA) which start off the replication of the specific DNA sequence and a supply of the DNA bases ATGC. When the mixture is heated up, the DNA in the fragment of interest is denatured causing the strands to separate. Subsequent rapid cooling causes the primers to "anneal" on complementary sequences of the DNA and to initiate the process of copying the sequences of interest on each of the two separated strands. Each cycle of heating and cooling produces doubling of the number of copies of the original DNA sequence. So in a matter of hours sufficiently large quantities of DNA are produced for characterisation.

The PCR has the advantage of:
(i) multiplying specific sequence of DNA depending on the primers used;
(ii) it is most effective for relatively short DNA sequences;
(iii) only small amounts of DNA are needed to start with, e.g. hair follicles, nails etc.

**Marker Assisted Selection**

Here, marker assisted loci are used either to identify and locate useful traits or to describe population structure. Although the same marker systems can be used for the two different approaches, experimental design however differs in the two approaches.

The characterization of production traits in livestock species using molecular markers is currently a very attractive area of research as we now have DNA maps, Fingegmap, Sheepmap, etc., in production in several laboratories all over the world. The identification of such markers requires however, the examination of large pedigrees or populations which are carefully phenotyped before genotyping. Some of these techniques in use include.

Development of markers

Any identifiable segment of DNA in the genome (the entire genetic code of animals) which shows variation between animals can be used as a marker. Markers may be all or part of a functional gene, or part of the genome which does not code directly for the production of a protein.

Several markers have been developed. They are of three basic types: genotyping, marker assisted selection, parentage verification and product identification. There are two types of markers currently of most value in livestock genome mapping and of value in marker assisted selection. The first is the Restriction Fragment Length Polymorphism (RFLP). This is a method that utilizes restriction enzymes to cut the DNA in the number and position of sites at which the animals vary. The variation in termed restriction polymorphism, i.e. different forms. The RFLPs were used to detect variation in the DNA sequence of different animals using:

(i) PCR to multiple the fragments containing sites;
(ii) Digesting the multiple samples with one or more restriction enzymes; and
(iii) Separating the digested fragments from each animal in adjacent columns of a gel.

(iv) Distinguishing different genotypes from the set of DNA fragments produced by staining or use of a labelled probe.
Restriction fragment length polymorphisms (RFLPs)
This involves use of DNA fragments generated by restriction enzymes which are blotted on to membranes that had previously been probed with cloned radio-labbed DNA bound to single locus. It has application in the study of nuclear and mitochondrial DNA for genetic distance, population variation, gene flow, effective population size, patterns of historical biogeography and the analysis of parentage relationships. The only problem is the lack of resolving power when dealing with very closely related groups (Thallman et al., 1989).

RFLPs are often located in functional genes which increases their value as potential markers. However, their major limitations is that a given RFLP only involves two different variants or alleles so animals can only be assigned to only a small number of classes or genotypes (Archibald and Haley, 1993).

Mini and micro-satellites
Throughout the genome, there are many regions where the same sequence of base pairs is repeated several times, and so end. These repeat sequences are termed minisatellites or microsatellites depending on the size of the sequence of the base pairs which get repeated. The repeated sequences in minisatellites are 10 to 60 pairs long while those in microsatellites are only 2 to 5 base pairs long (Archibald and Haley, 1993; Nicholas, 1996).

The number of times a given sequence of bases is repeated varies between animals. For example, the two-bias AC may be repeated anywhere between 16 and 22 times (Microsatellites). Because of this variation these repeat sequences are used as markers.

Simple Tandem Repeats (STRs) or Microsatellites are relatively new classes of genetic markers. In the past couple of years, they have become markers of choice for gene mapping and are increasingly being used for population studies (MacHugh et al., 1994). Microsatellites are simple di or tri-nucleotide tandem repeats of very short nucleotide motifs. The di-nucleotide repeats are found to be most common in mammalian genomes. A typical microsatellite locus may consist of a stretch of DNA with the base sequence CA, repeated 12 times, i.e. (CA)₁₂, when the unique sequence flanking both ends of the repeated sequence is known, the microsatellite is preferrentially amplified using聚合酶链式反应 (PCR). Different length classes (alleles) vary in the number of repeats and can be separated using polyacrylamide gel electrophoresis (PAGE) (Fig. 4). This class of marker is highly polymorphic, displaying many different alleles for a given locus. The primary disadvantage of this technique is that prior knowledge of the DNA sequence is required to allow the design of PCR primers to use. However, there are many private organisations with public domain data bases of accumulated sequence where many economically important species are well represented.

