



NATIONAL OPEN UNIVERSITY OF NIGERIA

SCHOOL OF AGRICULTURAL SCIENCES

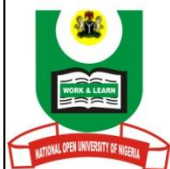
COURSE CODE: ANP 307

COURSE TITLE: ELEMENTARY TOPICS IN ANIMAL BREEDING

**COURSE
GUIDE**

**ANP 307
ELEMENTARY TOPICS IN ANIMAL BREEDING**

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INTRODUCTION

This course elementary topic in Animal Breeding (ANP 307) is a 2 credit course designed to stimulate the interest of all Agricultural Science students to adopt and apply the use of Animal breeding techniques to increase animal productivity and ensure food security in Nigeria. It introduces the basic principles and concepts of animal breeding for improvement of livestock to all Agricultural students in the third year. Students from other disciplines other than Animal science may decide to take up this area of Agriculture in their post-graduate studies. Also, 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 consists of six modules and fourteen units which comprised of Course Guide, Objectives and history of animal breeding, fundamental principles of inheritance, variations in animals population, repeatability and heritability estimates, genes and genes action as well as quantitative and qualitative characters and their inheritance.

This course guide tells you briefly what the course is about. What course materials you will be using and how you can work your way through these materials. In addition, it suggest some general guidelines for the amount of time you are likely to spend on each unit of the course in order to complete it successfully.

It gives you guidance in respect of your Tutor Marked Assignments, which will be made available in the assignment file. There will be regular tutorial classes that are related to the course. It is advisable for you to attend these tutorial sessions.

WHAT YOU WILL LEARN IN THIS COURSE

Elementary topics in Animal Breeding (ANP 307) is a compulsory introductory course that is design to introduces the basic principles and concepts of animal breeding and improvement of livestock to all Agricultural students in the third year. History of breeding and the principles that govern animal breeding will be discussed. Principles and problems in breeding animals for disease resistance and productivity are discussed. Past conceptions of people about heredity, Fundamental principle of inheritance, Mendel's work in the discovery of factors of inheritance, sex determination mechanism and sex ratio will be discussed. Qualitative and Quantitative traits, allelic relationships, exceptions to Mendel's rules, Application of Mendelian genetics to animal improvement and introduction of the concepts of Heritability and

Repeatability estimates will be introduced. Different types of gene actions; lethal or detrimental genes and their control will be discussed. The scope of discussion is limited to those specified in the course content above. Some areas that may not be covered will be given as assignments to students to explore.

COURSE AIMS

The aims of this course are

1. To explain the pathways of Animal genetic improvement through the applications of principles of genetics and breeding.
2. To provide a good knowledge base to future manpower for genetic improvement of Nigerian livestock resources towards a sustainable food production and food security.
3. Finally the course is aimed at providing a basic foundation for students intending to take up animal breeding and genetics as a career in the future.

COURSE OBJECTIVES

At the end of this course, you will be able to:

1. Define some important concept in animal breeding;
2. explain the historical perspective and objectives of animal breeding;
3. explain the fundamental principles of inheritance in animal breeding;
4. list and explain the types, causes and measurements of variations in animal populations;
5. explain the concepts of repeatability and heritability and their estimation;
6. explain different types of genes and genes action and
7. differentiate between quantitative and qualitative characters in animal

WORKING THROUGH THE COURSE

For a maximum benefits from the course and for fast grasping of many of the breeding concepts, the course requires that you should be familiar with basic cell structures and the structures that are important in heredity which include the genes, chromosome, and different types of gene actions, you should also refresh your memories on the basic probability theories and some basic knowledge in algebra.

Being a course that involves calculation, the course requires that each student for the course has a computer system with one or two different analytical software (SAS, SPSS, Matlab etc.) that can calculate variances in the introduction of estimation of heritability and repeatability. There will be tutorials of which your tutor will communicate the dates and time to you, failure to attend the tutorial classes could result in you having an incomplete grade.

