NATIONAL OPEN UNIVERSITY OF NIGERIA

FACULTY OF AGRICUTURAL SCIENCES

COURSE CODE:
ANP312

COURSE TITLE:
INTRODUCTION TO GENETICS AND BREEDING

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CONTENTS **PAGES**

Introduction

The course ANP312 (Introduction to genetics and breeding), is a two (2) credit unit course designed for 300 level undergraduate students pursuing a degree in Agricultural Science. The course is expected to provide a good knowledge base for the future manpower for genetic improvement of Nigerian livestock resources towards a sustainable production of livestock. It explains the rudimentary biology, starting with the cell. Major components of the cell were treated including the nucleus which contains the genetic materials. Since genetics is mainly concerned with transmission of genetic information from parents to offspring, pattern of inheritance was also discussed. The ingenious contributions made by fathers of genetics (Charles Darwin, Gregor Mendel and host of others) were highlighted. The course also provides basic knowledge for biotechnological applications in livestock genetic improvement and the development of genotypes that are adapted to Nigerian environment. The course will provide a basic foundation for students intending to take up Animal breeding and Genetics as a Career in the future.

The course is divided into four (4) modules with modules one (1), three (3) and four (4) consisting of four (4) units each while module two (2) consist of three (3) units. Each unit begins with a clear introduction and statement of objectives followed by the main content. The conclusion, summary and references (for further reading) were also provided for each unit. Tutor marked assignments were provided for each unit to enable you attempt some questions on the topics treated for onward submission to your tutor.

The Course Guide provides you with access to brief information and overview of the course content, course duration, what you are expected to know in each unit, what course material you need to use and how you can systematically go through the course materials.

What You Will Learn in This Course

You are expected to learn the basic knowledge of animal genetics and breeding. This is only possible through the understanding of the cell and its major components. The nucleus houses the DNA, which is crucial in transmission of genetic materials. You will also learn the fundamental principles of inheritance, Mendelian genetics, breeding value and genetic parameters (heritability and repeatability). Animal breeding, as the application of the principles of genetics, was well treated by avoiding much of the technicalities involved. Selection principles and methods of selection of high performing animals, breeding/mating methods were thoroughly explained. Thus, we intend to achieve the above through the following broad aim and other specific objectives.

Course Aim

The major aim of this course is to treat the fundamental principles of animal genetics and breeding through the highlights of the basic knowledge of biology and the contributions by founders of genetics. Using Mendelian genetics, some highly technical aspect of crossing was avoided; instead a simple technique was followed to arouse the interest of student into understanding fundamental principles of inheritance for both quantitative and qualitative traits, selection and mating of superior performing individuals for production of high performing offspring. The course is also aimed at preparing you rigorously for more advance courses in genetics and animal breeding.

Course Objectives

The following specific objectives have set out to ensure that the course achieves its aim. In addition, the 15 different units carry specific objectives designed to provide a systematic study of each module. The unit objectives are stated at the beginning of each unit. Attention should be given to these objectives in the course of your study to evaluate the progress you are making. At the completion of each unit, you are expected to look at the unit objectives again to ensure that you have covered the enumerated objectives.

After going through this course, you are expected to understand the following;

1. The cell as the basic unit of life, its major components and functions.
2. Chromosome is made of protein and DNA, which are responsible for storage of genetic information.
3. Differences between DNA and RNA and their roles in cell division and information transfer.
4. The contributions made to the field of genetics by Darwin, Mendel, Watson and Crick and others, without which the breakthrough in genetics and breeding would not have been possible.
5. The simple monohybrid crossing leading to the ratio of 3:1.
6. The use of Punnet Square for dihybrid crossing to get a ratio of 9:3:3:1.
7. Different types of gene action that caused deviations to Mendelian inheritance and ratios: incomplete dominance, multiple alleles, variable expressivity, sex limited trait, sex influenced trait and others.
8. The difference between quantitative traits (also called polygenic traits) and qualitative traits (also called monogenic traits).
9. Identify traits that are quantitative as against those that are qualitative.
10. The concept of heritability and repeatability of a trait, which are collectively called genetic parameters. Their significance to animal breeding and application.
11. Identify traits of economic importance with their heritability and repeatability values.

12. Define and distinguish between natural and artificial selection.
13. Explain the principles and methods of selection for single trait: mass selection, family selection and so on.
14. Enumerate the methods of selection for multiple traits: independent culling levels, tandem selection and selection index.
15. Enumerate different breeding methods available to the animal breeder: random mating, inbreeding and its consequences, crossbreeding and its various forms or schemes such as crisscrossing, backcrossing, top crossing, grading up and rotational crossing among others.

Working through this Course

For thorough understanding of this course, you are required to read the study units and be acquainted with the contents. Your devoted attention, self discipline and personal commitment is highly sought. In addition, kindly check on the references for further readings and read also other relevant materials that may be provided by the National Open University of Nigeria (NOUN) to aid your learning process. You should do the exercises in the Tutor-Marked Assignments provided and submit to your tutor as at when due.

The Course Materials

You will be provided with the following course materials:

1. The course guide
2. The study units
3. Other relevant reference materials
4. A file for your assignment and for records to monitor your performance/progress

Study Units

This course contains fifteen study units organized as follows:

Module 1	The Molecular Basis of Heredity – The Animal Cell, Its Components and the Genetic Code
Unit 1	Structure of an animal cell and functions of the major components
Unit 2	Chromosomes

Unit 3 DNA and RNA

Unit 4 The Genetic code

Module 2 Mendelism: The Fundamental Principles of Inheritance

Unit 1 Definitions of Some Genetic Terms

Unit 2 History of Genetics I (Darwin, Mendel and others)

Unit 3 History of Genetics II (Watson and Crick and others)

Module 3 Mendelian Genetics and Non Mendelian Inheritance

Unit 1 Mendelian genetics I (Mendel's first law and the law of dominance)

Unit 2 Mendelian genetics II (Mendel's second law and the Punnet Square)

Unit 3 Non Mendelian inheritance I (Types of gene action)

Unit 4 Non Mendelian inheritance II (Types of gene action)

Module 4 Quantitative and Qualitative Characters and their mode of Inheritance

Unit 1 Quantitative and qualitative inheritance

Unit 2 Heritability and repeatability

Unit 3 Animal variation and selection principles

Unit 4 Breeding methods

Each unit contains some tutor-marked assignments, these exercises will assist you in achieving the stated learning objectives for the course and the individual units. Make use of the course materials, do the exercises to enhance your learning.

Textbooks and References

Alberts B. Johnson A. Lewis J. Raff M. Roberts K. Walter P. (2002). Molecular Biology of the Cell, 4th Edition, Garland. ISBN 0815332181. http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=mboc4.TOC&depth=2

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Stansfield W.D. (1986) Genetics of livestock improvement. Schaum's Outline series, 2nd Edition, McGraw Hill Book Company, Pg 392.

Kay, L.E. (2001). Who wrote the book of life? Stanford University press, The story of how a group of mostly physicists-turned-biologists deciphered the genetic code in the 1960s. Pg 203

Genetic Interest Group (www.gig.org.uk), Online Mendelian Inheritance in Man www.ncbi.nlm.nih.gov/entrez/query.fcgi?db=ONIM (Accessed October, 2015)

Assessment

There are two aspects of assessments in this course; the first aspect is the Tutor-Marked Assignments (TMA) while the second is a written examination which comes up at the end of the semester. In tackling the assignments, you are expected to apply information,

knowledge and techniques gathered during the course. The assignments must be submitted to your tutor for formal assessment in accordance with the stipulated deadlines.

Tutor Marked Assignments (TMAs)

There are sixty-four tutor marked assignments in this course. You need to submit all the assignments. The assignment questions for the units in this course are contained in the Assignment File. You should be able to complete your assignments from the information and materials contained in your set textbooks, reading and study units. However, you may wish to use other references to broaden your viewpoint and provide a deeper understanding of the subject. When you have completed each assignment, send it together with form to your tutor. Make sure that each assignment reaches your tutor on or before the deadline given. If, however, you cannot complete your work on time, contact your tutor before the assignment is done to discuss the possibility of an extension.

This course endows you with the status of a teacher and that of a learner. This means that you teach yourself and that you learn, as your learning capabilities would allow. It also means that you are in a better position to determine and to ascertain the what, the how, and the when of your language learning. No teacher imposes any method of learning on you.

How to Get the Most from the Course

In distance learning, the study units replace the lecturer. This is an advantage over the conventional mode of learning. Do you know why? Because it accords you with the opportunity to read and work through all the specially designed materials at your pace, at a time and place that suits you best. Just as a lecturer might give you an in-class exercise, your study units provide exercises for you to do appropriately.

Each of the study units follows a common format. The first item is the introduction to a subject matter of the unit and the course as a whole. Next is a set of learning objectives. These objectives let you know what you should be able to do by the time you have completed the unit. You should use these objectives to guide your study. When you have finished the unit, you must go back and check whether you have achieved the objectives. If you make a habit of doing this, you will significantly improve your chances of passing the course.

CONTENTS **PAGES**

MODULE 1 THE MOLECULAR BASIS OF HEREDITY – THE ANIMAL CELL, ITS COMPONENTS AND THE GENETIC CODE

UNIT 1 STRUCTURE OF AN ANIMAL CELL AND FUNCTIONS OF THE MAJOR COMPONENTS

CONTENTS

1.0 INTRODUCTION

In this section, you will appreciate the basic unit of life called cell. A typical animal cell will be drawn and major components shall be clearly labeled. Functions of these major components of the animal cell shall be explained.

2.0 OBJECTIVES

It is expected that, by the end of this unit you will be able to;

- draw and clearly label a typical animal cell.
- explain the functions of some of the major components.

3.0 MAIN CONTENT

3.1 The structure of an animal cell

All cells share certain features that enable them perform the basic life functions of reproduction, growth, response to stimuli and energy use. Body cells also have specialized features, for instance, the more than 260 specialized or differentiated cell types in a human body arise because the cells express different genes. The body cells of human and other animals (sheep, goat, cattle, rabbit, chicken etc) fall into four broad categories: ***epithelium*** (lining cells), ***muscle***, ***nerve*** and ***connective tissues*** (blood, bone, cartilage, adipose and others).

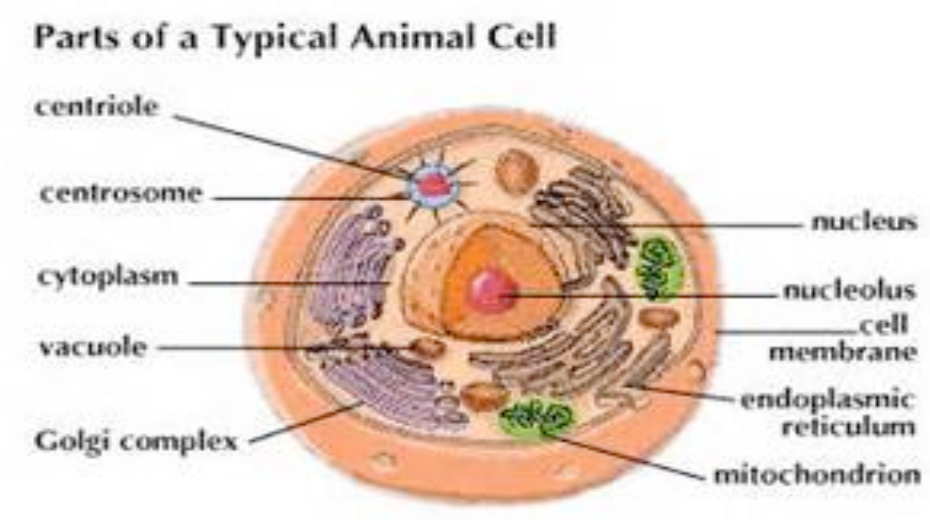

Figure 1, diagram of a typical animal cell

Biologists recognize three broad types of cells that define three major 'domains' of life: the Archaea, the Bacteria and the Eukarya. A domain is a designation that is broader than the familiar kingdom. The Archaea and Bacteria were in the past lumped together as prokaryotes, because they both lack a nucleus. They are recently recognized as separate domain and are both single-celled but they differ in many of their genetic molecules and in the types of molecules in their membranes. The third domain of life, the Eukarya or eukaryotes includes singled-celled organisms that have nuclei as well as all multicellular organisms.

3.1.1 Major components of animal cell and their functions

For a typical animal cell (Fig. 1) to carry out the activities of life, structures called organelles divide and share the labour. They keep related biochemicals and structures close enough to one another to interact efficiently retain as well as use its genetic instructions.

3.1.1.1 **Nucleus:** The most prominent organelle is the nucleus enclosed in a layer called the nuclear envelope. Within the nucleus, an area that appears darkened under a microscope called nucleolus, is the site of ribosome production. The nucleus is filled with DNA (deoxyribonucleic acid) and RNA (ribonucleic acid). The reminder of the cell, minus the nucleus, organelles and cell membrane is called cytoplasm (Fig. 2).

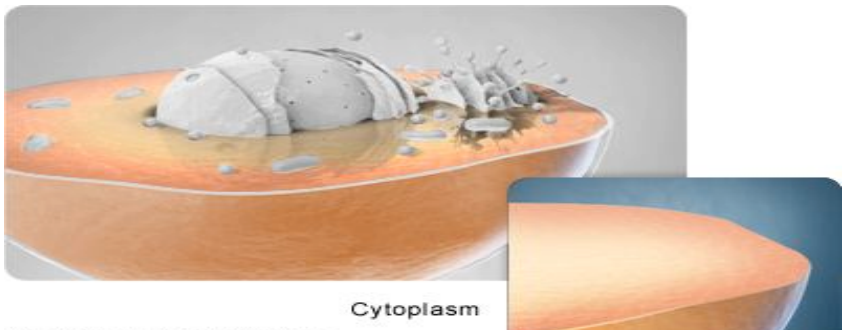

Figure 2, the cytoplasm of a cell

3.1.1.2 **Golgi apparatus:** The Golgi apparatus (Fig. 3) is a stack of flat, membrane-enclosed sac where sugars are synthesized and linked to form starches or attach to proteins to form glycoproteins or to lipids to form glycolipids.

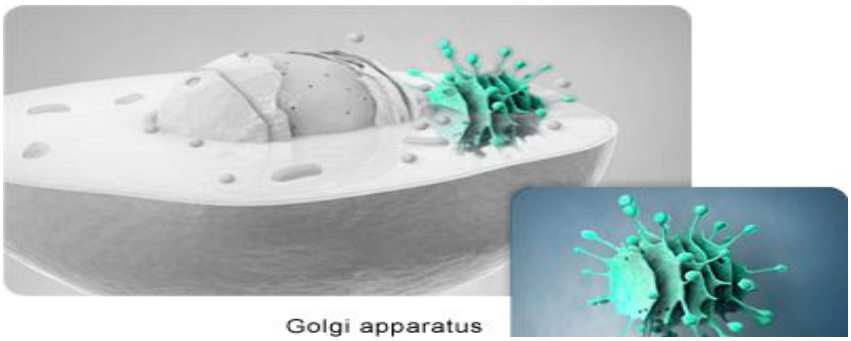

Figure 3, the golgi apparatus

3.1.1.3 **Lysosomes** and **peroxisomes:** The Lysosomes and peroxisomes are membrane-bounded sacs that contain enzymes that dismantle or digest captured bacterial remnants, worn-out organelles and other debris. A lysosome loaded with such 'garbage' moves toward the cell membrane and fuses with it, dumping its contents to the outside.

3.1.1.4 **Mitochondria:** The organelles called mitochondria (Fig. 4) provides energy by breaking down the products of digestion. They are especially interesting to geneticists because, like the nucleus, they contain DNA though in small amount.

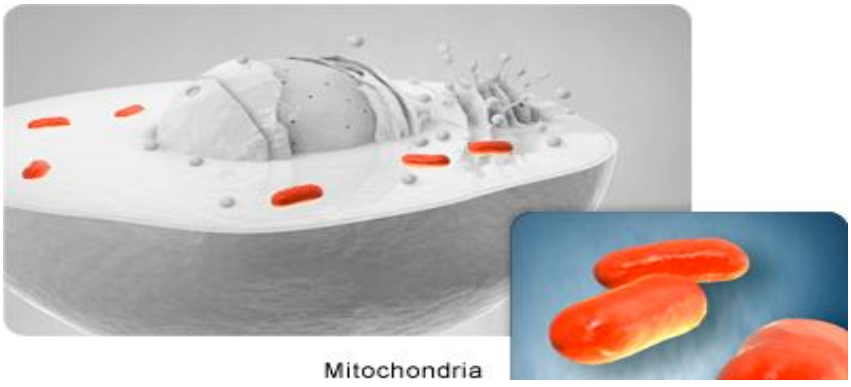

Figure 4, the mitochondria

4.0 CONCLUSION

It is hoped that you have learnt in this unit how to draw and clearly label the structure of a typical animal cell. The functions of these major components should be clearly understood, because these components and their functions are vital to the integrity of the cell and crucial in cell division.

5.0 SUMMARY

In summary, the structure and other major components of animal cell were clearly treated. The importance of each major component was highlighted, which include the nucleus, mitochondria, lysosomes, golgi apparatus and others.

6.0 TUTOR-MARKED ASSIGNMENT

Having gone through this unit, you are to attempt the following assignments and submit your answers to your tutor for this course.