The main advantage of microsatellite is the large number of variants or alleles present at a particular site or locus. Which means that animals can be assigned to many different classes or genotypes. Hence microsatellites are the markers of choice in livestock genome mapping and they are likely to be of most value in marker assisted selection.

Unique DNA

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AC   AC   AC
0000000000 0000000000
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PCR

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electrophoresis
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Electrophoresis of PCR fragment of DNA - There are 3 alleles at this locus. Individual animals have two copies of any of these alleles, as homozygous or heterozygous.

System involved in genotyping animals using RFLP or microsatellite

DNA extracted from parents and progeny

Parents

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A x B
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C D E F G
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Marker reagents are added to animals DNA
Restriction enzymes or Microsatellite primers ➔ A B C D E F G H
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Restriction length polymorphisms (RFLPs)

This involves use of DNA fragments generated by restriction enzymes which are blotted on to membranes that had previously been probed with cloned radio-labelled DNA bound to simple loci. It has application in the study of nuclear and mitochondria DNA for relatedness. The only problem is the lack of resolving power when dealing with very closely related groups (Thallman et al. 1989).

Fals and microsatellites

Throughout the genome, there are many regions where the same sequence of base pairs is repeated several times and in tandem. The repeat sequences are termed microsatellites or minisatellites depending on the size of the sequence of the base pairs which gets repeated. (Archibald and Haley, 1993; Nicholls, 1996).

The number of times a given sequence of bases is repeated varies between animals. For example, the two bases AC may be repeated anywhere between 15 and 22 times (Microsatellites). Because of this variation, these repeat sequences are used as markers.

Simple Tandem Repeats (STRs) or Microsatellites are relatively new classes of genetic markers. In the past couple of years, they have become markers of choice for genetic mapping and are increasingly being used for population studies (MacHugh et al., 1984). Microsatellites are simple di or tri-nucleotide tandem repeats of very short nucleotide motifs. The dinucleotide repeats are found to be most common in mammalian genomes. A typical microsatellite locus may consist of a stretch of DNA with the base sequence CA, repeated 12 times, i.e., (CA)12. When the unique sequence flanking both ends of the repeated sequence is known, the microsatellite is preferentially amplified using polymerase chain reaction (PCR). Different lengths classes (alleles) vary in the number of repeats and can be separated using gel electrophoresis (Fig. 4). This class of markers is highly polymorphic, displaying many different alleles for a given locus. The primary disadvantage of this technique is that prior knowledge of the DNA sequence is required to allow the design of genotypically important markers to be made.

The main advantage of microsatellites is the large number of variables or alleles present at a particular site or locus. This means that animals can be assigned to many different classes or genotypes. Hence microsatellites are the markers of choice in livestock genotyping and they are likely to be of most value in marker assisted selection.

Unique DNA (AC) (AC) (AC) 000000000000

PCR

Electrophoresis


Electrophoresis of PCR fragment of DNA. There are 3 alleles at this locus. Individual animals have two copies of any of these alleles, as homozygotes or heterozygotes.

System involved in genotyping animals using RFLP or microsatellite

DNA extracted from parents and progeny

Parents

A x B

Progeny:

ABCDEF

Marker reagents are added to animals DNA

Restriction enzymes or Microsatellite primers 

A B C D E F G H
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**Inheritance pattern of marker alleles**

This system had been used to type for genetic diversity in some Nigerian cattle, sheep and goat breeds as well as genetic linkage studies of some 5 markers on chromosomes 17, 19 and 20 using the International Resource Families (Adebowale, et al, 1996, 1995a & b).

Due to their exceptional variability and relative ease of scoring, microsatellites are considered the most powerful genetic marker. It is typical to observe loci with more than 10 alleles and heterozygosity above 0.60.