COURSE MATERIALS

The main components of the course are:

1. Course Guide
2. Study Units
3. References
4. Assignments
5. Presentation schedule

STUDY MODULES AND UNITS

In this course, there are six modules and fourteen study units. The modules and units are presented thus:

Module 1 Objectives and History of Animal Breeding

- Unit 1 Definition of Terms and Objectives of Animal Breeding
- Unit 2 History of Animal Breeding

Module 2 Principles and Problems in Breeding Animals for Disease Resistance and Productivity

- Unit 1 Principles and problems in breeding animals for increase productivity
- Unit 2 Principles and Problems in breeding animals for disease resistance

Module 3 Fundamental Principles of Inheritance

- Unit 1 Historical Perspectives of Principles of Heredity
- Unit 2 Mendel's laws and Principles of Inheritance
- Unit 3 Types of Gene action and Exceptions to Mendelian ratio
- Unit 4 Sex Determination Mechanism

Module 4 Traits Characters and their Inheritance in Animals

Unit 1	Qualitative and Quantitative characters and their inheritance
Unit 2	Gene and Gene types

Module 5 Variation and its Statistical Measurements

Unit 1	Variations in Animal population
Unit 2	Measurements of variation

Module 6 Heritability and Repeatability

Unit 1	Heritability
Unit 2	Repeatability

Every unit contains a list of references and further reading. You should try and get the textbooks and materials listed. The textbooks and materials are meant to deepen your knowledge of the course.

Apart from the print course material, you will equally have the soft copy of the material in NOUN web site www.nou.edu.ng . When you get to the site, click on courseware and select this course.

This course will be facilitated through face-to-face at the study centers and also through online i-Learn platform. In the platform you will receive both synchronous and asynchronous facilitations. To get to i-learn platform, click on www.nou.edu.ng and click on i-Learn

UNIT STRUCTURE

Each Study Unit is structured in the following format;

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor-Marked Assignment
- 7.0 References/Further Reading

PRESENTATION SCHEDULE

Your course material gives you important scheduled for timely completion and submission of your tutor marked assignments and attending tutorials. Remember that you would be required to submit all your assignments and practical log books at a stipulated time. Make sure you submit them on time to your facilitator /tutor.

ASSESSMENT

There are four aspects to the assessment of the course. First are self-assessment exercises, second are the Tutor-Marked Assignments (TMAs), third is practical and the fourth is a written examination. All of these are very important for successful completion of the course and are therefore, allotted marks accordingly.

The assignments and practical log books must be submitted to your tutor for assessment in accordance with the deadlines stated in the presentation schedule and the assignment file. The work you submit to your tutor for assessment will count for 30% of your total course mark. At the end of the course, you will be required to sit for final examination of two hours duration. This examination will count for 70% of your total course mark. You are expected to apply information, knowledge and techniques acquired during the course in tackling the assignments and the exam questions.

TUTOR-MARKED ASSIGNMENT

Tutor-marked assignments (TMAs) account for 30 per cent of your total course work. There are seven hours tutor-marked assignments in this course. You are to submit only five of the seven assignments to your Facilitator/Tutor for grading. You are encouraged, however, to submit all eight assignments in which case the best five of the eight assignments will be counted. The Tutor Marked Assignments (TMA) questions for the units in this course are contained in the assignment file. When you have completed each assignment, send it, together with a TMA form to your Tutor; make sure that each assignment reaches your tutor on or before the deadline given in the presentation schedule and assignment file. If for any reason, you cannot complete your work on time, contact your Tutor before the assignment is due to discuss the possibility of an extension. Otherwise, extension will not be granted after the due date unless in exceptional cases.

The assignments would be marked and returned to you for your review. The course materials and suggested further reading references will assist learners to complete their assignments and prepared for final examination. You are however; advised to undertake independent reading of relevant materials, extract useful points. The totality of your comprehension of the subject matter from the study units, references and other relevant materials would broaden your understanding to address

problems and give professionals insights and practical skills to the subject of animal breeding.

PRACTICAL ASSIGNMENT

There are six practicals (one at the end of each module). You are expected to conduct 4 out of the 6 practical and record them in your practical logbooks. The log books are to be submitted for grading as part of your assessment. The practical assignment would account for 20 per cent of your total course work.

FINAL EXAMINATION AND GRADING

The final examination at the end of this course will hold for about 2 hours and it will be graded on a score of 50 per cent of total course work. The examination questions will reflect understanding of the subject matter or topics discussed in this course material. As much as possible the entire course content will be covered in the assessment, sound grasp of every discussion on the main content through reading formalization with reference materials may be very helpful to you. A revision of TMAs and comments of facilitators prior to the examination is strongly advised.

COURSE MARKING SCHEME

The following table shows how the actual course marking is broken down.