1. The body cells of humans and other animals fall into four broad categories, list them.
2. A prokaryote is a cell that lacks a nucleus True …….False …….
3. What is the major function of the nucleus?
4. …….. is where sugars are synthesized and linked to form starches or attach to proteins to form glycoproteins or to lipids to form glycolipids (a) Golgi apparatus (b) Mitochondria (c) Nucleus (d) Lysosomes
5. The mitochondria provide ……. to the cell by breaking down the products of digestion. (a) energy (b) protein (c) enzymes (d) vitamin
6. Membrane-bounded sacs that contain enzymes that dismantle or digest captured bacterial remnants, worn-out organelles and other debris are the …….. (a) Golgi apparatus (b) Mitochondria (c) Nucleus (d) Lysosomes

7.0 REFERENCES/FURTHER READING

- Alberts B. Johnson A. Lewis J. Raff M. Roberts K. Walter P. (2002). Molecular Biology of the Cell, 4th Edition, Garland. ISBN 0815332181. http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=mboc4.TOC&depth=2
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UNIT 2 THE CHROMOSOME

CONTENTS

1.0 INTRODUCTION

This is a section where you will be taken through another important hereditary component of the cell called chromosome. It is a thread-like structure that consists of DNA and protein. Diagramatic structure and some essential parts of the chromosome have been explained.

2.0 OBJECTIVES

By the end of this unit, it is expected that you will be able to;

- identify the structure of a chromosome

- explain the essential parts of a chromosome
- mention the crucial role of each of the segment mentioned

3.0 MAIN CONTENT

3.1 The Chromosome

Chromosomes (Fig. 5) are thread-like materials that can be seen (with the help of a microscope) within the nucleus of a cell when stained at the proper stages of cell division. Each chromosome is made of protein and a single molecule of deoxyribonucleic acid (DNA). Passed from parents to offspring, DNA contains the specific instructions that make each type of living creature unique. In other words it is a structure that consists of DNA and proteins, which is duplicated and transmitted to the next generation (via mitosis and meiosis). The term chromosome comes from the Greek words for color (chroma) and body (soma). Scientists gave this name to chromosomes because they are cell structures, or bodies, that are strongly stained by some colorful dyes used in research.

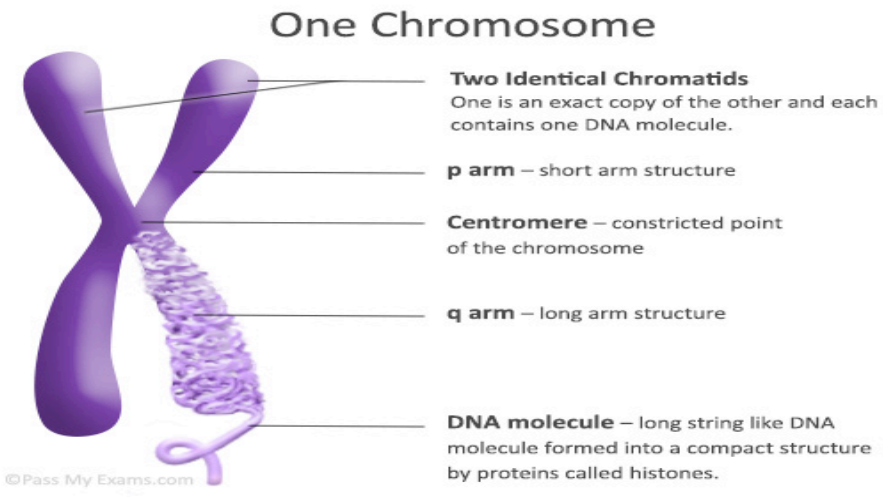

Figure 5, a chromosome showing the p and q arms

The unique structure of chromosomes keeps DNA tightly wrapped around spool-like proteins, called histones. Without such packaging, DNA molecules would be too long to fit inside cells. For example, if all of the DNA molecules in a single human cell were unwound from their histones and placed end-to-end, they would stretch 6 feet. For an organism to grow and function properly, cells must constantly divide to produce new

cells to replace old, worn-out cells. During cell division, it is essential that DNA remains intact and evenly distributed among cells. Chromosomes are a key part of the process that ensures DNA is accurately copied and distributed in the vast majority of cell divisions.

3.1.1 Essential parts of a chromosome

The absolutely essential parts of a chromosome (in terms of navigating cell division) are (1) centromere (2) telomere, and (3) origin of replication sites where replication forks begin to form.

3.1.1.1 Centromere

The constricted region of linear chromosomes is known as the centromere (Fig. 6). Although this constriction is called the centromere, it is usually not located exactly in the center of the chromosome and, in some cases, is located almost at the chromosome's end. The regions on either side of the centromere are referred to as the chromosome's arms.

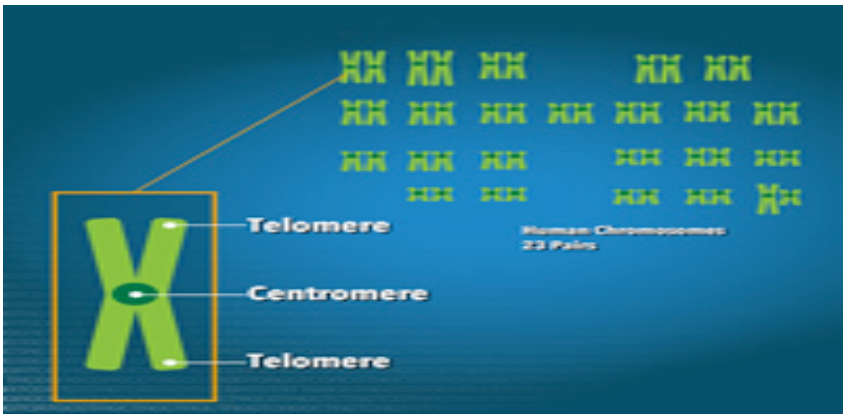

Figure 6, a human chromosome showing the telomere and centromere

The centromere is the largest constriction of a chromosome and where spindle fibres attach. A chromosome without a centromere is no longer a chromosome (it disappears from the cell as division begins because it cannot attach to the spindle). Centromeres help to keep chromosomes properly aligned during the complex process of cell division. As chromosomes are copied in preparation for production of a new cell, the centromere serves as an attachment site for the two halves of each replicated chromosome, known as sister chromatids. The set shown here is from a male, since it contains an X and a Y chromosome; if the chromosome set were from a female, it would contain XX only. All

chromosomes other than the sex chromosomes are known as autosomes. Human cells contain two sets of chromosomes, one inherited from the mother and one from the father. Each set has 23 single chromosomes (22 autosomes and a sex-determining chromosome, either X or Y).

3.1.1.2 Telomere

Telomeres are repetitive stretches of DNA located at the ends of linear chromosomes. They protect the ends of chromosomes in a manner similar to the way the tips of shoelaces keep them from unraveling. In many types of cells, telomeres lose a bit of their DNA every time a cell divides (Fig. 7). Eventually, when all of the telomere DNA is gone, the cell cannot replicate and dies. The telomeres are the tip of the chromosome, each consisting of many repeats of the sequence TTAGGG that are whittled down with each mitotic cell division. White blood cells and other cell types with the capacity to divide very frequently have a special enzyme that prevents their chromosomes from losing their telomeres. Because they retain their telomeres, such cells generally live longer than other cells. Telomeres also play a role in cancer. The chromosomes of malignant cells usually do not lose their telomeres, helping to fuel the uncontrolled growth that makes cancer so devastating.

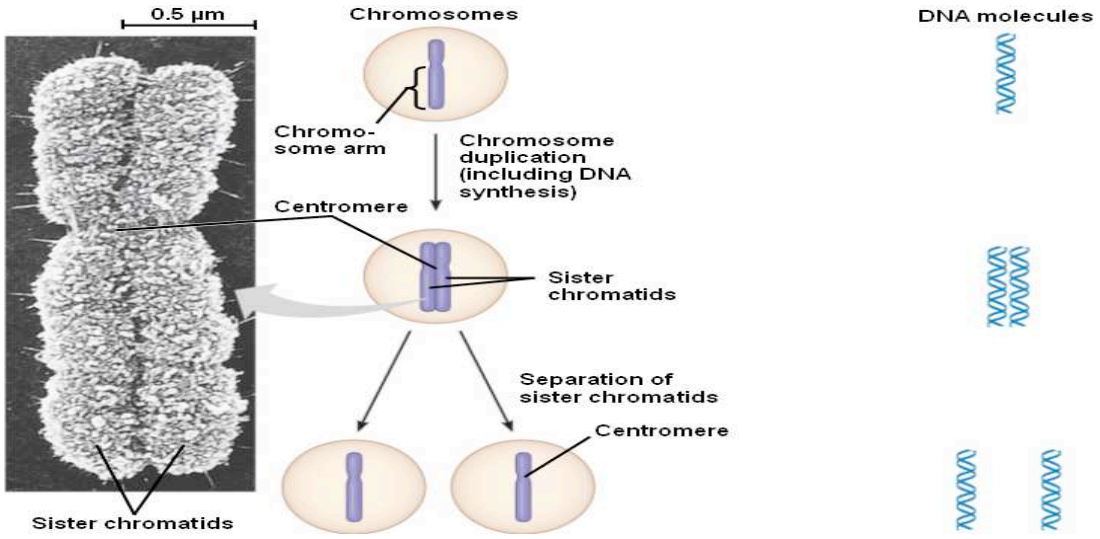

Figure 7, stages of divisions in the chromosome

The number of pair characteristics for a given species is as shown in Table 1.

Table 1: Diploid chromosome number of some mammals

Common/scientific names	No of Chromosome
Human (Homo sapiens)	64
Horse (Equus caballus)	64
Ass (Equus asinus)	62
Cattle (Bos Taurus, Bos indicus, Bison bison)	60
Buffalo (Bubalus bubalus)	48
Ox (Ovbus moschatus)	48
Reindeer (Rangifer tarandus)	70
Sheep (Ovis aries)	54
Goats (Capra hicus)	60
Swine (Sus scrofa)	38
Dog (Canis familiaris)	78
Cat (Felis catus)	38
Rabbit (Oryctalagus cunniculus)	44
Mouse (Mus musculus)	40
Rat (Rattus norvegicus)	42
Chicken (Gallus gallus)	36

4.0 CONCLUSION

In conclusion, we have learned that chromosomes are found in the nucleus of all body cells except for red blood cells which have no nucleus and therefore do not contain chromosomes. There are two chromosomes that have been given the labels X and Y.

These are the sex chromosomes. It is these sex chromosomes that determine whether the chromosomes have come from a male or a female. The chromosomes, including the genes, are made up of a chemical substance called DNA (Deoxyribo Nucleic Acid). Essential parts of the chromosome and the crucial role(s) each part plays in cell division have been taught.

5.0 SUMMARY

Chromosomes can be thought of as being made up of strings of genes (DNA that codes for proteins) with non-coding DNA between them. The chromosomes, including the genes, are made up of a chemical substance called DNA (Deoxyribo Nucleic Acid).

6.0 TUTOR-MARKED ASSIGNMENT

Having gone through this unit, you are to attempt the following assignments and submit your answers to your tutor for this course.

1. What are the names given to the short and long arms of a chromosome?
2. List any two essential part of a chromosome
3. Fill-in the blank spaces by provided the correct number of chromosome against the species of animal in the table given below:

S/No	Common/scientific names	No of Chromosome
1	Cattle (Bos Taurus, Bos indicus)	
2	Horse (Equus caballus)	
3	Sheep (Ovis aries)	
4	Goats (Capra hicus)	
5	Swine (Sus scrofa)	
6	Dog (Canis familiaris)	
7	Chicken (Gallus gallus)	
8	Human (Homo sapiens)	

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UNIT 3 DNA AND RNA

CONTENTS

1.0 INTRODUCTION

DNA simply stands for Deoxyribo Nucleic Acid and is double-stranded. RNA, which stands for Ribo Nucleic Acid is single-stranded. Remember in unit 2 we said that the DNA is found in the nucleus of a cell and its main function is to store genetic information passed from parents to offspring. RNA has multiple functions and we shall discuss them in this unit. There are basic and distinct differences between DNA and RNA, which you need to clearly understand.

2.0 OBJECTIVES

By the end of this unit, it is expected that you will be able to;

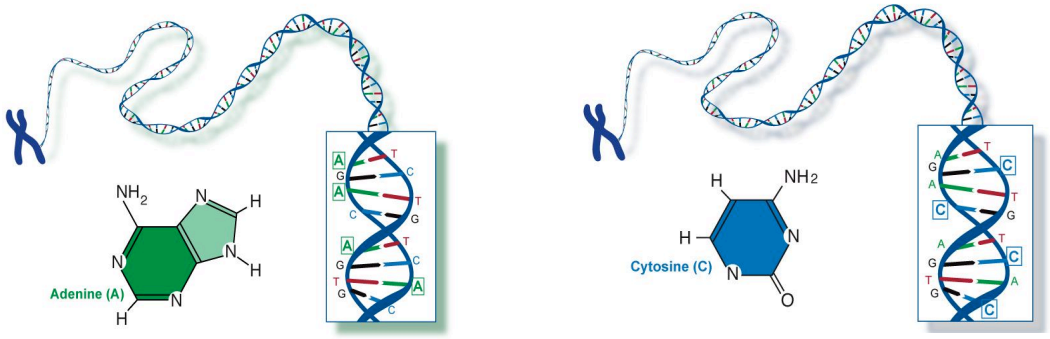
- explain the meaning of DNA and RNA and state their roles
- list the 4 different types of bases contained by each of DNA and RNA
- understand the structural component of DNA and RNA
- differentiate between DNA and RNA in terms of structure and function

3.0 MAIN CONTENT

3.1 The DNA and RNA

The most common nucleic acids are deoxyribonucleic acid (DNA) and ribonucleic acid (RNA). The main role of DNA is the long-term storage of genetic information. DNA is often compared to a blueprint, since it contains instructions for constructing other components of the cell, such as proteins and RNA molecules. The DNA segments that carry genetic information are called *genes*, but other DNA sequences have structural purposes or are involved in regulating the expression of genetic information. RNA may also serve more than one purpose, but it is most commonly identified as the intermediate between the DNA blueprint and the actual workings of the cell, serving as the template for the synthesis of proteins from the genetic information stored in DNA. ACGT is an acronym for the four types of bases found in a DNA molecule: adenine (A), cytosine (C), guanine (G), and thymine (T) as shown in Fig. 8.

Adenine (A) Cytosine (C)



Thymine (T) Guanine (G)

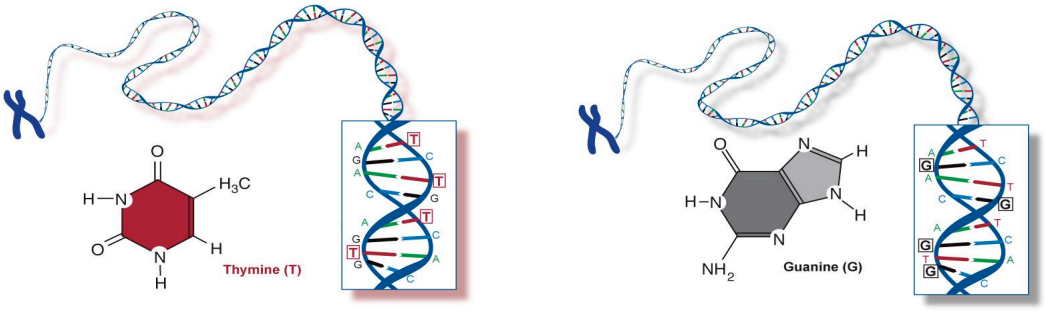


Figure 8, structures of adenine, cytosine, guanine and thymine

A DNA molecule consists of two strands wound around each other, with each strand held together by bonds between the bases. Adenine pairs with thymine, and cytosine pairs with guanine. The sequence of bases in a portion of a DNA molecule, called a gene, carries the instructions needed to assemble a protein. RNA is a nucleic acid, complex, high-molecular-weight macromolecule composed of nucleotide chains whose sequence of bases conveys genetic information. A nucleotide is a chemical compound comprising three components: a nitrogen-containing base, a pentose (five-carbon) sugar, and one or more phosphate groups. The nitrogen-containing base of a nucleotide (also called the nucleobase) is typically a derivative of either purine or pyrimidine. The most common nucleotide bases are the purines adenine and guanine while the pyrimidines are cytosine and thymine (or uracil in RNA).

3.1.1 Types of RNA molecule

There are 3 principal types of RNA involved in protein synthesis:

• Messenger RNA (mRNA) serves as the template for the synthesis of a protein. It carries information from DNA to the ribosome.

• Transfer RNA (tRNA) is a small chain of nucleotides that transfers a specific amino acid to a growing polypeptide chain at the ribosomal site of synthesis. It pairs the amino acid to the appropriate three-nucleotide codon on the mRNA molecule.

• Ribosomal RNA (rRNA) molecules are extremely abundant and make up at least 80 percent of the RNA molecules found in a typical eukaryotic cell. In the cytoplasm, usually three or four rRNA molecules combine with many proteins to perform a structural and essential catalytic role, as components of the ribosome.

3.1.2 Differences between RNA and DNA: They differ in three main ways (Fig. 9);

(1) Unlike DNA which is double-stranded, RNA is intrinsically a single-stranded molecule in most of its biological roles and has a much shorter chain of nucleotides.

(2) While DNA contains *deoxyribose*, RNA contains *ribose*. There is no hydroxyl group attached to the pentose ring in the 2' position in DNA, whereas RNA has two hydroxyl groups. These hydroxyl groups make RNA less stable than DNA because it is more prone to hydrolysis. ("Deoxy" simply indicates that the sugar lacks an oxygen atom present in ribose, the parent compound).

(3) The complementary nucleotide to adenine is not thymine (as it is in DNA), but rather uracil, which is an unmethylated form of thymine.