**Random Amplified Polymorphic DNAs (RAPD).**

This is another recently identified genetic technique which does not require a prior knowledge of DNA sequence. The levels of genetic variation utilizing this technique is also very high although it has not yet been accepted as a tool in population studies.

**Other Genetic Systems**

Under these systems, parts of the genome with distinct modes of inheritance are sample such as autosomal, mitochondrial and Y-chromosomal DNA. Autosomal DNA are sexually-inherited, mitochondrial are maternally inherited, while Y-chromosomal DNA are paternally inherited. With appropriate technology, it is envisaged that the livestock industry in Nigeria could be revolutionized for example through characterization, conservation and utilization of rare genetic variants among the different livestock breeds.

**Livestock Improvement Stations**

There is an urgent need to establish species/community specific livestock research stations and in particular regional livestock research stations to take care of the improvement, development, utilization and intensive breed development of our livestock breeds specifically adapted to the different ecologies (Table 3). Nigeria could boast of dairy cattle breed development and improvement in the NW zone and middle-belt (Plateau) of the country using the Open Nucleus Breeding Scheme if a Dairy Research Station could be established. Even and Grassland Research, and more importantly Poultry Research Institutes are essential for the country to forge ahead in order to meet the basic animal protein demands of the populace. Not only are the animals to be developed but industrial units to process and distribute livestock products will similarly be expanded thereby creating job opportunities for the growing populace.

Niger’s manufacturing sector has continued to decline for lack of appropriate local input. Caputty utilization in most industries declined steadily from 73.3% in 1981 to 33% in 1997. One major reason for this anomaly was the reliance of manufacturers on imported inputs, the procurement of which has been complicated by movements in the exchange rate of the Naira.

The present administration should look critically at these problems of animal livestock vis-a-vis livestock products industrial base. It is suggested that:

- increased expertise in the areas of breeding and genetic improvement
- collaborative and more strategic research
- specialized institutes
- focus on facilitating basic research on problems specific to livestock production be vigorously pursued.

**Development opportunities**

Opportunities abound to increase nonruminant milk and meat production. These opportunities take different forms according to ecological zone and region:

- in the humid areas south of the country there is great and long term potential to increase production if trypanosomiasis and dermatophilosis can be controlled through multiplication of appropriate cattle breeds.
- in the sub-humid zone, there is ample opportunity in the medium term to increase forage production, hence this combined with freedom from trypano allowed greater concentration of cattle herds.
- In the semi-arid zone, seasonal mild fluctuations are available hence the potential for dairy development.

**Gel electrophoresis**

**Gel exposed to X-ray film for a hard copy**
Cattle production

- Age at first calving in the neighborhood of 36-50 months could be reduced through selection.
- Animal calving rates usually less than 50% could be increased.
- Successive calving intervals of more than 2 years could also be reduced.
- Calves from birth to weaning of 20-30% could be reduced through management.

At the same time, the southern zone could concentrate on monogastric, poultry, pigs and rabbit production.

Trypanosomiasis breeds

- In Africa, over the last 2 decades, an estimated 180 million zebu cattle have progressively entered the sub-humid savannas and in large countries the cattle livestock industry depends on trypanotolerant breeds kept in low to medium fly challenge. These production systems rely heavily on the use of chemophylactic and chemotherapeutic drugs as proven by high percentage that is over 50% of drugs used in those countries are on trypanocidal drugs.

- Economic need for carry out research in:
  - The extent of drug resistance.
  - The dynamics of resistance, and
  - Specific conditions that trigger resistance.

- Genetic differences have been reported within and between even trypanotolerant breeds. For example, reports between Timor and Galama Boran cattle breed by Murray, A. (1986) give an indication of what could be achieved if concerted effort had been directed at the selection of resistant/bound animals within the trypanotolerant breeds over the years.

- Several cattle populations in West Africa have evolved under a permanent tsetse challenge and might exhibit major difference in trypanotolerance.