Assessment	Marks
Tutor Marked Assignment 1-8	Select the best 5 at 6% each = 30%
Practical	4 practical at 5% each = 20%
Final Exams	Account for 50% of the total course work
Total marks	100% of the course work

COURSE OVERVIEW

This table brings together the modules and units. The number of weeks you should take to complete them and the assignment that follows them

Module	Unit	Course Guide	Activity	Assignment
1	1	Definition of Terms and Objectives of Animal Breeding	1	1
	2	History of Animal Breeding	1	1

2	3	Principles and problems in breeding animals for increase productivity	1	2
	4	Principles and Problems in breeding animals for disease resistance	1	2
3	5	Historical Perspectives of Principles of Heredity	1	3
	6	Mendel's laws and Principles of Inheritance	1	3
	7	Types of Gene action and Exceptions to Mendelian ratio	1	4
	8	Sex Determination Mechanism	1	4
4	9	Qualitative and Quantitative characters and their inheritance	1	5
	10	Gene and Gene types	1	5
5	11	Variations in Animal population	1	6
	12	Measurements of variation	1	6
	13	Heritability	1	7
	14	Repeatability	1	7

HOW TO GET THE MOST FROM THIS COURSE

One of the great advantages of distant learning is that it is flexible in such a way that you can read and work through the specially designed study materials at your own pace and at a time and place of your choice. It tries to marry between your work and study scheduled.

The study unit tells you when to read your other materials. In addition, the study units provide exercise for you to do at appropriate point.

Each of the study unit follows a common sequence. The first item in the sequence is an introduction to the subject matter of the unit and how a particular unit is integrated with the other unit and the course as a whole. Next is a set of learning objectives, which enable learners to know what they are expected to achieved at the end of each units. You should use these objectives as a guide in your study. When you have completed the unit, you must go back and check whether you have achieved the set objectives.as this will significantly improve your learning and comprehension of the course materials. The main body of the units guides you through the required reading sections and from other sources. Self-assessment tests (exercises) are interpreted throughout the units and answers are given at the end of the units. Working through these tests

will help you to achieve the objectives of the unit and prepare you for the assignments and the examination. You should make sure you attempt each self-tests in each of the study unit, don't skip any. There will also be numerous examples given in the study units. Work through these when you come across them in the course material.

The following is a practical approach for working through the course. If you run into any difficulty, don't hesitated to call your facilitator for assistant.

1. Study this course guide carefully
2. Organize a study schedule, which is most convenient for you. Refer to the course overview for more details. Whatever method you choose you should decide on and write your own dates for working each unit.
3. Once you create your own study schedule do everything you can to stick to it. The major reason that makes students to fail is that they get behind with their course work.
4. Use the unit to guide your reading. Note the time you are expected to spend on each unit and how the assignments relate to the units.
5. Assemble the reading materials. Information about what you need for a unit is given in "time overview" at the beginning of each unit. You will almost always need both the study unit you are working on and one of your references on your desk at the same time.
6. Work through the unit, the content of the unit itself has been arranged to provide a sequence for you to follow. As you work through the units you will be instructed to read sections from other sources.
7. Well before the relevant schedule dates check your assignment file and make sure you attend to the next required assignment keeping in mind that you will learn a lot by doing the assignments carefully. They have been designed to help you meet the objectives of the course and therefore will help you pass the examination. Submit all assignments not later than the schedule date.
8. When you have submitted an assignment to your tutor for marking, do not wait for its return before starting on the next unit. Keep to your schedule.
9. When the assignment is returned, pay particular attention to your tutor's comments. Both on the Tutor-Marked Assignment form and also written on the assignment. Consult your tutor as soon as possible if you have any questions or problems.
10. After completing the last unit, review the course and prepare yourself for the final examination. Check that you have achieved

the unit objectives (listed at the beginning of each unit) and the course objectives (listed in the course guide).

11. Visit information e.g details of your tutorials and the date of the first day of the semester will be made available. You need to gather together all this information writes them in your diary or a wall calendar.

TUTORS AND TUTORIALS

Fourteen (14) hours tutorials have been slated to assist you in assimilating this course, you will be notified of the dates, times and location of these tutorials as well as the names and contact phone number(s) of your tutor as soon as you are assign to a tutorial group.

You must mail your tutor-marked assignment to your tutor before the schedule date (at least two working days are required). They will be marked by your tutor and returned to you as soon as possible.

Do not hesitate to contact your tutor by either phone, e-mail or discussion board if you need help.

The following might be circumstances in which you would find help necessary.

Contact your tutor if :

1. You do not understand any part of the study units or the assigned readings.
2. You have difficulty with the self-test or TMAs
3. You have a question or problem with an assignment or with the grading of an assignment.

You should try your best to attend the tutorials. This is the only chance to have face to face contact with your tutor and to ask questions which are will be answered instantly.

You can raise any problem encountered in the course of your study. To gain the maximum benefit from course tutorials prepare a question list before attending them.

You will learn a lot from participating in discussing actively.