3.1.3 Comparing RNA with DNA

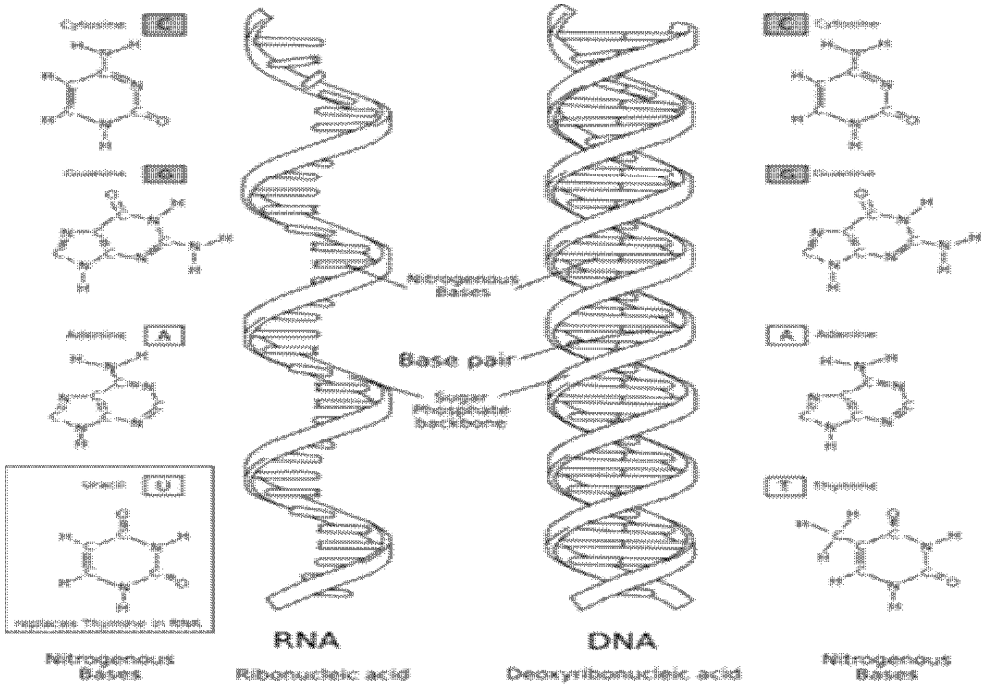


Figure 9, Left: RNA strand, with its nitrogenous bases. Right: Double-stranded DNA

3.1.4 Synthesis of RNA

Synthesis of RNA is usually catalyzed by an enzyme, RNA polymerase, using DNA as a template. Initiation of synthesis begins with the binding of the enzyme to a promoter sequence in the DNA. The DNA double helix is unwound by the helicase activity of the enzyme. The enzyme then progresses along the template strand in the 3' > 5' direction, synthesizing a complementary RNA molecule with elongation occurring in the 5' > 3' direction. The DNA sequence also dictates where termination of RNA synthesis will occur. There are also a number of RNA-dependent RNA polymerases as well that use RNA as their template for synthesis of a new strand of RNA. For instance, a number of RNA viruses (e.g. poliovirus) use this type of enzyme to replicate their genetic material. Also, it is known that RNA-dependent RNA polymerases are required for the RNA interference pathway in many organisms.

4.0 CONCLUSION

In this unit, we have understood that DNA is deoxyribonucleic acid while RNA is ribonucleic acid. While DNA is double stranded, RNA is single stranded molecule. DNA is the blueprint for storing genetic information of the cell. We also leaned that the four types of bases contained by both DNA and RNA differ.

5.0 SUMMARY

- The DNA molecule consists of two strands wound around each other, with each strand held together by bonds between the bases. Adenine pairs with thymine, and cytosine pairs with guanine.
- In RNA, the complementary nucleotide to adenine is not thymine (as it is in DNA), but rather uracil, which is an unmethylated form of thymine.
- There are 3 principal types of RNA: Messenger RNA (mRNA), Transfer RNA (tRNA) and Ribosomal RNA (rRNA).

6.0 TUTOR-MARKED ASSIGNMENT

The following assignments are set for you to attempt and submit your answers to your tutor for this course.

1. Write the full meaning of DAN and RNA
2. List the four types of bases contained in DNA and RNA, respectively
3. Mention the three different types of RNA involved in protein synthesis

7.0 REFERENCES/FURTHER READING

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UNIT 4 THE GENETIC CODE

CONTENTS

1.0 INTRODUCTION

The genetic code, in a simple term, is the relationship between the bases and amino acids. The genetic code is the same in all organisms of the world (whose genetic code have been studied), except in mitochondria and protozoan nuclear DNA. Recall that in unit 3, we discussed that the DNA has four nucleotide bases: adenine, guanine, cytosine and thymine, while RNA also has four nucleotide bases: adenine, guanine, cytosine and uracil. This ‘alphabet’ of four letters is responsible for carrying the code that results in the synthesis of many protein molecules.

2.0 OBJECTIVES

By the end of this unit, it is expected that you will be able to;

- Understand the concept of genetic code in its simplest term
- name the scientists that were among the first to crack the code
- understand the components of amino acids
- list the six characteristics of the genetic code

3.0 MAIN CONTENT

3.1 The Genetic code

The pathway of protein synthesis is called Translation because the language of nucleotide sequence on mRNA is translated in to the language of an amino acid sequence. The process of Translation requires a Genetic code, through which the information contained in nucleic acid sequence is expressed to produce a specific sequence of amino acids. In other words, the genetic code is found in the sequence of nucleotides in mRNA that is translated from the DNA. A codon is a triplet of bases along the mRNA that codes for a particular amino acid. The flow of information is unidirectional: information is transferred from nucleotide sequences into the amino acid sequence of proteins, but it never transfers from protein back into the sequence of DNA – a phenomenon Francis Crick called the central dogma of molecular biology.

The Genetic Code

nonpolar polar basic acidic (stop codon)

Standard genetic code

1st base	2nd base								3rd base
	U		C		A		G		
U	UUU	(Phe/F) Phenylalanine	UCU	(Ser/S) Serine	UAU	(Tyr/Y) Tyrosine	UGU	(Cys/C) Cysteine	U
	UUC		UCC		UAC		UGC		C
	UUA	(Leu/L) Leucine	UCA		UAA	Stop (*Ochre*)	UGA	Stop (*Opal*)	A
	UUG		UCG		UAG	Stop (*Amber*)	UGG	(Trp/W) Tryptophan	G
C	CUU		CCU	(Pro/P) Proline	CAU	(His/H) Histidine	CGU	(Arg/R) Arginine	U
	CUC		CCC		CAC		CGC		C
	CUA		CCA		CAA	(Gln/Q) Glutamine	CGA		A
	CUG		CCG		CAG		CGG		G
A	AUU	(Ile/I) Isoleucine	ACU	(Thr/T) Threonine	AAU	(Asn/N) Asparagine	AGU	(Ser/S) Serine	U
	AUC		ACC		AAC		AGC		C
	AUA		ACA		AAA	(Lys/K) Lysine	AGA	(Arg/R) Arginine	A
	AUG[A]	(Met/M) Methionine	ACG		AAG		AGG		G
G	GUU	(Val/V) Valine	GCU	(Ala/A) Alanine	GAU	(Asp/D) Aspartic acid	GGU	(Gly/G) Glycine	U
	GUC		GCC		GAC		GGC		C
	GUA		GCA		GAA	(Glu/E) Glutamic acid	GGA		A
	GUG		GCG		GAG		GGG		G

Figure 10, standard genetic code

3.2 Deciphering the genetic code

Marshall Nirenberg and Heinrich Matthaei at the National Institutes of Health used a precise and logical series of experiments to "crack" the code (Fig. 10). They were among the first to characterize specific coding sequences. This was made possible by advancements that:

- Allowed protein synthesis in vitro
- Synthesizing RNA strands in vitro

3.3 Amino acids

These are the subunits of protein and they all have the same basic structure: a central carbon atom (the **a** carbon), an amino group (NH_2) at the **a** carbon, a carboxyl group (COOH), a side group (R).

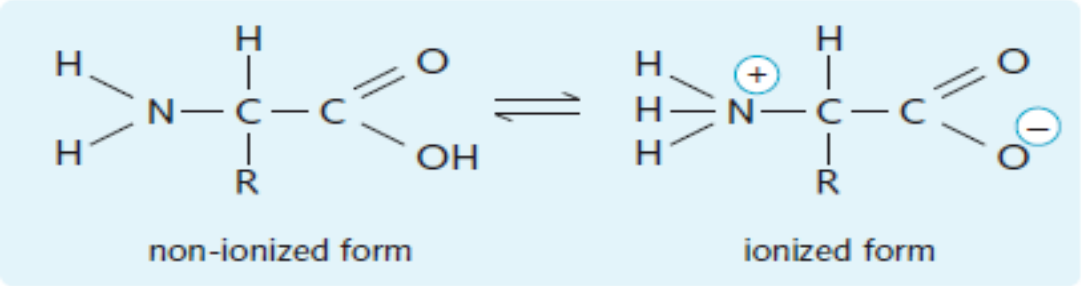

Figure 11, structure of an amino acid

There are 20 naturally occurring amino acids, which differ in their side group. All amino acids (Fig. 11), except glycine, have asymmetrical α-carbon atom, giving rise to D or L stereoisomer forms; however, only the L form is found in humans. The dynamic structure of haemoglobin (Hb) is responsible for its ability to transport oxygen (O_2) within mammalian blood. A change in single amino acid causes Hb to form fibers. The specific sequence of amino acids results in a unique three-dimensional structure for that protein and the three-dimensional structures of protein are related to their function. Some are simple structural molecules, like the fibers formed by the protein collagen. Proteins can bind to other proteins and simple molecules, sometimes acting as enzymes by facilitating chemical reactions within the bound molecules (without changing the structure of the protein itself). Protein structure is dynamic; the protein Hb bends into slightly different forms as it facilitates the capture, transport and release of O_2 molecules within mammalian blood. For example, sickle-cell anaemia is a human genetic disease that results from a single base difference within the coding region for the ß-globin section of Hb, causing a single amino acid change that changes Hb's physical properties. Sickle-cell versions of Hb stick to themselves, stacking to form fibers that distort the shape of red blood cells carrying the protein. These sickle-shaped cells no longer flow smoothly through blood vessels, having a tendency to clog or degrade, causing the medical problems associated with this disease.

3.3.1 Amino acids code

Nonpolar and uncharged

A	Ala	Alanine
F	Phe	Phenylalanine
G	Gly	Glycine
I	Ile	Isoleucine
L	Leu	Leucine
M	Met	Methionine
P	Pro	Proline
V	Val	Valine
W	Trp	Tryptophan

Polar and uncharged

C	Cys	Cysteine
N	Asn	Asparagine
Q	Gln	Glutamine
S	Ser	Serine
T	Thr	Threonine
Y	Tyr	Tyrosine

Positively charged (basic)

H	His	Histidine
K	Lys	Lysine
R	Arg	Arginine

Negatively charged (acidic)

D	Asp	Aspartic acid
E	Glu	Glutamic acid

Ambiguous codes

B	Asx	Asparagine or aspartic acid
Z	Glx	Glutamine or glutamic acid

Figure 12, polar, non polar, acidic basic and ambiguous amino acids

Almost all amino acids are specified by two, three or four different codons. Three amino acids (arginine, serine, and leucine) are specified by six codons. Methionine and tryptophan are encoded by single codons. In many codons specifying the same amino acid (synonymous codons), the first two positions are the same but the third position differs (Proline). Chemical analysis (Fig. 12) revealed that the code includes directions for starting and stopping translation. The codon AUG signals "start" and the codons UGA, UAA and UAG signify "stop". The genetic code has six features or better called characteristics as discussed below:

3.4 The six features or characteristics of genetic code

1. **Triplet code**: Each code is a triplet of nucleotides, this means each codon should have 3 nucleotides to impart specificity to each of the amino acid for a specific codon. There are 3 codons out of 64 in the genetic code, which do not encode for any amino acid and they are called termination codons or stop codons or nonsense codons. They include UAA, UAG and UGA.

2. **Specificity**: The genetic code is unambiguous but rather specific. Because a specific codon always codes for the same amino acid. Example, UUU only code for Phenyl alanine, it cannot code for any other amino acid.

3. **Degeneracy**: The code is degenerate meaning that a given amino acid may be coded for by more than one codon. Example Valine: GUU, GUC, GUA, GUG. Lysine: AAA, AAG. Tyrosine: UAU, UAC. It should be noted here that, the third base is usually less specific than the first two. This is known as the Wobble hypothesis because the third base can change but the amino acid remains the same. Wobble position of a codon refers to the 3^{rd} nucleotide in a codon. One advantage of degenerate code is that, it allows for possible mutations to be less damaging.

4. **Universality**: The code is nearly universal as it is the same in almost all organisms, except in mitochondria and protozoan nuclear DNA. This exception can however be tolerated because mitochondria and ciliated protozoa do not affect the major repositories of DNA. The universality of the genetic code is among the strongest evidence that all living things share a common evolutionary heritage.

5. **Non-overlapping**: No base of a given triplet contributes to part of the code of the adjacent triplet. The genetic code is read in groups (or 'words') of three nucleotides. After reading one triplet, the 'reading frame' shifts over the next three letters, not just one or two.

6. **Unpunctuated or commaless**: Once translation of mRNA begins, the codons are read one after the other with no breaks between them until a stop signal is reached.

4.0 CONCLUSION

By the end of this unit, it is hoped that you have learnt about the central dogma of molecular genetics, the phenomenon referring to the genetic code. It should be emphasized that, you should clearly understand the features or characteristics of the genetic code.

5.0 SUMMARY

The background information regarding the genetic code was explained. The genetic code has some unique features or characteristics summarized as follows; it is written in linear form; each word consists of 3 ribonucleotide letters; the code is specific (unambiguous); it is degenerate; it contains 1 start and 3 stop codons; the code is commaless; it is non-overlapping; and finally the code is (nearly) universal.

6.0 TUTOR-MARKED ASSIGNMENT

Having gone through this unit, you are to attempt the following assignments and submit your answers to your tutor for this course.

1. What is a codon?
2. Describe the six characteristics of genetic code
3. Describe the basic structure of amino acid
4. List any two basic and acidic amino acids
5. List any three polar and three non-polar amino acids

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MODULE 2 MENDELISM: THE FUNDAMENTAL PRINCIPLES OF INHERITANCE

Unit 1 **Definitions of Some Genetic Terms**

Unit 2 **History of Genetics I (Darwin, Mendel and others)**

Unit 3 **History of Genetics II (Watson and Crick and others)**

UNIT 1 DEFINITIONS OF SOME GENETIC TERMS

CONTENTS

3.1 Definitions of Some Genetic Terms

3.1.1 Distinction between Animal Genetics and Animal Breeding

3.1.1.1 What is Animal Genetics

3.1.1.2 What is Animal Breeding

3.1.2 Definitions of some genetic terms

(i) Trait
(ii) Gene
(iii) Allele
(iv) Dominant
(v) Recessive
(vi) Genotype
(vii) Homozygous
(viii) Heterozygous
(ix) Phenotype
(x) Heredity
(xi) Variation

4.0 Conclusion

5.0 Summary

6.0 Tutor Marked Assignment

7.0 References/Further Reading

1.0 INTRODUCTION

Having read through the Course Guide, you will now go through this first unit of the course, which is fundamental to the understanding of genetics. This includes definitions of some terminologies used in genetics as well as going through the memory lane to appreciate the contributions made by some ingenious scientists to the field of genetics and animal breeding. Now let us go through your study objectives for this unit.

2.0 OBJECTIVES

At the end of this unit, you should be able to:

- define genetics and animal breeding.
- distinguish between animal genetics and animal breeding
- define other genetic terminologies as gene, allele, dominant, recessive, homozygous, heterozygous, genotype, phenotype, heredity and variation.

3.0 MAIN CONTENT

3.1 Definitions of Some Genetic Terms

3.1.1 Distinction between Animal Genetics and Animal Breeding

3.1.1.1 What is Animal Genetics? Genetics is the science that deals with study of heredity and variation. It is a branch of biology that studies how characters (traits) are transferred from parents to their offspring. It came from the word ***gen, genetikos*** meaning generative and ***genesis*** meaning beginning.

3.1.1.2 What is Animal Breeding? Animal breeding refers to the application of the principles of animal genetics for the improvement of economically important characteristics (traits) in domestic animals. Examples of economically important traits include improvement milk production in dairy cow, egg production in chickens or meat yield in beef cattle. Advantages of animal breeding include improving the existing trait, producing new traits or producing individuals with superior merits.

3.1.2 Definitions of other genetic terminologies

(i) Trait: Simply means a character. Genetic traits are passed down through the genes from parents to offspring.

(ii) Gene: Is defined as the ***smallest unit of inheritance***. It is the hereditary material that controls which trait should be expressed in an animal. Gene occurs in pairs and offspring inherit one copy of each gene from each parent. Recently gene is defined as a specific sequence of nucleotide bases, whose sequences carry the information required for constructing proteins, which provide the structural components of cells and tissues as well as enzymes for essential biochemical reactions. The human genome is estimated to comprise at least 100,000 genes.

(iii) Allele: Refers to the other form of a gene. Remember we said gene occurs in pairs (AA or AB or BB) (Fig. 13). The uppercase (R) is called dominant gene while the lowercase (r) is known as a recessive allele.

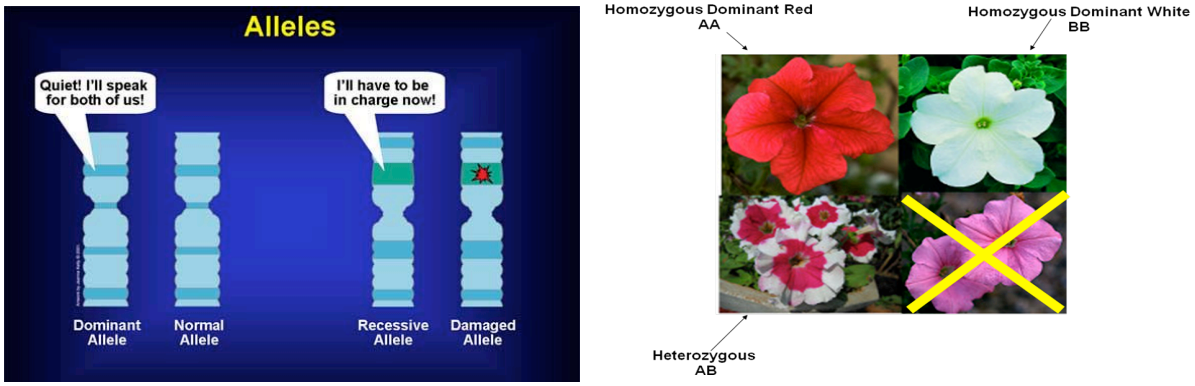

Figure 13, dominant and recessive alleles

(iv) Dominant: Is the stronger of the two genes expressed in the hybrid (Fig. 13). A dominant gene is always represented by a capital letter (uppercase) e.g. R.