- A better characterization and understanding of the scope of these differences would greatly contribute to the more efficient production of Zebu cattle in tsetse affected areas. Research to enhance trypanotolerance through genetic improvement, including genetic and gene transfer might be especially applicable here.

- A further use of trypanotolerant cattle is presently constrained by their population size of 183,668 (FRA, 1991). The present 100 million head of trypanotolerant cattle breed in Africa is far below the potential carrying capacity of the tsetse zone of 34 million, head estimated by Tchifer (1982) or 110 million estimated by FAO (1979). Africa's tsetse affected areas constitute one of the continent's underutilized resources and could play a pivotal role in alleviating its food deficit, provided appropriate research and development in Sub-Saharan Africa (de Haan, 1983) an estimated $100 million was distributed or committed to livestock development in the infested area of West and Central Africa. Approximately $60 million out of this amount was used to finance credit programmes (small holder farming and animal husbandry), $50 million for importation and distribution of trypanotolerant breeds, $10 million for basic annualization and $100 million to strengthen veterinary and livestock extension services.

- The performance of these investments had been rather disappointing the main reasons being:
  - Inappropriate macro-economic policies.
  - Inadequate institutional framework.
  - Inadequate technological packages.
  - Policy differences and exchange rates that frequently favoured the consumer, relatively unattractive to producer and not conducive to increasing productivity.
  - Introduction of parametric ranching.
  - Excessive salary costs and inflexible central administrative procedures on these ranches which is in compatible with the assertive management required in livestock farming.
  - Adaptation problem of imported trypanotolerant cattle to their new environment.
  - Inadequate use of appropriate technology in range management and sustainable cash cow eradication.

- The current trend in World Bank's funding programmes is to move away from parametric and private ranching and use of trypanotolerant cattle import, hence we would demand that World Bank lending should be directed at increasing animal production through establishment of specialized livestock breeding and research stations and the development and utilization of specialized indigenous livestock breeds.

Demand for increased animal production

- One of the major reasons for the domestication of animals was to supply food for the family of the owner. In the last century, animal food supply in the developed world concentrated on specialized farms and farm-animals that are bred and managed to express production and quality traits more efficiently. Under intensive circumstances, there is need to diversify animal products, hence need to search for genetic variation and enhancement of selection activities in farm animals in Africa in general and Nigerina in particular in the present millennium.

Driving forces

- In Europe, breeding organisations strongly influenced the composition of farm animals populations used for food production. Economic, social and environmental developments encouraged selection of highly productive breeds for use in intensive animal production systems. This decreased the contribution of low input-low output breeds to food production thereby threatening the existence of these breeds.

- Applications of the genetic sciences in the improvement of genetic ability of farm animals and the use of artificial reproduction techniques led to the development of advanced breeding schemes and advanced methods to identify the genetically superior animals within selected high productive breeds. These improvements are obtained for only a few traits. The other traits which were ignored in the selection were compensated by increasing management efforts. In worldwide animal production, molecular genetics are searching for genes which influence production, quality of products, health, and reproduction play an important role. They guarantee a high degree of heterogeneity and linkage disequilibrium which is required to detect associations between highly polymorphic markers and performance or quantitative and qualitative traits.

- Many breeds are the results of long domestication process and a long period of adaptation to local circumstances. They reflect a long history of selection between mankind and farm animals and can help to classify adaptation processes which can be worthwhile for the management of animal genetic resources in the present production system.
Within community, there is a growing awareness for the ecological value of regions as a result of vegetation, nature and farm management. Within the complex, presence of animals interwining with this complex is of great ecological significance. Hence the need to develop animal breeds that can contribute to the development of local products with an ecological image.

Rule of Nigeria in international animal genetic resources context

In 1992, the Second United Nations Conference on the Environment in Rio de Janeiro recognized the importance of farm animal genetic resources in Agenda 21 and in the Convention on Biological Diversity (CBD). Nearly all countries have signed this convention which resulted in political and social awareness of national animal genetic resources. Specific activities are now in place, directed towards the conservation of all indigenous livestock genetic resources most especially in countries whose major of these resources has been eroded over the years. The CBD considers diversity and similarly recognizes the sovereignty of each country over its own genetic resources which implies also the obligation to conserve these resources.