SUMMARY

Elementary Topics in Animal Breeding is a compulsory introductory course that is design to introduce the basic principles and concepts of animal breeding and improvement of livestock to all Agricultural students in the third year.

Upon completion of this course, learners will be equipped with the basic knowledge of the concepts, scope, principles and techniques of breeding farm animals for increase productivity and diseases resistance. In addition, learners will be able to answer such question as:

- Explain briefly the concept of animal breeding.
- State the basic aim and objectives of animal breeding
- Briefly explain the principles and problems in breeding animals for increase production and disease resistance
- Enumerate the reasons why Bakewell is considered the founder of systematic modern breeding
- List some ancient theories of inheritance prior to the discovery of Mendel's work
- State two laws of Gregor Mendel
- Enumerate some reasons that made Mendel's research work unique compare to the other early theories
- States some implication of Mendel's work
- Briefly explain some exceptions to classical Mendelian ratios
- Briefly explain the systems of sex determination in mammals, insect and avian
- Explain the differences between qualitative and quantitative traits
- Identify qualitative and quantitative traits in farm animals
- What is lethal or detrimental genes and how can they be control
- List and explain the types and causes of variation in animal population
- How can you measure variation in farm animals
- Define heritability and repeatability
- States the importance of heritability and repeatability

The list of the questions that you can answer is not limited to the one listed above. We wish you success in the course and hope that you will find it very interesting and useful.

BEST OF LUCK

**MAIN
COURSE**

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MODULE 1 OBJECTIVES AND HISTORY OF ANIMAL BREEDING

Unit 1	Definition of Terms and Objectives of Animal Breeding
Unit 2	History of Animal Breeding

UNIT 1 DEFINITION OF TERMS AND OBJECTIVES OF ANIMAL BREEDING

CONTENTS

1.0.	Introduction
2.0.	Objectives
3.0.	Main Content
3.1.	Definition of terms in Animal Breeding
3.1.1	What is breeding?
3.1.2	Animal breeding
3.1.3	Common terms Used in Animal Breeding
3.2.	Aim and objectives of Animal Breeding
4.0.	Conclusion
5.0.	Summary
6.0.	Tutor Marked Assignment
7.0.	References / Further Reading

1.0 INTRODUCTION

Apart from the interest of esthetic and fancier reasons, Animal breeding is an economic undertaking. As such, the breeding goals and programme need to be determine with proper consideration of the economic concerns dictated by the system of management and market for the end products.

2.0 OBJECTIVES

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

- Explain the meaning of breeding and animal breeding
- Define important basic terms in animal breeding
- State the general and specific objectives of animal breeding

3.0 MAIN CONTENT

3.1. Definition and scope of Animal Breeding

3.1.1 What is breeding?

It is the production of plants and animals, especially for the purpose of developing new or better types. Breeding can be done in both plants and animals as in case of animals it is called animal breeding or livestock breeding.

3.1.2 Animal breeding

Is the application of scientific knowledge to the genetic improvement of animals. For better understanding of the meaning of breeding we need to know what genetics is. **Genetics** is the branch of biology that deals with the study of heredity (similarity) and genetic variations (differences). Genetics study how living organisms inherit features from their ancestors. It tries to identify which features are inherited, and work out the details of how these features are passed from generation to generation. Therefore, animal breeding is the application of genetic principles in the development of new breeds of animals with improved characteristics. Genetic principles are employed in the improvement of animals through selection and mating. Genetic principles are utilized and synthesized into breeding programmes, and breeding programmes involve a system of management as well as systems of breeding.

3.1.3 Common terms Used in Animal Breeding

- i. **Gene**—is the basic unit of heredity, which carries genetic information from parents to offspring or from generation to generation.
- ii. **Alleles**—is an alternate form of a gene; two genes that occupy the same position or locus in a homologous chromosome and cover the same trait
- iii. **Locus** - a fixed location on a strand of DNA where a gene or one of its alleles is located
- iv. **Homozygous** - having identical genes (one from each parent) for a particular characteristic
- v. **Heterozygous** - having two different genes for a particular characteristic
- vi. **Dominant** - the trait that appears in the heterozygous condition and masks the effect of the other
- vii. **Recessive** - the trait that is masked in the heterozygous condition

- viii. **Phenotype** – the physical expression or appearance of an organism.
- ix. **Genotype** - genetic makeup or genetic composition of an organism
- x. **Hybrid**- the offspring of parents which are genetically pure for one or more pairs of different hereditary factors
- xi. F_1 : first filial generation form from a given mating (i.e the hybrid), offspring from mating the F_1 generation are the F_2 etc
- xii. **Monohybrid cross** - cross involving a single pair of genes, or one trait
- xiii. **Dihybrid cross**- cross involving two pairs of gene or traits
- xiv. **Segregation** : separation of members of a pair of gene at gamete formation.