(v) Recessive: Gene or allele that shows up less often in a cross. It is represented by a small letter (lowercase) e.g. r.

(vi) Genotype: Gene combination for a given trait (e.g. RR, Rr, rr). It is the genetic make-up of an individual. Genotype can be homozygous (e.g. RR, rr) or heterozygous (e.g. Rr).

(vii) Homozygous genotype: Is a situation where you have gene combination involving 2 dominant (RR) or 2 recessive (rr) genes. That is, having identical alleles. Homozygote individual is also called ***pure***.

(viii) Heterozygous genotype: Situation where you have gene combination of one dominant and one recessive allele (e.g. Rr). Heterozygotes are also called ***hybrid***.

(ix) Phenotype: Is the physical feature resulting from a genotype (e.g. red and white colour).

(x) Heredity: Simply means the transmission of traits from parents to offspring.

(xi) Variation: Refers to similarities and differences in creation, behavior, traits etc.

4.0 CONCLUSION

As you have learnt in this unit, the definitions of genetics and animal breeding was treated, it is expected that you will be able to distinguish between the two. Further terminologies were given to refresh and update your knowledge. Understand them well so that you will be able to attempt the questions in the Assignment section.

5.0 SUMMARY

In this unit, we have learned that:

- Animal genetics is a branch of biology that deals with the study of genes and their transmission from parents to offspring through reproduction.
- Animal breeding simply entails using or applying the principles of animal genetics in the improvement of livestock for human benefit.
- Other basic genetic terminologies were also clearly explained. These terminologies provide the knowledge to the bedrock of the science of genetics and animal breeding.

6.0 TUTOR MARKED ASSIGNMENT

You are to attempt the following assignments and submit your answers to your tutor for this course.

1. Define the following terms: (i) Homozygous genotype (ii) Allele (iii) gene
2. Distinguish between Animal Genetics and Animal Breeding.
3. A gene that shows up less often in a cross is called: (a) dominant (b) recessive (c) weak
4. The other form of a gene is called (a) allele (b) trait (c) phenotype
5. Similarities and differences in creation, behavior or traits is known as (a) heredity (b) variation (c) genotype

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UNIT 2 HISTORY OF GENETICS I (Darwin, Mendel and others)

1.0 Introduction

2.0 Objectives

3.0 Main content

3.1 History of genetics I

3.1.1 Charles Darwin

3.1.2 Gregor Mendel

3.1.3 Carl Correns,

3.1.4 Hugo De Vries

3.1.5 Erich Von Ischermak

1.0 INTRODUCTION

This unit seeks to provide an overview of modern genetics and will examine the major aspects of contemporary genetics in terms of current knowledge and how earlier discoveries fit into the overall picture, with little concern about the chronology of discovery. It will include a brief historical perspective, as well as an analysis of the major contributions to the field of genetics and the society in general. The brief details on the foundation of genetics and early philosophers, thinkers and workers in the field of genetics pave way to the appreciation of their great contributions. The works of Gregor Mendel and Charles Darwin as the founding fathers of genetics cannot be over emphasized.

2.0 OBJECTIVES

The objective is to provide a broad foundation that will allow you understand and appreciate major contributors in the area of genetics. At the end of this unit you should be able to:

- Mention some important dates in the historical lives of Charles Darwin, Gregor Mendel and others.
- Highlight major contributions made by Gregor Mendel regarding principles of genetics.

3.0 MAIN CONTENT

3.1 History of genetics I

3.1.1 Charles Darwin (1809 – 1882)

The English naturalist (Charles Darwin) (Plate 1) was an attending physician who brought the concept of the theory of evolution into the world. Most scholars had abandoned the notion of fixed species since their origin in the grand creation of life, long before publication of Darwin's "The origin of species" in 1859. By that time, most biologists agreed that new species arise through some process of evolution from older species. Butler said "Darwin's chief glory is not that he discovered evolution but that he made men to believe in it". He sailed the world from 1831–1836, studied the rich fauna and flora of South America and several islands.

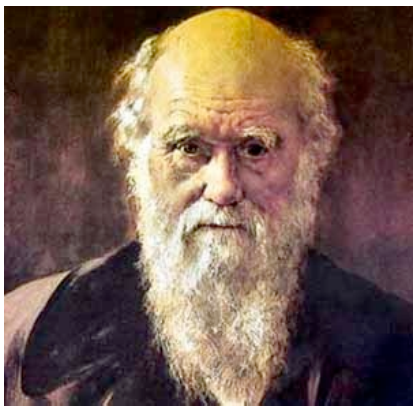

Plate 1, Charles Darwin

The three principles of Darwin's theories:

1. ***Principle of Variation***: Natural variation occurs in every species in the world. Organisms vary (differ) from one another indicating that no two individuals are exactly alike; offspring are not exactly like their parents. There is variation in morphology, physiology and behaviour.

2. ***Principle of Heredity***: The variations may be hereditary and can be passed onto descendants, which resemble their parents more than unrelated individuals. Competition occurs when two individuals of the same species compete for the same resources; be it food, water, space or even mate.

3. ***Principle of Selection***: This explains the continual struggle for existence in nature due to the dynamics of reproduction in all species. Some individuals successfully survive and reproduce than others in a given environment. The best adapted individuals will be the most likely to survive and therefore produce many offspring. This entails survival of the fittest. Natural selection coincides with evolution because the process can change a given species or even create a new one.

3.1.2 Gregor Mendel (1822 – 1884)

The Austrian Monk (Gregor Johann Mendel) (Plate 2) was regarded as the 'father of genetics'. Between the year 1856 and 1863, he cultivated and tested about 28,000 garden pea plants (*Pisum sativum)* and found that the offspring of these plants retained traits of their parents. He discovered the principles of heredity called particulate inheritance.

Plate 2, Gregor Johann Mendel

Mendel's work showed that:

1. Each parent contributes one factor of each trait to its offspring.
2. The two members of each pair of factors segregate from each other during gamete formation.
3. Males and females contribute equally to the traits in their offspring.
4. The blending theory of inheritance was not correct.
5. Acquired traits are not inherited.

THE THREE SCIENTISTS WHO RE-DISCOVERED THE WORK OF MENDEL

Hugo de Vries, Carl Correns and Erich von Tschermak-Seysenegg were the three scientists who rediscovered Mendel's laws. They were all working independently on different plant hybrids, and came to the same conclusions about inheritance as Mendel.

3.1.3 Carl Correns (1864 – 1933)

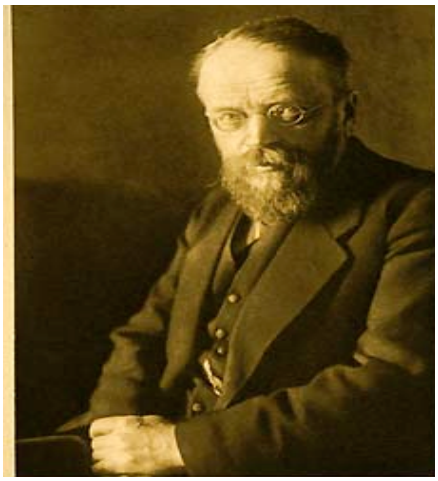

Plate 3, Carl Correns

Carl Erich Correns (Plate 3) was born on 10th September, 1864 in Munich, Germany and died on 14th February, 1933 in Berlin, Germany. In 1885, he entered the University of Münich to study botany. Carl Nägeli, the botanist to whom Mendel wrote to about his pea plant experiments, was no longer lecturing at Münich. Nägeli, however, knew Correns' parents and took an interest in him. Nägeli was the one who encouraged Correns' interest in botany and advised Correns on his thesis subject. Nägeli and Correns' connection was more than just scientific; Correns eventually married Nägeli's grandniece. Correns was a tutor at the University of Tübingen when he began to experiment with trait inheritance in plants in 1892. Correns already knew about some of Mendel's plant experiments from Nägeli.

However, by 1900, when Correns submitted his own results for publication, the paper was called: G. Mendel's Law Concerning the Behavior of the Progeny of Racial Hybrids. Correns and de Vries were the ones who most clearly "redefined" Mendel's laws. Mendel, in his paper, spoke about the "law of combination of different characters" and talked about "the law of independent assortment." Mendel implied that the segregation of factors occurred in the production of sex cells. Correns (with credit to de Vries) restated Mendel's results, giving us Mendel's law of segregation and Mendel's law of independent assortment.

Correns was active in genetic research in Germany, and was modest enough to never have a problem with scientific credit or recognition. He believed that his other work was more important, and the rediscovery of Mendel's laws only helped him with his other work. Correns was supposedly indignant that Hugo de Vries did not mention Gregor Mendel in the first printing of de Vries' paper. Credit should be given where due. In 1913, Correns became the first director of the newly founded Kaiser Wihelm Institut für Biologie in Berlin-Dahlem. Unfortunately, most of his work was unpublished and destroyed when Berlin was bombed in 1945.

3.1.4 Hugo De Vries (1848 – 1935)

Plate 4, Hugo De-Vries

Hugo Marie de Vries (Plate 4) was a Dutch botanist and one of the first geneticists. He is known chiefly for suggesting the concept of genes, rediscovering the laws of heredity in the 1890s. He was born on 16th February, 1848 in Haarlem, Netherlands and died May 21st, 1935 in Lunteren, Netherlands. A Dutch botanist and geneticist who introduced the experimental study of organic evolution, his rediscovery in 1900 (simultaneously with the botanists Carl Correns and Erich Tschermak von Seysenegg) of Gregor Mendel's principles of heredity and his theory of biological mutation, though considerably different from a modern understanding of the phenomenon, resolved ambiguous concepts concerning the nature of variation of species that, until then, had precluded the universal acceptance and active investigation of Charles Darwin's system of organic evolution.

3.1.5 Erich Von Tschermak (1871 – 1962)

Erich Tschermak, Edler von Seysenegg (Plate 5) was an Austrian agronomist who developed several new disease-resistant crops. He was a son of the Moravia-born mineralogist Gustav

Plate 5, Erich Von Tschermak

In 1898, he started doing plant-breeding experiments using peas, and by 1900, he had written up his results. Tschermak, like de Vries and Correns, independently derived "Mendelian" laws of inheritance from his plant experiments. Because he was younger, and not as established in the scientific community, Tschermak was worried about the acceptance of his paper given those of de Vries' and Correns'. However, he was able to rush his paper to press, and was accorded his share of attention as one of the rediscoverers of Mendel's laws.

Tschermak was a plant breeder, and his hybridization experiments were done with the idea of improving crops using the laws of heredity. He did most of the work himself, and produced high-yielding food crops such as wheat, barley, and oats. In 1903, Tschermak was appointed associate professor at the University of Agricultural Sciences in Vienna, and later became a full professor. He was a major influence in agriculture and plant breeding in Austria.

4.0 CONCLUSION

You should have noted in this unit, some important dates, historical background and major contributions made by some ingenious scientists to genetics and animal breeding. It can be concluded from our discussion that basic principles of evolution put forward by Darwing and the principles of particulate inheritance by Mendel are fundamental.

5.0 SUMMARY

The details of the foundation of genetics and early philosophers, thinkers and workers in the field of genetics pave way to the appreciation of their great contributions. The works of Gregor Mendel and Charles Darwin as the founding fathers of genetics cannot be over emphasized.

6.0 TUTOR MARKED ASSIGNMENT

The following are assignments for you. You should attempt all and submit your answers to your tutor as at when due.

1. Enumerate the three principles of Darwin's theories.
2. Name the two founding fathers of genetics.
3. Name the three scientists who independently re-discovered Mendel's work.
4. Watson and Crick shared a Nobel Prize in the year (a) 1960 (b) 1962 (c) 1964
5. Who is the researcher that cloned a sheep (Dolly) at the Roslin Institute in Scotland?
   (a) Carl Correns in 1986 (b) Ian Wilmut in 1996 (c) Thomas Hunt Morgan in 2006

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UNIT 3 HISTORY OF GENETICS II (Watson and Crick and others)

CONTENTS

3.0 INTRODUCTION

This unit shall provide an overview of major contributions made in the field of modern genetics by other great researchers and scientists. The great discovery by Thomas Hunt Morgan in his work with fruit flies in 1907 proved that chromosomes have a definite function in heredity. He established mutation theory that led to the fundamental understanding of the mechanisms of heredity. Thomas Hunt also discovered the white-eye and its sex-linkage in Drosophila and received a Nobel Prize in 1933. Other researchers like Watson and Crick whose work shook the world with an elegant double stranded, helical complementary, anti-parallel model through observations of the X-ray crystallographic images of the deoxyribonucleic acid (DNA).

4.0 OBJECTIVES

At the end of this unit you should be able to:

- Highlight the major contributions made by Morgan Thomas, Watson and Crick as well as Ian Wilmut.

- Briefly explain the Human genome project

5.0 MAIN CONTENT

3.1 History of genetics II

3.1.1 Morgan Thomas Hunt (1866 – 1945)

Plate 6, Thomas Morgan Hunt

Thomas Hunt Morgan (Plate 6) was an American evolutionary biologist, geneticist, embryologist, and science author who won the Nobel Prize in Physiology or Medicine in 1933 for discoveries elucidating the role that the chromosome plays in heredity. He was born on 25th September, 1866 at Lexington, Kentucky, U.S.A and died on 4th December, 1945. The eldest son of Charlton Hunt Morgan, he was educated at the University of Kentucky, where he took his B.S. degree in 1886, subsequently doing postgraduate work at Johns Hopkins University, where he studied morphology with W. K. Brooks and physiology with H. Newell Martin.

In 1890 he obtained his Ph.D. degree at Johns Hopkins University. In that same year he was awarded the Adam Bruce Fellowship and visited Europe, working especially at the Marine Zoological Laboratory at Naples which he visited again in 1895 and 1900. At Naples he met Hans Driesch and Curt Herbst. The influence of Driesch with whom he later collaborated, no doubt turned his mind in the direction of experimental embryology. In 1891 he became Associate Professor of Biology at Bryn Mawr College for Women, where he stayed until 1904, when he became Professor of Experimental Zoology at Columbia University, New York. He remained there until 1928, when he was appointed Professor of Biology and Director of the G. Kerckhoff Laboratories at the California Institute of Technology, at Pasadena. Morgan was made a Foreign Member of the Royal Society of London in 1919, where he delivered the Croonian Lecture in 1922. In 1924, he was awarded the Darwin Medal, and in 1939 the Copley Medal of the Society. For his

discoveries concerning the role played by the chromosome in heredity, he was awarded the Nobel Prize in 1933.

3.1.5 Watson and Crick

Plate 7, James Watson Plate 8, Francis Crick

In 1953, James Watson and Francis Crick shook the world with an elegant double stranded, helical complementary, anti-parallel model through observations of the X-ray crystallographic images of the deoxyribonucleic acid (DNA). James Dewey Watson is an American molecular biologist, geneticist and zoologist, best known as one of the co-discoverers of the structure of DNA in 1953 with Francis Crick. James Dewey Watson (Plate 7) was born in Chicago on April 6th, 1928. He received a tuition scholarship to the University of Chicago, and in the summer of 1943 entered their experimental four-year college. In 1947, he received a B.Sc. degree in Zoology. Watson received a Fellowship for graduate study in Zoology at Indiana University in Bloomington, where he received his Ph.D. degree in Zoology in 1950. Watson's Ph.D. thesis, done under Luria's able guidance, was a study of the effect of hard X-rays on bacteriophage multiplication. From September 1950 to September 1951 he spent his first postdoctoral year in Copenhagen as a Merck Fellow of the National Research Council. Part of the year was spent with the biochemist Herman Kalckar, the remainder with the microbiologist Ole Maaløe. Again he worked with bacterial viruses, attempting to study the fate of DNA of infecting virus particles. He soon met Crick and discovered their common interest in solving the DNA structure.

Francis Harry Compton Crick (Plate 8) was born on June 8th, 1916, at Northampton, England, being the elder child of Harry Crick and Annie Elizabeth Wilkins. He has one

brother, A. F. Crick, who is a doctor in New Zealand. Crick was educated at Northampton Grammar School and Mill Hill School, London. He studied physics at University College, London, obtained a B.Sc. in 1937, and started research for a Ph.D. under Prof E. N. da C. Andrade, but this was interrupted by the outbreak of war in 1939. During the war he worked as a scientist for the British Admiralty, mainly in connection with magnetic and acoustic mines. He left the Admiralty in 1947 to study biology. A critical influence in Crick's career was his friendship, beginning in 1951, with J. D. Watson, then a young man of 23, leading in 1953 to the proposal of the double-helical structure for DNA and the replication scheme. Crick and Watson subsequently suggested a general theory for the structure of small viruses. The two shared a Nobel Prize in 1962.

3.1.6 Wilmut Ian (1944 – date)

Plate 9, Sir Wilmut Ian

Sir Ian Wilmut, (Plate 9) is a British embryologist and Chair of the Scottish Centre for Regenerative Medicine at the University of Edinburgh. He was born on 7th July, 1944 (age 71) at Hampton Lucy, Warwickshire, England. He was the first to use nuclear transfer of differentiated adult cells to generate a mammalian clone, a Finn Dorset sheep named Dolly, born in 1996.