In 1980, the European Association for Animal Production established a working group in the field of animal genetic resources. Their major activities were to organize regular surveys of breeds of farm animals in different European countries and to improve the genetic science in conservation activities. Hence, from 1988 to 1994, the FAO and the EAAP managed the Global data bank, 21 million animal genetic resources at the Hamburg Veterinary University in Germany. To date, the Domestic Animal Diversity Information System (DAD-IS) reported 332 cattle, 407 sheep, 123 goats, 156 pig and 233 horse breeds maintained at 37 European countries (FAO, 1998). If through concerted efforts, within such a short duration, these communities could characterize and define their indigenous livestock genetic resources, Nigeria has nothing to lose but rather lack to gain if her very few animal diversity could be defined. There is something definitely inherent in these animal breeds, deposited over the years by nature that could be exploited for global utilization in the nearest future and definitely within the present millennium.

In prospects countries of the European Community, the demand for specialized feed from animal origin increases; also is the situation in Nigeria where we import several specialized animal products to feed our growing population. Besides this, prosperity increases the use of other animals like hobby farming and use of animals for sports (for example, horses in polo and house sports) in Nigeria to see is a very prosperous future. These animal breeds are available in Nigeria. Despite the fact that their development requires a large variability in the genetic variation of the species used. These breeds in Nigeria that can qualify for all the criteria. They need to be characterized, explored and properly utilized.

Growing global population

The global human population hit the 5 billion mark in 1999 and is expected to hit the 7 billion mark before the year 2030. In the past, the demand for increased food production has been satisfied by a combination of genetic improvements, greater farming inputs and cultivation of more land for agriculture. It can hardly be expected that in the future, the agricultural inputs can still be increased and that more land can be utilized. Therefore, genetic improvement is the most viable approach to meet increasing demand for food from animal origin under intensive system, while rural areas might continue to serve in food production under that require low input and low output breeds which are locally developed and adapted to these areas.

Responsibility of Scientists

Scientists are expected to develop, monitor and signal scientific work that will help governmental institutions to work over population that might be exploited or threatened with extinction. Genetic science shows that the developed guidelines for conservation plans individual breeders and breeding organizations are to help in conservation activities by collecting materials for genebank and performing breeding programs for small populations at risk. There is however, the need for government initiatives and national stability for breeders and breeding organizations to be able to play a key role in the success of animal genetic resources conservation and utilization activities.

SUMMARY

The current estimated animal population in Nigeria comprises 31.8 million cattle, 22 million sheep, 34.5 million goats, 104.3 million poultry and 3.4 million pigs (RIM, 1992) which is over 12 million Tropican livestock breeds and about 10% of animal population in sub-Saharan Africa. The livestock industry provides a mean of livelihood for a large percentage of the population. The indigenous breed forming the backbone of livestock production because of their ability to survive and reproduce under stressful conditions and being highly diversified.

Because of the rapidly increasing population, there is need to increase substantially, productivity of food especially from the livestock resources to meet the ever-increasing food and industrial demand for livestock and livestock products.

Although restrictions in economic financial conditions do not permit the production environment to be altered sufficiently to suit high potential of temperate breeds, early efforts at increasing production levels were based on, and emphasized by breeding policies and strategies that encouraged the replacement of indigenous breeds with those from temperate regions.

With full effect of most of these replacement programmes, it is now very obvious that Nigeria will only develop productively and well adapted domestic breeds in selection programmes if rural needs could be used as point of collection of breeds into regional open nucleus breeding systems.

Nigeria is far better equipped to achieve the much desired objective of becoming self-sufficient in livestock production. The human and material resources at the disposal of the nation should guarantee the sustained physical effects necessary if this could be backed up with readily available modern agricultural technology. The most essential element missing or inadequately expressed is the political will of the government and people of Nigeria to persist until the ultimate success is achieved.

Both politicians, technocrats and farmers must be totally committed because success in animal production and genetic improvement can only be realized where there is wholehearted commitment and sustained involvement.

References


FAO (1998): Primary guidelines for development of national farm animal genetics resources management plans. FAO Rome, Italy.