The news of Dolly's birth was reported in every major newspaper and magazine around the world, and Dolly became the most celebrated (and certainly the most photographed) lamb in the history of animal husbandry. Wilmut was invited to speak before the Parliament of the United Kingdom and the Congress of the United States, after which the team leaders were interviewed to the point of exhaustion. Cloning a mammal sparked the public's imagination in a way that had not been seen since American astronauts got their white suits dirty on the surface of the moon. Cloning a sheep brought the technology closer, making it both fascinating and frightening to a great many people.

3.1.7 The Human Genome project

The completion of a "working draft" of the human genome (an important milestone in the Human Genome Project) was announced in June 2000 at a press conference at the White House USA, and was published in the February 15, 2001 issue of the journal *Nature*. In February 2001, two competing research programs published working drafts of the human genome. A genome is the total of all genetic material in an organism. Genomics is a branch of science concerned with development and utilization of DNA sequences and genetic maps that represent the architecture of the genome. The first genetic sequence of a cow was published in 2009. This milestone was achieved through an international collaboration with 300 scientists in 25 countries and took six years to complete. The first cow to be sequenced was the Hereford breed, but other additional breeds that were sequenced included Holstein, Angus, Jersey, Limousin, Norwegian Red and Brahman.

4.0 CONCLUSION

In this unit we discussed the Nobel Prize winner's salient contributions to the field animal breeding and genetic engineering.

- Morgan T.H. was awarded the Darwin Medal in 1924, and in 1939 the Copley Medal of the Society for his discoveries concerning the role played by the chromosome in heredity, he was awarded the Nobel Prize in 1933.
- In 1953, James Watson and Francis Crick shook the world with an elegant double stranded, helical complementary, anti-parallel model through observations of the X-ray crystallographic images of the deoxyribonucleic acid (DNA). The two shared a Nobel Prize in 1962.
- Wilmut Ian was the first to use nuclear transfer of differentiated adult cells to generate a mammalian clone, a Finn Dorset sheep named Dolly, born in 1996. He received several awards for his discoveries.

5.0 SUMMARY

In this unit you have been taken through the history lane of some great researchers and scientists in the world of animal breeding and genetic engineering. You are expected to read your notes very well so as to clearly understand how their discoveries have changed the world of science.

6.0 TUTOR MARKED ASSIGNMENT

1. The evolutionary biologist, geneticist, embryologist and scientist who won the Nobel Prize in Physiology/Medicine in 1933 for discoveries elucidating the role that the chromosome plays in heredity was;
   (a) Wilmut Ian (b) Morgan T. Hunt (c) James Watson (d) Francis Crick

2. The two great scientists who shared a Nobel Prize in 1962 were; (a) Wilmut Ian and Morgan T.H. (b) Morgan T. H and Francis Crick (c) James Watson and Francis Crick (d) Francis Crick Wilmut Ian

3. Dolly the Sheep was born in 1996 by the use of nuclear transfer of differentiated adult cells through a team of researchers lead by; (a) Wilmut Ian (b) Morgan T. Hunt (c) James Watson (d) Francis Crick

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MODULE 3 MENDELIAN GENETICS AND NON MENDELIAN INHERITANCE

Unit 1 Mendelian genetics I (Mendel's first law and the law of dominance)

Unit 2 **Mendelian genetics II (Mendel's second law and the Punnet Square)**

Unit 3 **Non Mendelian inheritance I (Types of gene action)**

Unit 4 **Non Mendelian inheritance II (Types of gene action)**

UNIT 1: MENDELIAN GENETICS I (Mendel's first law and the law of dominance)

CONTENTS

1.0 INTRODUCTION

You will now be taken through another unit of the course, which is fundamental to the understanding of genetics and is called Mendelian genetics. The section will discuss how Gregor Mendel conducted his experiment and the results he obtained. Mendel's first law will be explained in detail. The basic calculation on monohybrid ratio of 1:3 will also be treated.

2.0 OBJECTIVES

At the end of this unit, you should be able to;

- explain how Mendel conducted his experiment
- state Mendel's first law and show how to calculate the monohybrid ratio of 1:2:1

3.0 MAIN CONTENT

3.1 Mendelian theory and the fundamental principles of genetics

The modern science of genetics traces its roots to Gregor Johann Mendel, a German Czech Augustinian monk and scientist who studied the nature of inheritance in plants. In his paper 'Experiments on Plant Hybridization' presented to the Society for Research in Nature in 1865 at Brünn, Mendel traced the inheritance patterns of certain traits in pea plants and described them mathematically. Although this pattern of inheritance could only be observed for a few traits, Mendel's work suggested that heredity was particulate, not acquired, and that the inheritance patterns of many traits could be explained through simple rules and ratios. The importance of Mendel's work did not gain wide understanding until the 1890s, after his death, when other scientists working on similar problems re-discovered his research.

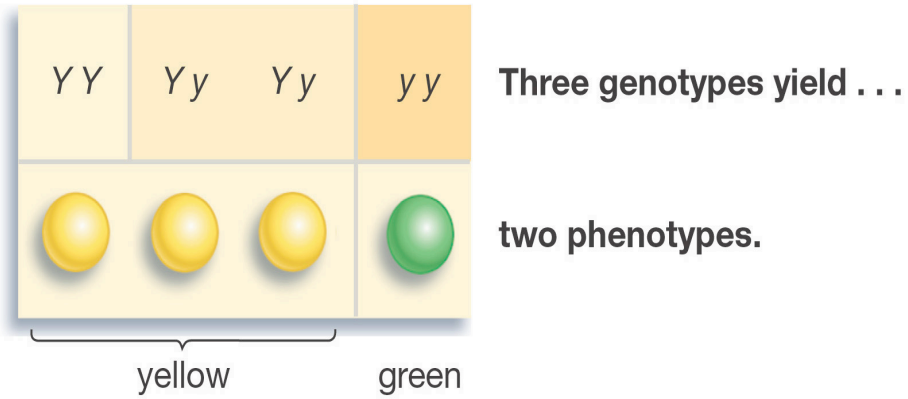
At its most fundamental level, inheritance in organisms occurs by means of discrete traits, called *genes*. Gregor Mendel, who studied the segregation of heritable traits in pea plants, first observed this property. In his experiments studying the trait for flower color, Mendel observed that the flowers of each pea plant were either purple or white but never intermediate between the two colors. These different, discrete versions of the same gene are called *alleles*. In the case of pea plants, each organism has two alleles of each gene, and the plants inherit one allele from each parent. Many organisms, including humans, have this pattern of inheritance. Organisms with two copies of the same allele are called *homozygous*, while organisms with two different alleles are *heterozygous*. The set of alleles for a given organism is called its *genotype*, while the observable trait the organism has is called its *phenotype*. When organisms are heterozygous, often one allele is called *dominant* as its qualities dominate the phenotype of the organism, while the other allele is called *recessive* as its qualities recede and are not observed. Some alleles do not have complete dominance and instead have *incomplete dominance* by expressing an intermediate phenotype or *codominance* by expressing both alleles at once. When a pair

of organisms reproduces sexually, their offspring randomly inherit one of the two alleles from each parent.

3.1.1 Dominancy and recessiveness

It is a result of interaction between alleles at a singe locus in which one allele completely suppresses or covers the expression of the alternative allele which is said to be **recessive**. **Dominance** is said to be complete when both the heterozygotes and dominant homozygotes cannot physically be distinguished (i.e. phenotypically). That is, they have the same phenotypic value. For example, some poultry breeds used for meat production, the gene for white skin (**WW**) is dominant to the gene for yellow skin (**ww**). F1 progeny have white skin but heterozygotes.

3.1.1.1. The **Law of Dominance** explains that, in a cross of parents (Fig. 14) that are pure for contrasting traits (e.g. **Y** for yellow and **y** for green), only one form of the trait will appear in the next generation (**Yy** = all yellow). All the offspring will be heterozygous and express only the dominant trait.



(Figure 14, parental genotypes and phenotypes)

3.1.2 Mendel's first law (The law of segregation)

Mendel's first law is also called the law of segregation and it states that "two members of a gene pair segregate from each other into the gametes, so that half of the gametes carry one member of the pair and the other half of the gametes carry the other member of the pair". For example, during the formation of gametes (eggs or sperm) the two alleles

responsible for a trait separate from each other. Alleles for a trait are then "recombined" at fertilization, producing the genotype for the traits of the offspring (Fig. 15).

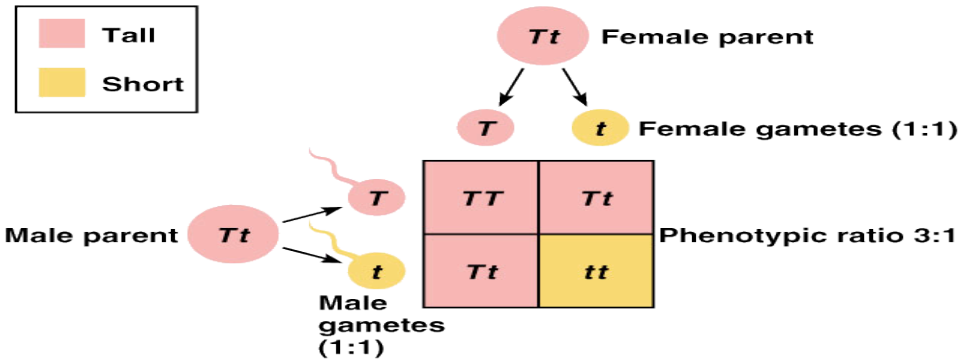


Figure 15, monohybrid cross

3.1.2.1 The monohybrid crossing:

Mono means one hence this cross simply involves just one single trait, example flower colour. Mendel mated two parents each having only one contrasting trait. He called the parents 'parental generation' (i.e P_1). Their offspring are called the first filial generation offspring (ie F_1 generation). F_2 generation are obtained when individuals from the F_1 generation are mated inter se, (i.e 2nd filial generation).

How Mendel began his experiment:

He produced pure strains by allowing the plants to self-pollinate for several generations. He considered 8 contrasting traits or characters (Fig. 16). The cross between true breeding pea plants with tall stems and dwarf stems represents Mendel's monohybrid crosses. *Tall* and *dwarf* represent contrasting forms of one character (stem height). When **true breeding** tall plants (**TT**) were crossed with dwarf (**tt**) plants, the resulting F1 generation consisted of only tall plants.

The Eight Pea plant traits used by Mendel in his experiment are shown in Fig. 16

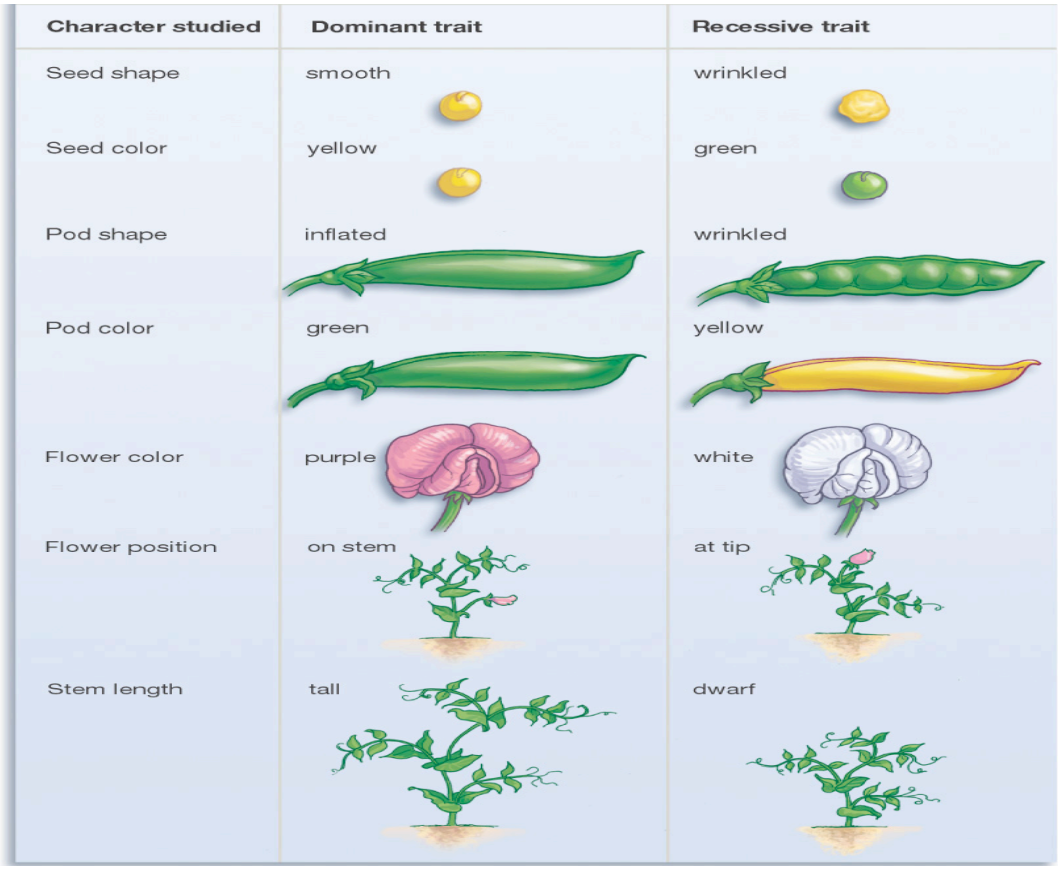


Figure 16, the eight traits used by Mendel

Parental phenotype: Tall Short
Parental genotype (2n): **T T X t t**

Gametes (n) **T T t t**

F_1 Genotype (2n): **T t T t T t T t**

Phenotype: All Tall

From the above cross, all the observed phenotypes are the same (Tall) with similar genotypes (Tt). Next, was the mating of the F_1 individuals *inter se,* which is otherwise called selfing. So when members of the F1 generation were selfed, Mendel observed that 787 of 1064 F2 plants were tall, while 227 of 1064 were dwarf. This gives a ratio of approximately 2.8:1 or about 3:1. That is, three-quarter (3/4) appeared like F1 plants

while one-quarter (1/4) exhibited the contrasting trait which has disappeared in the F1 generation, only to reappear in the F2. Summary of Mendel's monohybrid cross experiment is given in Fig. 17)

P2 phenotype: Tall Tall

P2 genotype (2n): **T t** **X** **T t** (*Selfing*)

P2 gametes (n) **T** **t** **T** **t**

F2 Genotype (2n): **T T** **T t** **T t** **t t**

Genotypic ratio: 1TT : 2Tt : 1 tt

Phenotypic ratio: 3 Tall : 1 Dwarf (ie 3/4 tall: 1/4 dwarf)
(787/1064) (227/1064)

Self - Assessment work:

Practice your crosses using the P_1, F_1 and both F_2 crosses for each of the other seven Pea Plant Traits.

Dominant trait	Recessive trait	Ratio of dominant to recessive in F_2 generation
Smooth seed	Wrinkled seed	2.96:1 (5,474 smooth, 1,850 wrinkled)
Yellow seed	Green seed	3.01:1 (6,022 yellow, 2,001 green)
Inflated pod	Wrinkled pod	2.95:1 (882 inflated, 299 wrinkled)
Green pod	Yellow pod	2.82:1 (428 green, 152 yellow)
Purple flower	White flower	3.14:1 (705 purple, 224 white)
Flower on stem	Flower at tip	3.14:1 (651 along stem, 207 at tip)
Tall stem	Dwarf stem	2.84:1 (787 tall plants, 277 dwarfs)
	Average ratio, all traits:	**3:1**

Figure 17, summary of Mendel's monohybrid cross

4.0 CONCLUSION

This unit indicated how you can clearly state the first law of Mendel. We were able to discuss how Mendel conducted his experiments. The 8 characters used by Mendel were shown and the step-by-step methods he followed in the cross were highlighted. You should be able to calculate the monohybrid ratio of 3:1

5.0 SUMMARY

In this unit you have been introduced to Mendelian genetics, the principle of monohybrid crossing using the simple arrow method. You have also been introduced to the works of Mendel looking at the eight traits he used.

6.0 TUTOR MARKED ASSIGNMENT

1. Clearly state Mendel's first law otherwise called the law of segregation.
2. Explain the law of dominance
3. The ratio obtained from a monohybrid cross is
   (a) 1:3 (b) 3:1 (c) 9:3 (d) 3:9

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UNIT 2 MENDELIAN GENETICS II (Mendel's second law and the Punnet Square)

CONTENTS

1.0 INTRODUCTION

In this unit, Mendel's second law otherwise called the law of independent assortment will be explained in detail. The basic calculations involving dihybrid crossing using the punnet square will be treated.

2.0 OBJECTIVES

By the end of this unit, you are expected to be able to;

- State Mendel's second law also known as the law of independent assortment
- Use the Punnet square in solving dihybrid crossing and calculations leading to the dihybrid ratio of 9:3:3:1

3.0 MAIN CONTENT

3.1 Mendel's Second Law

This is also called the law of independent assortment, which states that "gene pairs assort independently during gamete formation". This law simply means alleles for *different* traits are distributed to sex cells (and offspring) independently of one another. Dihybrid crosses are best used to illustrate Mendel's second law.

3.1.1 Dihybrid cross: Di means two and a dihybrid cross is a cross involving two traits; example flower colour and plant height. It is a breeding experiment that tracks the inheritance of two traits. Dihybrid cross is a cross between two different lines (varieties, strains) that differ in two observed traits. In the Mendelian sense, between the alleles of both these loci there is a relationship of complete dominance - recessive. A dihybrid cross involves a study of inheritance patterns for organisms differing in two traits. Mendel invented the dihybrid cross to determine if different traits of pea plants, such as flower color and seed shape, were inherited independently. Our objective is to understand the principles that govern inheritance of different traits in a dihybrid cross that led Mendel to propose that alleles of different genes are assorted independently of one another during the formation of gametes.

3.1.2 The Punnet Square is a method used to help solve genetics problems. It is named after Punnet R.C., who first devised the method in which gametes are arranged in rows and columns. You can predict the next generation offspring by combining the gametic information of both male and female parent. Punnet square is a tool to predict the probability of certain traits in offspring that shows the different ways alleles can combine. It is a chart that shows all the possible combinations of alleles that can result when genes are crossed. Letters stand for dominant and recessive alleles; uppercase letter stands for a dominant allele while lowercase letters stand for recessive alleles (Fig. 18). Reginald Punnet worked with William Bateson on genetics research. Punnet later became the first Professor of Genetics at Cambridge University.

	RY	Ry	rY	ry
RY	RRYY	RRYy	RrYY	RrYy
Ry	RRYy	RRyy	RrYy	Rryy
rY	RrYY	RrYy	rrYY	rrYy
ry	RrYy	Rryy	rrYy	rryy

Figure 18, typical punnet square for dihybrid cross

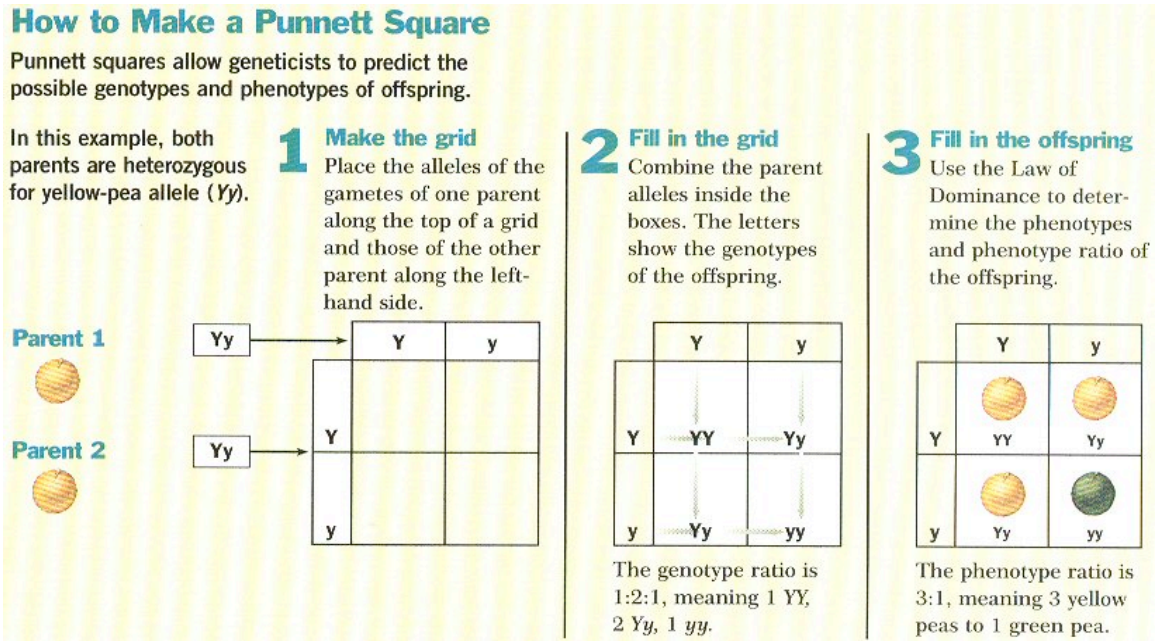

Figure 19, steps in using punnet square

Let us consider pure breeding (Fig. 19) homozygous plants having round and yellow peas (**RRYY**) were crossed with pure breeding recessive plants having wrinkled and green peas (**rryy**) to produce F1 generation seeds that were round and yellow (**RrYy**).

Round (**R**) is dominant to wrinkle (**r**), and Yellow (**Y**) is dominant to green (**y**)

Phenotype of Parent: Round-yellow wrinkled-green

Genotype of Parent (2n): **RRYY** X **rryy**

Gametes (n): **R Y** **r y**

F1 Genotype (2n): **RrYy** (*Round-yellow*)

F1 heterozygote plants were self pollinated to produce F2 generation from four kinds of gametes R, r, Y, y. The Punnet Square below (Fig. 20) illustrates dihybrid cross and the resultant genotypic and phenotypic ratios given in the summary (Fig. 21).

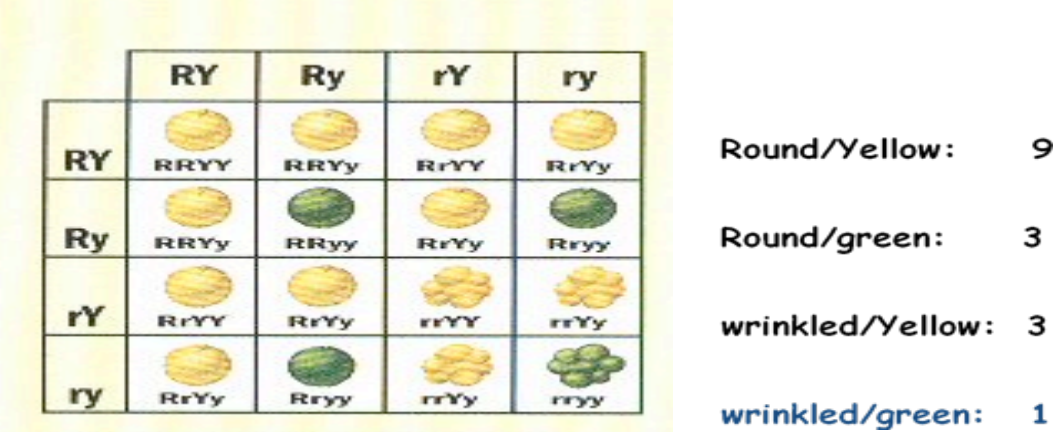

Figure 20, result of dihybrid cross yielding ratio of 9:3:3:1

LAW	PARENT CROSS	OFFSPRING
DOMINANCE	TT x tt tall x short	100% Tt tall
SEGREGATION	Tt x Tt tall x tall	75% tall 25% short
INDEPENDENT ASSORTMENT	RrGg x RrGg round & green x round & green	9/16 round seeds & green pods 3/16 round seeds & yellow pods 3/16 wrinkled seeds & green pods 1/16 wrinkled seeds & yellow pods

Figure 21, Summary of Mendel's laws and ratios obtained

4.0 CONCLUSION

This unit is concluded if you;

- can clearly state the second law of Mendel.
- will be able to explain what the Punnet square is all about.
- can as well solve a problem on dihybrid crossing and get ratio of 9:3:3:1.

5.0 SUMMARY

In this unit you have been introduced to Mendelian principle of dihybrid crossing using the punnet square. Step-by step method of solving dihybrid crossing leading to the ratio of 9:3:3:1 was explained using the Punnet Square.

6.0 TUTOR MARKED ASSIGNMENT

1. Clearly state Mendel's second law.
2. What is a dihybrid cross?
3. What is a Punnet Square?
4. How many gametes will be produced for the following allele arrangements? {Remember the formula: 2^n (n = number of heterozygotes}

   (i) RrYy

   (ii) AaBbCCDd

   (iii) MmNnOoPPQQRrssTtQq

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UNIT 3 NON MENDELIAN INHERITANCE I (Types of gene action)

1.0 INTRODUCTION

In this lecture unit, you will examine traits that deviate from the simple dominant/recessive relationship. The inheritance patterns of these traits still obey Mendelian laws. However, they are more complex and interesting than Mendel had realized. Mendelian inheritance describes inheritance patterns that obey two laws: Law of segregation and Law of independent assortment as we treated in the previous module.

2.0 OBJECTIVES

By the end of this unit, you should be able to explain the various inheritance patterns that disobeys Mendel laws, which include;

- incomplete dominance
- multiple alleles
- incomplete penetrance and
- variable expressivity

3.0 MAIN CONTENT

3.1 Deviations from Mendelian inheritance I

Non Mendelian inheritance, exceptions or deviations from Mendelian laws are terms used to refer to any pattern of inheritance in which traits do not segregate in accordance with Mendelian inheritance. The following are several circumstances that appear to contradict Mendel's Laws.

3.1.1 Incomplete dominance: This is a situation in which the heterozygous phenotype is intermediate between the two homozygous. In other words, it is a form of intermediate inheritance where one allele for a specific trait is not dominant over the other allele. There are two types of incomplete dominance: co-dominance and over-dominance.

(a) Co-dominance: The four-o'clock paint plants may have red, white or pink flowers (Fig. 22). Plants with red flowers have two copies of the dominant allele *R* for red flower color (*RR*). Plants with white flowers have two copies of the recessive allele *w* for white flower color (*ww*). Pink flowers result in plants with one copy of each allele (*RW*), with each allele contributing to a blending of colors.

Figure 22, co-dominance gene action

- The ABO blood system in man provides another good example of codominance. Heterozygote I^A/I^B individuals are blood group AB because both the A antigen (product of the I^A allele) and the B antigen (product of the I^B allele) are produced. Thus, the I^A and I^B alleles are codominant.

(b) ***Overdominance:*** This is another type of incomplete dominance gene action in which the performance of heterozygote is more extreme than that of both homozygotes. In other words, it is the inheritance where the heterozygotes have traits that are more beneficial to the individual than the homozygotes, e.g. sickle cell anaemia (Fig. 23). The sickle cell trait is an autosomal recessive disorder in which affected individuals produce abnormal form of haemoglobin.

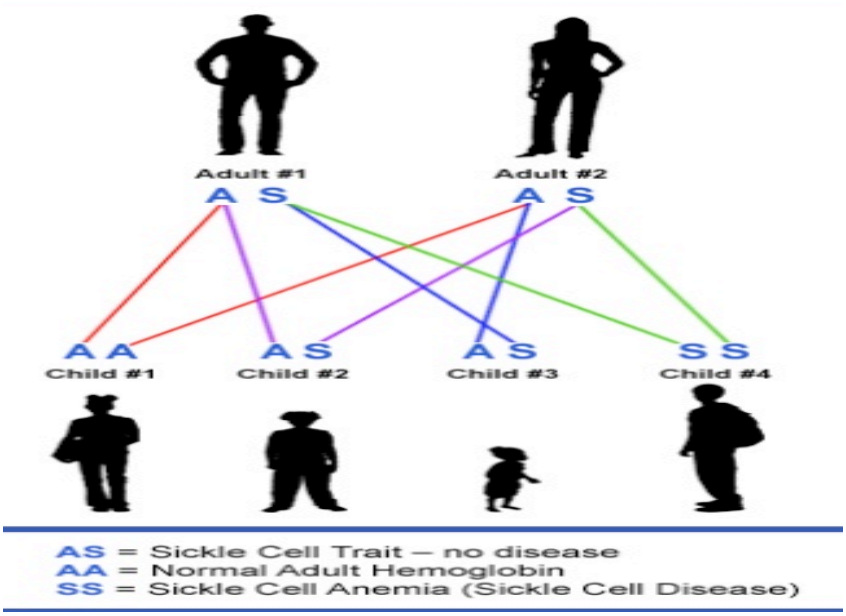

Figure 23, breeding for sickle cell disease

Another example is found in white Wyandotte breed of poultry. The gene for Rose comb **R**, is dominant to the gene for single comb **r**. Heterozygous males have normal fertility while homozygous dominant males have lowered fertility.

	RR (Rose comb)	**Rr** (Rose comb)	**rr** (Single comb)
Male:	*Lower fertility	Normal fertility	Normal fertility
Female:	Normal fertility	Normal fertility	Normal fertility

3.1.2 Multiple alleles: A trait that is controlled by more than two alleles is said to be controlled by multiple alleles. Traits controlled by multiple alleles produce more than three phenotypes of that trait. For Example, blood group in humans is controlled by

autosomal gene locus I, which stands for Isohaemaglutinogen, and the alleles are called A, B, and O. The O allele is recessive to both the A and B alleles. When a person inherits one A allele and one B allele for blood type, both alleles are expressed. The person has the blood phenotype AB. A person with phenotype A blood inherited an A and an O allele (AO) or an A and an A allele (AA). Someone with phenotype B blood has the genotype BB or BO. This person inherited either a B and an O allele, or two B alleles. A person with phenotype O blood has the genotype OO (Table 2).

Table 2: Human blood group genotypes

Genotype	Blood group
I^AI^A	A
I^AI^O	A
I^BI^B	B
I^BI^O	B
I^AI^B	AB
I^OI^O	O

Presence of single dominant allele results in the blood producing a substance called agglutinin which acts as an antibody. E.g. I^AI^O produces Agglutinin A.

3.1.3 Incomplete penetrance: The term indicates that a dominant allele does not always 'penetrate' into the phenotype of the individual, i.e. the dominant allele is not expressed in a heterozygote individual. A good example is the case of polydactyl, which is an autosomal dominant trait where affected individuals have additional fingers and or toes. A single copy of the allele is usually sufficient to cause this condition. In some cases however, individuals carry the dominant allele but do not exhibit the trait. Generally, in any particular individual, the trait is either penetrant or not.

3.1.4 Variable expressivity: This is the degree to which a trait is expressed. In the case of polydactyl, the number of digits can vary. A person with many extra digits has high expressivity of this trait, while another with single extra digit has low expressivity. Generally, the molecular explanation of variable expressivity and incomplete penetrance

may not clearly be understood, because the range of phenotypes might be due to influences of the environment and/or other genes.

4.0 CONCLUSION

As you have learnt in this unit, although alleles are transmitted from parent to offspring according to Mendelian principles, they sometimes fail to display the clear-cut dominant-recessive relationship observed by Mendel. The result of the various exceptions to Mendelian principles is the occurrence of phenotypes that differ from those resulting from mono-, di-, and tri-hybrid crosses. Another exception to Mendelian inheritance is the presence of genes on sex chromosomes, where males only receive a single copy of genes on that chromosome. In many cases contrast to Mendelian genetics, two or more genes are known to influence the phenotype of a single characteristic.

5.0 SUMMARY

In this unit, we have examined that the Mendelian inheritance pattern is rare in nature (too complex). Other patterns include polygenic inheritance, incomplete dominance, multiple alleles, and codominance. You were also told that genes that have three or more possible alleles are said to have multiple alleles and such control the ABO blood groups (blood types) in humans. Codominance is a condition in which both alleles for the same gene are fully expressed. The genetics of human blood groups is an example of codominance.

6.0 TUTOR MARKED ASSIGNMENT

1. There are two types of incomplete dominance, mention them
2. The ABO blood system in man provides a good example of: (a) codominance
   (c) over dominance (c) lethal allele (d) recessive allele
3. The sickle cell anaemia is another good example of: (a) codominance
   (b) over dominance (c) lethal allele (d) recessive allele
4. Polydactyl in man is a situation where the individual possesses extra fingers or toes and such a condition is due to: (a) lethality (b) variable expressivity (c) incomplete penetrance
5. The following questions (a) and (b) relate to codominance and multiple allele:

(a) If a boy has a blood type O and his sister has blood type AB. What are the genotypes and phenotypes of their parents?
(b) A man whose blood group is A was married to a woman whose blood group is B and the marriage was blessed with a child whose blood group is AB.
    (i) What are the genotypes of the 3 individuals?
    (ii) What is the probability of the couple's next child having blood group AB?

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UNIT 4 NON MENDELIAN INHERITANCE II (Types of gene action)

1.0 INTRODUCTION

Non-Mendelian inheritance is a general term that refers to any pattern of inheritance in which traits do not segregate in accordance with Mendel's laws. These laws describe the inheritance of traits linked to single genes on chromosomes in the nucleus. In Mendelian inheritance, each parent contributes one of two possible alleles for a trait. If the genotypes of both parents in a genetic cross are known, Mendel's laws can be used to determine the distribution of phenotypes expected for the population of offspring. Some of the several situations in which the proportions of phenotypes observed in the progeny do not match the predicted values have been enumerated under Unit 3. The few others will be discussed under this unit.

2.0 OBJECTIVES

At the end of this unit, you should be able to explain the various inheritance patterns that disobey Mendel laws. These include (but not limited to) the following:

- Sex limited traits

- Sex influenced traits
- Sex linked traits and
- Lethal ganes

3.0 MAIN CONTENT

3.1 Deviations from Mendelian inheritance II

This is the second phase of discussion on exceptions or deviations to Mendelian laws, which we said are terms used to refer to any pattern of inheritance in which traits do not segregate in accordance with Mendel's laws. The following are yet other several circumstances that appear to contradict Mendel's Laws, further constituting different types gene action.

3.1.1 Sex limited traits: Sex limited genes are autosomal genes (genes located on autosome chromosomes, i.e. not located on the sex chromosomes) that affect traits which appear only in one sex, but not in the other sex. Good examples are milk production in dairy cattle, the formation/enlargement of breast in human and the ability to produce eggs in chicken. The genes involved in these traits operate in females but not in males. Another example is feather plumage in chicken where the pattern of hen feathering depends on the production of sex hormone. If the single ovary is surgically removed from a newly hatched female (hh), she will develop cock feathering and look exactly like a cock.

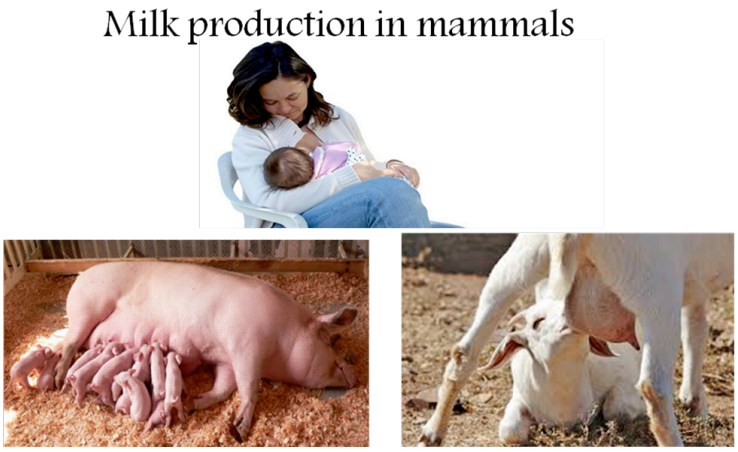

Plate 10, sex limited inheritance

Inheritance of sex-limited trait e.g. the feathering pattern in chickens

P generation: Female x Male
Phenotype: hen-feathered cock-feathered
Genotypes: h^+/h^+ h/h
Gametes: All h^+ all h
F_1 genotypes: All h^+/h
F_1 Phenotypes: All hen-feathered

Interbreeding of F_1
F_1 generation: Female x Male
F_1 phenotype: hen-feathered hen-feathered
F_1 genotypes: h^+/h h^+/h
F_1 gametes: ½ h^+, ½ h ½ h^+, ½ h

F_1 female gametes	F_1 male gametes	
	½ h^+	½ h
½ h^+	¼ h^+/h^+	¼ h^+/h
½ h	¼ h^+/h	¼ h/h

F_2 Genotypes ¼ h^+/h^+, ½ h^+/h, ¼ h/h
F_2 Phenotypes in females h^+/h^+, h^+/h and h/h are hen-feathered
in males h^+/h^+, h^+/h are hen-feathered while h/h are cock-feathered.

3.1.2 Sex influenced traits: The expression of some genes may be sex influenced, which are autosomal and appear in both sexes. But either the frequency of occurrence in the two sexes is different or the relationship between genotype and phenotype is different. Typical example is pattern baldness in humans (Table 3). The BB genotype specifies pattern baldness in males and females and the bb genotype gives a nonbald phenotype in both sexes. The difference is in the heterozygotes where in males Bb leads to the bald phenotype but in females it leads to the nonbald phenotype. In other words, the b allele acts as a dominant in males but a recessive in females.

Table 3: Inheritance of baldness in male and female human

Genotype	Male phenotype	Female phenotype
BB	Bald	Bald
Bb	Bald	Nonbald
Bb	Nonbald	Nonbald

3.1.3 Sex linked traits: Genes located on the sex chromosomes are said to be sex linked and have different patterns of inheritance. They display different patterns of inheritance than genes located on autosomes. In human females (Plate 11), the sex chromosomes consist of two X chromosomes (**XX**), while males have an X chromosome and a shorter Y chromosome with many fewer genes (**XY**). A male's X chromosome may contain a recessive allele associated with a genetic disorder, such as hemophilia or muscular dystrophy. In this case, males do not have a normal second copy of the gene on the Y chromosome to mask the effects of the recessive gene, and disease typically results. Red-green colour blindness (Table 4) in humans and baldness are also sex-linked traits.

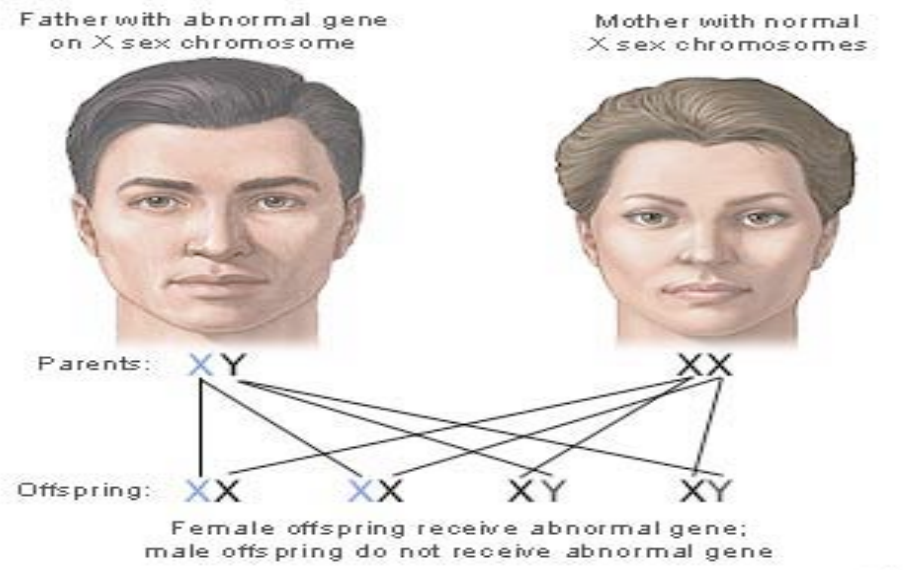

Plate 11, sex linked inheritance

Table 4, Genotypes and phenotypes of Colour blindness in human

Genotypes	Phenotypes
1. XX	Normal female
2. XX^c	Normal female,carrier of the gene
3. X^cX^c	Color-blind female
4. XY	Normal male
5. X^cY	Color-blind male

3.1.4 Lethal genes: An allele that results in the death of an organism is called a lethal allele, and the gene involved is called an essential gene. Essential genes are genes which, when they are mutated can result in a lethal phenotype. If the mutation is due to a dominant lethal allele, both homozygotes and heterozygotes for that allele will show the lethal phenotype. If the mutation is due to a recessive lethal allele, only homozygotes for that allele will be lethal.

In chickens, when an embryo contains two copies of the recessive gene known as creeper, the embryo dies inside the eggshell. Chicks that are heterozygous for the gene survive. Also in chickens that are homozygous for an allele controlling feather structure called 'frizzled', several phenotypic effects results from the incomplete development of the feathers. These chicken lack adequate feather insulation and suffer from heat loss leading to high mortality rate. The effect of lethal gene is also clearly illustrated by the inheritance of fur, a condition known as agouti. Some mice have yellow fur. Crossbreeding yellow mice produces offspring in the ratio, 2 yellow: 1 agouti (Yellow is dominant to agouti and all yellow coat mice are heterozygous). A ratio of 2:1 instead of the typical Mendelian ratio of 3:1 is explained by the fetal death of the dominant homozygous coat mice.

Inheritance of lethal allele in mice

P generation	Female parent	x	Male parent
Parental phenotype	Yellow mouse		Yellow mouse
Parental genotype	A^Y/A		A^Y/A
Gametes	½ A^Y, ½ A		½ A^Y, ½ A

F_1 generation

Female gametes	Male gametes	
	½ A^Y	½ A
½ A^Y	¼ A^Y/A^Y	¼ A^Y/A
½ A	¼ A^Y/A	¼ A/A

F_1 genotypes ¼ A^Y/A^Y, ½ A^Y/A, ¼ A/A
F_1 phenotypes ¼ die, ½ yellow, ¼ nonyellow
Birth ratio 2/3 A^Y/A yellow, 1/3 A/A nonyellow
A^Y allele is a recessive lethal allele because it causes death in the homozygous state.

7.0 CONCLUSION

As you have learnt in this unit, sex-influenced inheritance occurs when some alleles are dominant in one sex and recessive in the other e.g. baldness in humans. Sex-limited inheritance is a situation where some traits occur in only one of the sexes e.g. breast development in mammals. A lethal allele is one that has the potential to cause the death of an organism. These alleles are typically the result of mutations in essential genes. They are usually inherited in a recessive manner. Many lethal alleles prevent cell division. These will kill an organism at an early age. Some lethal alleles exert their effect later in life. Huntington disease is an example, which is characterized by progressive degeneration of the nervous system, dementia and early death. The age of onset of the disease is usually between 30 to 50 years. Conditional lethal alleles may kill an organism only when certain environmental conditions prevail, example Temperature-sensitive allele.

8.0 SUMMARY

In this unit, we have learned that several other situations do exists as to deviate from the Mendelian inheritance pattern. Situations such as sex limited and sex influenced inheritance were explained. Sex linked traits and lethal traits were also discussed.

9.0 TUTOR MARKED ASSIGNMENT

1. Define sex limited trait and give few examples
2. Give an example of a trait that is sex influenced?
3. Explain the type of gene action called sex linked inheritance
4. What is a lethal gene?

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- Alberts B. Johnson A. Lewis J. Raff M. Roberts K. Walter P. (2002). Molecular Biology of the Cell, 4th Edition, Garland. ISBN 0815332181. http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=mboc4.TOC&depth=2

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MODULE 4 QUANTITATIVE AND QUALITATIVE CHARACTERS AND THEIR MODE OF INHERITANCE

Unit 1 **Quantitative and qualitative inheritance**

Unit 2 **Heritability and repeatability**

Unit 3 **Animal variation and selection principles**

Unit 4 **Breeding methods**

UNIT 1 QUANTITATIVE AND QUALITATIVE INHERITANCE

CONTENTS

1.0 INTRODUCTION

Polygenic traits are traits that are governed by many gene pairs and so are called quantitative traits. Such traits are influenced to some extent by environmental factors. Qualitative traits on the other hand are determined by few pairs of genes and are less affected by environmental factors. In this section, details will be given on quantitative and qualitative inheritance with examples given to many traits being quantitative or qualitative. Heritability and repeatability are genetic parameters that will be explained in detail as we go through the unit.

2.0 OBJECTIVES

The end of this unit, expects you, to be able to;

- define quantitative trait as well as qualitative trait
- give some examples of traits that are quantitative and those that are qualitative
- understand the concept of heritability of a trait
- explain what repeatability of a trait is all about

3.0 MAIN CONTENT

3.1 Quantitative traits

Inheritance of quantitative traits, also called polygenic inheritance or multifactorial inheritance refers to the inheritance of a phenotypic characteristic (trait) that varies in degree and can be attributed to the interactions between two or more genes and their environment. Unlike monogenic traits, polygenic traits do not follow patterns of Mendelian inheritance (qualitative traits). Instead, their phenotypes typically vary along a continuous gradient depicted by a bell curve. An example of a polygenic trait is human skin color. Many genes factor into determining a person's natural skin color, so modifying only one of those genes changes the color only slightly. Many disorders with genetic components are polygenic, including autism, cancer, diabetes and numerous others. Most phenotypic characteristics are the result of the interaction of multiple genes. Generally, multifactorial traits apart from illness, contribute to what we see as continuous characteristics in organisms, such as height, skin color, and body mass. All of these phenotypes are complicated by a great deal of interplay between genes and environment. The continuous distribution of traits such as height and skin colour described above reflects the action of genes that do not quite show typical patterns of dominance and recessiveness. Instead the contributions of each involved locus are thought to be additive. Researchers have distinguished this kind of inheritance as *polygenic*, or *quantitative inheritance.* Thus, due to the nature of polygenic traits, inheritance will not follow the same pattern as a simple monohybrid or dihybrid cross. Polygenic inheritance can be explained as Mendelian inheritance at many loci, resulting in a trait, which is normally distributed. Environmental effects may obscure genetically caused differences between

phenotypic classes. For example, nutrition affects the adult size in many organisms. The distribution of phenotypes (Table 5) then becomes even more continuous. The distribution of quantitative traits often approximates a bell-shaped curve when you plot phenotypic value (height, for example) against the frequency of individuals in particular phenotypic classes. Such a plot is called a frequency histogram.

3.1.1 Features of quantitative traits

1. They are governed by many pairs of genes.

2. They demonstrate considerable variation and are not easily categorized into distinct phenotypic classes, i.e. they show variation from one phenotypic extreme to another.

3. Their study depends on measurement instead of counting.

4. The traits are usually affected by environment to a large extend. Phenotypes are the outcome of interaction among genes and between genes and the environment.

5. The type of variation exhibited by quantitative characters is called continuous variation.

3.2 Qualitative traits

Qualitative characters (traits) are sharply defined inherited characters which can be placed into distinct phenotypic classes or categories. Many simple inherited traits of qualitative nature are important in animal breeding. They may be of direct economic importance or they exert harmful effects which completely prevents the expression of genes controlling desired quantitative traits. The expression of many qualitative traits can be related to one or a few pairs of genes. Numerous qualitative traits have been identified as having a genetic basis in farm animals. For many the mode of inheritance is well established. In others a hereditary basis is known to exist but the exact mode of inheritance is not known with certainty. It is sometimes assumed that continuous variation in a character is necessarily caused by a large number of segregating genes so that continuous variation is taken as *prima facie* evidence for control of the character by many genes. But this is not necessarily true. If the difference between genotypic mean is small compared with the environmental variation then even a simple one gene Z allele can result in continuous phenotypic variation. Of course the range of a character is

limited and if there are many segregating loci influencing it then we expect the character to show continuous variation because each allelic substitution must account for only a small difference in the trait.

3.2.1 Features of qualitative traits

1. They are governed by single or few pairs of genes each of which segregate independently of others during gamete formation, e g. coat colour in cattle, presence or absence of horns, quality of pea plants, its pods, seeds etc.

2. Individuals in a population can be placed into discrete phenotypic classes. Genes are not linked on the same chromosome and therefore assort independently of one another at gamete formation.

3. Their expression is usually not affected by environment.

4. The variation in qualitative characters is called discontinuous or discrete variation.

5. Their study depends on counting. With characters that show discontinuous distribution of phenotypic values, ratios are usually calculated. Test of these ratios with respect to hypothesis are performed using Chi-square statistic.

Table 5: Quantitative traits and their heritability values in some domestic livestock

Specie	Trait	Heritability (h^2)
Cattle (Dairy)	Adult body weight	65
	Weaning weight	48
	Efficiency of weight	35
	Milk yield	35
	Butter fat yield	35
	Protein yield	25
	Type score	30
Cattle (Beef)	Birth weight	35
	Weaning weight	30
	Weaning score	25
	Feedlot gain	45
	Marbling	42
	Conception rate	5
	Calving interval	8
Sheep/goat	Litter size	10
	Birth weight	40
	Weaning weight	40
	Milk yield	33
	Survival to weaning	18

	Fertility	14
Poultry (Broilers)	7-week weight	45
	Feed consumption	70
	Feed conversion	35
	Breast fleshing	10
Poultry (Layer)	Adult body weight	55
	Egg weight	50
	Egg production at peak	15
	Fertility	5
	Hatchability	5
	Chick livability	5
	Adult livability	10

Characters with lowest heritability are those related to reproductive fitness.

4.0 CONCLUSION

In this unit, the terms quantitative and qualitative inheritance were discussed and some examples of traits were respectively given on the two terms. You are expected to read and understand you notes very well.

5.0 SUMMARY

In summary;

- Quantitative traits are those determined by many gene pairs and influenced by the environment
- Qualitative traits are governed by few gene pairs and are not affected by the environmental forces
- Egg number, milk yield and examples of quantitative traits while coat colour and presence or absence of horn are examples of qualitative traits

6.0 TUTOR-MARKED ASSIGNMENT

As we have come to the end of this unit, you are to attempt the following assignments and submit your answers to your tutor for this course.

1. Describe concept of quantitative inheritance and give some clear examples
2. What is a qualitative trait?
3. Enumerate 3 features each of quantitative and qualitative trait
4. List three traits each that belong to quantitative and qualitative traits

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UNIT 2 HERITABILITY AND REPEATABILITY

CONTENTS

1.0 INTRODUCTION

The importance of the concept of genetic parameter (which includes heritability and repeatability) to animal breeder cannot be overemphasized. Heritability is the proportion of observed variation in a particular trait that can be attributed to inherited genetic factors in contrast to environmental ones. It has two definitions: Statistical definition, defines heritability as the proportion of phenotypic variance attributable to genetic variance. While the second definition is more common 'sensical' and defines heritability as the extent to which genetic individual differences contribute to individual differences in observed behavior (or phenotypic individual differences). It measures the degree to which the offspring resemble their parents in performance for a trait: if a trait has a large heritability, animals with high performance for the trait will produce offspring with high performance. Repeatability in simple term, refers to the ability of an animal to repeat a record more than once in its lifetime, like milk yield by a cow or egg production by a hen.

2.0 OBJECTIVES

At the end of this unit, you should be able to;

- define heritability and repeatability of a trait
- categorize heritability into its two components and explain each
- mention the importance of both heritability and repeatability

3.0 MAIN CONTENT

3.1 Heritability

Heritability is defined as the proportion of the total variance that is attributable to the average effects of genes. The concept of heritability plays a central role in estimating the breeding value of animals and it analyzes the relative contributions of differences in genetic and non genetic factors to the total phenotypic variance in a given population. It measures the fraction of phenotype variability that can be attributed to genetic variation. Heritability can change without any genetic change occurring (e.g. when the environment starts contributing to more variation). Heritability can be in broad sense and in narrow sense.

3.1.1 Heritability in the broad sense

Is the proportion of the phenotypic variance that is due to genetic effects including additive, dominance and epistasis. Broad sense heritability is denoted as H^2.

$$H^2 = \frac{V_G}{V_P} = \frac{V_A + V_D + V_I}{V_P}$$

Broad sense heritability measures the strength of the relationship between the phenotypic values and genotypic values of a trait.

3.1.2 Heritability in narrow sense

Is defined as the proportion of the phenotypic variance that is due to additive genetic effects only. Narrow sense heritability is denoted as h^2.

$$h^2 = \frac{V_A}{V_P} = \frac{V_A}{V_A + V_D + V_I + V_{EP} + V_{ET}}$$

Heritability (h^2) measures the strength of the relationship between the phenotypic values and the breeding values (BV) for a trait in the population. It can be viewed as the coefficient of regression of the BV on the phenotypic value. It also measures the degree to which the offspring resemble their parents in performance for a trait: if a trait has a large h^2, animals with high performance for the trait will produce offspring with high performance. If however, the trait has small h^2, performance records of parents reveal little information about the performance of their offspring. Generally, heritability is always positive ranging from 0 to 100 (or 0–1) and is categorized as being low (0–20%), moderate (21–39%) and high (above 40%). It is also a measure of the entire population not for a single individual. This means that an estimate of heritability varies from one population to another and from one environment to another.

3.1.3 Importance of heritability

1) It is vital in selection: the accuracy of selection is higher for a highly heritable trait than a low heritable trait. The larger the accuracy of selection, the larger is the expected response due to selection.

2) It is also crucial in prediction of breeding values (BV) and producing ability: Prediction of BV of animal (i) based on its phenotypic value (P_i), is obtained as;
   $BV = h^2 (P_i - P)$, where P is the population mean.

3) Heritability is important in management: trait with large h^2 indicates that genetic factors have important role, as in growth, which further means that the trait can be improved by selection; however, traits with small h^2, indicate that environmental factors are more vital than genetic, e. g reproductive traits. To improve such trait, environmental effects must be given greater priority like improving nutrition and management practices.

3.2 Repeatability

Denoted as R, it is defined as proportion of the phenotypic variance that is due to permanent effects i.e genetic effects and permanent environmental effects.

$$R = \frac{V_A + V_D + V_I + V_{EP}}{V_P}$$

Repeatability measures the strength of the relationship between repeated records. Therefore, repeatability can be estimated as the correlation between repeated records on the same animals. It also measures the strength of the relationship between single performance record and producing ability. In simple terms, R refers to the ability of an animal to repeat a record more than once in its lifetime. Table 6 show estimates of repeatability for various economic traits in different livestock species.

3.2.1 Importance of repeatability

1) Useful in prediction of animal's next performance record from the current and previous records; if R is high, you can predict the animal's next record more accurately. However, if R is low then the prediction of the next record will have low accuracy.

2) Repeatability is important in making culling decisions; if R is high for a trait (e. g. milk production) you can cull animal with poor milk yield on the basis of her first record. However, if R is low for the trait, you should wait for more records before making culling decision on the poor performing animal(s).

Table 6: Repeatability estimates for some traits in domestic livestock

Specie	Trait	Repeatability (R)
Cattle (Dairy)	Service per conception	15
	Calving interval	15
	Milk yield	50
	Percentage fat	60
Cattle (Beef)	Calving date (dam trait)	35
	Birth weight (dam trait)	20
	Weaning trait (dam trait)	40
	Body measurements	80
Sheep/goat	Number born	15
	Birth weight (dam trait)	35
	60-day weaning weight	25
Poultry (Layer)	Egg weight	90
	Egg shape	95
	Shell thickness	65

4.0 CONCLUSION

In this unit, we were able to discuss the concept of genetic parameters (heritability and repeatability). The broad and narrow sense heritability was also discussed. Importance of the two terms with respect to animal breeding and general animal improvement was also highlighted.

5.0 SUMMARY

The definition of heritability and repeatability was treated. The 2 divisions of heritability into broad and narrow sense was clearly explained. Lastly, the importance of heritability and repeatability was mentioned.

6.0 TUTOR-MARKED ASSIGNMENT

As we have come to the end of this unit, you are to attempt the following assignments and submit your answers to your tutor for this course.

1. Define heritability of a trait
2. Give the two divisions of heritability and define each
3. Mention any two importance of heritability to an animal breeder
4. Define repeatability of a trait

7.0 REFERENCES/FURTHER READING

- Genetics Schaum's outline series by Susan Elrod and William Stansfield. Fifth Edition (2009)
- Klung W.S. and Cummings M.R. (2000). Genetics, 6th Edition, Prentice Hall, Inc. Pg 816.
- Ricky Lewis (2003). Human genetics: Concepts and Applications. 5th Edition, McGraw Hill Companies Inc. New York, Pg 454

UNIT 3 ANIMAL VARIATION AND SELECTION PRINCIPLES

CONTENTS

1.0 INTRODUCTION

The importance of the concept of genetic parameter, which includes heritability and repeatability, to animal breeder cannot be overemphasized. Heritability in the simplest term refers to the portion of the heritable parts, which parents transmit to their offspring. It measures the degree to which the offspring resemble their parents in performance for a trait: if a trait has a large heritability, animals with high performance for the trait will

produce offspring with high performance. Repeatability in simple term, refers to the ability of an animal to repeat a record more than once in its lifetime, like milk yield by a cow or egg production by a hen.

2.0 OBJECTIVES

At the end of this unit, you should be able to;

- define heritability and repeatability of a trait
- categorize heritability into its two components and explain each
- mention the importance of both heritability and repeatability

3.0 MAIN CONTENT

3.1 Animal variation

Natural variation occurs in every species in the world. No two individuals are exactly alike. Variation therefore refers to similarities and differences in creation, behavior, traits etc. One of the major functions of an animal is to survive. One popular saying derived from Charles Darwin's work is "survival of the fittest", which basically means that only the organism that is best equipped to survive will live to reproduce. Competition occurs when two individuals of the same species compete for the same resources, may be food, water, space or even a mate. Competition paves way for selection. Selection simply means choosing high performing male to mate with high performing female so that they produce high performing offspring. There are two types of selection: ***Natural*** and ***Artificial***.

3.1.1 Natural selection

Charles Darwin is the man accredited with the theory of natural selection, which he originally came up with to explain variation. Natural selection is the influence of the environment on the survival and reproductive ability of an individual. Variation occurs among the individuals of a population of any species. These natural variations have either beneficial or detrimental effect on organism and allow one organism to survive better than the other. The organism that is better equipped to survive will live to reproduce, therefore passing on that favorable trait to the subsequent generations. This is the process

of natural selection. Another main function of an animal is to reproduce and pass on its genes to ensure that the next generations will have their traits. Natural selection is not an overnight process. It takes time and the birth of several new generations to completely alter a species. Genetic variation cannot be forced. Because of this, no individual organism can adapt to its environment by its own will. This is why natural selection occurs within a species, not an individual. Adaptations are only useful in the process of natural selection when the favorable trait spreads throughout the gene pool of a species and the population at large begins to display the beneficial variation of the trait.

3.1.2 Artificial selection

Edward M. East from the United States worked out the formal basis for modern artificial selection. Artificial selection is the efforts of man to increase the frequency of desirable genes in his herd. This is done by choosing for breeding purpose, those individuals with superior performance or which have the ability to produce superior performing offspring. Animals with the best sets of genes are said to have the best breeding values.

3.2 Selection Principles/Methods

3.2.1 Selection for single trait

3.2.1.1 Mass selection

This type of selection is also called individual selection. Under this method, animals are selected or rejected on the basis of their own merit. The criteria are that, the heritability for the trait must be high and the trait should be measurable in the animal. In addition, the traits should be observed in both sexes. Animals to be tested must be brought under similar environmental condition of feeding and management.

3.2.1.2 Pedigree selection

In this system, animals are selected or rejected on the basis of the performance of their ancestors. This is used when selection is done for traits that are not

measurable in the animals themselves either because they are too young or because the expression of the trait is sex-linked.

3.2.1.3 Family selection

This method is also called selection based on collateral relatives. Collateral relatives are those that are neither direct ancestors nor direct descendants of an individual. They include siblings, aunts, uncles, nieces and nephews. This method is most useful when family size is large, traits are highly inherited, there is close genetic relationship between members of the family and when the mean generation interval is short. It is best suited for poultry, rabbit or swine than for cattle.

3.2.1.4 Progeny selection

Animals are selected on the basis of the performance of their offspring. The system is used when the trait of interest cannot be measured in the individual animal. For example, increasing milk yield in dairy cattle can be achieved by selecting dairy bulls on the performance of their daughters.

3.2.2 Selection for multiple traits

3.2.2.1 Tandem selection

The simplest way of selecting for many traits is to select each trait at a time. That is; trait A is selected for some generations and then trait B is selected. After some further generations, trait C is selected and so on. If the traits involved are unrelated then as A improves, B and C will stay at their original level. If there are positive relationships between the traits, then as A improves B and C also improve. But if they are negatively correlated, then as A improves B and C become worse. Consequently, selecting to correct the problem in B will lead to loss of gains already made in A. Tandem selection is thus useful if only few traits are involved and they are all positively related or better unrelated.

3.2.2.2 Independent culling levels

These refer to minimum standards for traits undergoing multiple trait selection. When selecting animals using independent culling levels, those animals that fail to meet any one standard are rejected regardless of merit in other traits. The system has the advantage of being easy to operate even with large numbers of traits. Its disadvantage is that, an animal which is outstanding in a particular trait but fails (even slightly) on another, would be culled. Hence, in using this system it is important to limit traits to those of major interest and to set realistic targets. The system operates better than tandem selection especially when traits are negatively correlated.

3.2.2.3 Selection index

This is the most efficient method. It uses one single value for any number of traits each of which is weighted by its economic value. The value of Index (I) equals the sum of traits each of which is multiplied by a certain factor 'b' called regression coefficient. The aim of an index is to give the best prediction of an animal's breeding value. To construct an index, the following data are needed; heritability of each trait in the index, phenotypic variance of each trait, genetic and phenotypic correlation. Construction of selection indices is highly complex and certainly requires not only considerable data on each parameter but complex computer assistance in evaluation.

4.0 CONCLUSION

In this unit, we learned that variation is the reason for selection. No two individuals that are exactly alike, not even the monozygotic twins. We discussed the principles of selection both natural and artificial. Comprehensive explanation on methods of selection for single and multiple traits were provided.

5.0 SUMMARY

Definition of variation, natural and artificial selection were given in this unit. Further details on selection principles and methods for single as well as multiple traits were also

provided. You are therefore expected to memorize and understand these important aspects of animal breeding, because they are the tools, which an animal breeder uses to bring about improvement in his livestock.

6.0 TUTOR-MARKED ASSIGNMENT

As we have come to the end of this unit, you are to attempt the following assignments and submit your answers to your tutor for this course.

1. Define variation
2. Differentiate between natural and artificial selection
3. List three methods of selection for a single trait
4. Name any three multiple trait selection methods for livestock improvement
5. Name the most efficient method among the three listed in question 4

7.0 REFERENCES/FURTHER READING

- Alberts B. Johnson A. Lewis J. Raff M. Roberts K. Walter P. (2002). Molecular Biology of the Cell, 4th Edition, Garland. ISBN 0815332181. http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=mboc4.TOC&depth=2

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UNIT 4 BREEDING METHODS

CONTENTS

1.0 INTRODUCTION

Breeding methods is the same as mating systems. It refers to different schemes designed to bring male and female of the selected individual animals to serve as parent for the future offspring. This means that, the next step after selection is breeding methods or mating systems. Various types of schemes were discussed in this unit. You are to study these different systems and learn how to apply each depending on the objective for which the scheme is used.

2.0 OBJECTIVES

At the end of this unit, you should be able to;

- define breeding method or mating system
- explain the various methods available
- categorize the various schemes of crossbreeding

3.0 MAIN CONTENT

3.1 Breeding methods

After selecting individuals to be used as parents, the breeder must decide how the selected animals will be mated. The various ways of bringing this about is known as breeding method or mating system. There is no limit as to the number of possible mating or breeding system to adopt but there are few strategies. Some are based on animal performance or expected performance (like random mating) while others are based on pedigree relationship (like inbreeding and outbreeding).

3.1.1 Random mating

This is the simplest method of mating, where all the males in the population have equal chance of mating with any female in the same population. It requires no performance records or genetic predictions and little time is involved in making breeding decisions. The method is required to establish control populations, which are used to monitor long term selection response. It is popular in commercial breeding programmes where performance information is unavailable or where there are so many animals that other methods are impractical. Random mating is also best for estimation of genetic parameters such as heritability and genetic correlation from randomly unselected populations.

3.1.2 Inbreeding

This is the mating of individuals that are genetically related. They have some genes in common as a result of common ancestors. Thus, it can be defined as mating of individuals that are more closely related than average of the population from which they come. Inbreeding increases homozygousity in population. Continuous inbreeding can result to negative effects on certain traits, which we call inbreeding depression.

Some characters that may be affected by inbreeding depression are;

a) Dairy cattle: reduced milk yield, butterfat yield, growth rate, calf viability
b) Beef cattle; Weaning weight
c) Swine; Body weight, litter size, piglet viability
d) Sheep; Weaning weight, yearling weight, wool traits such as clean wool, staple length
e) Poultry; Body weight, egg number and weight, hatchability, sexual maturity, viability

3.1.2.1 Disadvantages of inbreeding

(i) Mating of closely related stock increases the chances of deleterious genes coming together giving rise to abnormal progeny.

(ii) It leads to loss of vigour.

(iii) Inbreeding depression (i.e decline in performance) could set-in. This is the gradual lowering of performance with increasing inbreeding. Traits that could be affected are usually fitness traits and include; reduced fertility, embryonic mortality, decline in progeny survival, lowered growth rate, decline in milk yield. Carcass traits may not be affected.

3.1.3 Outbreeding

This is the opposite of inbreeding and is a means of introducing new genes into an otherwise closed population. It is the mating of animals of the same breed but with minimal relationship between them. Outbreeding increases variation and heterozygousity in a population.

3.1.4 Crossbreeding systems

The basis of this system is that, if two breeds are crossed, it is expected that the progeny will be at the mid-point between the parental means for any trait. If the offspring exceed the means of the two parents then the extent to which they exceed the mid-point is a measure of heterosis (which means hybrid vigour). Traits that are non-additive in nature will show the greatest heterosis. Crossbreeding is therefore, crossing of two genetically unrelated populations or lines. These could be different breeds, strains, lines or even different species. It is aimed at combining the genes in both populations in the resulting progeny, thereby creating greater variability. For example, the basis of the modern broiler industry is as result of crossbreeding, the sire line (White Cornish) is selected for growth

and conformation, while the dam line (White Rock) is a large sized strain selected for egg production and egg size. The dam line may also incorporate the dwarf genes, which confer some advantage for egg production, hatchability and feed conversion. By crossing two specialized lines, the favourable genes for the composite trait are brought together in the progeny resulting in increased performance.

The breeder may decide and wish to use his first generation crossbred individuals for further breeding and different schemes are possible such as backcrossing, crisscrossing, top crossing, rotational crossing and grading-up.

3.1.4.1 Backcrossing

Backcrossing occurs when the first cross animal is mated back to one of its parent breed. it is used to increase the proportion of genes from a good parent in the future generation. The resultant progeny is 75% of one breed and 25% of the other.

3.1.4.2 Crisscrossing

This is an extension of backcrossing where two breeds (A and B) are initially crossed. The crossbred is then mated to A to give 75% : 25% B. This crossbred is then mated back to B to give 62.5% B : 37% A. Thereafter, breeds A and B are used in alternate generation.

3.1.4.3 Top crossing

Top crossing usually refers to a breeding system in which the breeder returns to the original genetic stock to gain new genetic material for improving the population by using stud sire from the original genetic stock. For example, Friesian breeders in Britain returning to Holland for bulls, or American Hereford breeders returning to England for bulls.

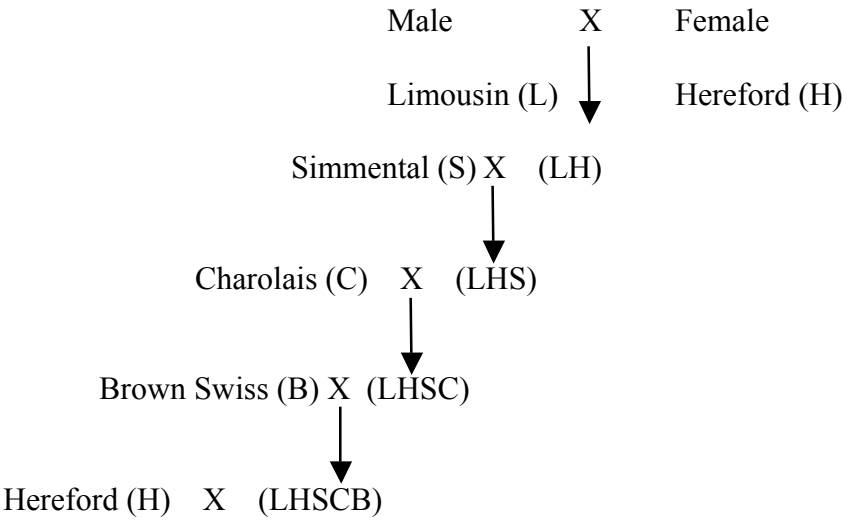
3.1.4.4 Grading-up

Grading-up consists of a series of crosses aimed at upgrading an unproductive native stock by infusing into them genes from improved breeds or strains. Usually, sires of the

improved stock are used on unimproved low-grade females. The scheme increases in the progeny, frequencies of favourable genes possessed by the improved male. It is commonly used in many developing countries to improve local stock. Example, Friesian sire on Bunaji dams.

3.1.4.5 Rotational crossing

In this system, a series of breeds (three, four or more) are used in succession. In principle, the use of several breeds ought to have been greater than using two breed. Below is an example showing rotational crossing using five breeds of cattle.



4.0 CONCLUSION

It can be concluded that, the various breeding methods discussed in this unit are for guide, so that the breeder can achieve the maximum benefit from his livestock enterprise. Inbreeding should be utilized for a short generation so as to avoid the effect of inbreeding depression. Crossbreeding is the best method to use especially if you have two or more different breeds to cross. This will improve the performance of the stock by taking advantage of hybrid vidor (heterosis).

5.0 SUMMARY

Various mating schemes were discussed, which include inbreeding, crossbreeding and their different forms. Inbreeding was shown to have detrimental effect on some traits of economic importance and therefore should be used with caution. The advantages of crossbreeding abound and should be utilized to benefit from heterosis.

6.0 TUTOR-MARKED ASSIGNMENT

As we have come to the end of this unit, you are to attempt the following assignments and submit your answers to your tutor for this course.

1. Define breeding method
2. What is random mating?
3. What is inbreeding?
4. What are the disadvantages of inbreeding?
5. List some crossbreeding schemes you know

7.0 REFERENCES/FURTHER READING

- Alberts B. Johnson A. Lewis J. Raff M. Roberts K. Walter P. (2002). Molecular Biology of the Cell, 4th Edition, Garland. ISBN 0815332181. http://www.ncbi.nlm.nih.gov/books/bv.fcgi?rid=mboc4.TOC&depth=2

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