3.2 Aim and Objectives of Animal Breeding

The aim of any breeding programme is to genetically improve one or more traits of economic importance. The choice of the appropriate breeding programme depends on the degree of inheritance, the selection pressure and the generation interval. Hence the first step in developing an improvement programme is to define the breeding goals or objectives and device techniques appropriate for their measurement. Although breeding objectives are peculiar to the types and purpose for which the animals are bred. However the basic objectives of animal breeding are to enhance the efficiency of production and quality of the product for the ultimate consumer through well planned genetic and environmental improvement. The specific objectives of Animal Breeding are to

1. Improved growth rate
2. Increase production of animal and animal products e.g milk, meat, egg, wool etc
3. Improve quality of animals and their products
4. Improved resistance to various diseases
5. Increase productive life span of the animals
6. Increase the reproductive rate

4.0 CONCLUSION

This unit serves as a general introduction to highlight the meaning of the concepts of breeding and animal breeding, the aim and objectives of animal breeding and the choice of the appropriate breeding programme which depends on the degree of inheritance, the selection pressure and the generation interval of the animals

5.0 SUMMARY

Animal breeding, which is the application of scientific knowledge to the genetic improvement of animals, evolves overtime to form the basic principles to which modern animal breeding is being practiced. The first step in developing an improvement programme is to define the breeding goals or objectives and devise techniques appropriate for their measurement. Although breeding objectives are peculiar to the types and purpose for which the animals are bred, however, the basic objectives of animal breeding are to enhance the efficiency of production and quality of the product for the ultimate consumer through well planned genetic and environmental improvement.

6.0 TUTOR MARKED ASSIGNMENT

1. Briefly explain the concept of animal breeding
2. State the aim and basic objectives of animal breeding
3. Define the following terms: i. gene, ii. Allele iii. Genotype, iv. Phenotype, v. Dominant, vi. Recessive, vii. Hybrid, viii. Homozygote, ix. Heterozygote

7.0 REFERENCES / FURTHER READING

- Malcolm B Willis (1998). Dalton's Introduction to Practical Animal Breeding. Blackwell Scientific Publication, 2nd edition ,London Edinburgh Boston
- J.E Legate and E.J. Warwick (1990). Breeding and Improvement of Farm Animals. McGraw-Hill Publishing Company Singapore
- Payne, W.J.A. and Wilson, R.T (1999) An Introduction to Animal Husbandry in the Tropics, 5thEdition, Wiley-VCH, Germany

UNIT 2 HISTORY OF ANIMAL BREEDING

CONTENT

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main content
 - 3.1 Historical background of Animal Breeding
 - 3.2 Reasons why Bakewell is consider the founder of modern systematic Animal breeding
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References / Further Reading

1.0 INTRODUCTION

Long before the appearance of the science that is now called “Genetics”, animal breeding had been practiced by humans following intuitive criteria, although less efficient than the present scientific ones, but criteria that had provide success along many generations of selection.

Under this unit we will examine a brief historical background of animal breeding.

2.0 OBJECTIVES

At the end of this unit, you will be able to

- Give a brief historical background of animal breeding
- Explain how modern systematic breeding started

3.0 MAIN CONTENT

3.1 Historical Background of Animal Breeding

The science of animal breeding is defined as the application of the principles of genetics to improve the efficiency of production in farm animals. These principles were applied to change animal populations thousands of years before the sciences of genetics were formally established. The practice of animal breeding dates back to the Neolithic period (approximately 7000 BC), when people attempted to domesticate wild species such as, goats, hogs, horse and dogs. Man's attempts to breed livestock to serve his purpose go far back into man's own history.

More than a thousand years ago, the Arabs in their horse breeding were memorizing the genealogies of their horses but the way they used these genealogies to breed their horses is not known. After the Second World War, several regional projects, patterned after the successful regional swine-breeding laboratory, were started with adequate funding from state experiment stations and the U.S. Department of Agriculture to initiate some large-scale animal breeding research projects. Today the fruits of these long-term investigations are seen in the dairy, poultry, swine, sheep and beef industries. The extent of breeding technology utilized by the various industries is related to their reproductive potential or to a reproductive innovation such as artificial insemination. However, modern breeding practices started with the self-taught work of Robert Bakewell (1725-1795), who produced new breeds and had a high reputation as a breeder. Robert Bakewell, an English animal breeder of the 18th century, is considered the founder of systematic animal breeding. He was the first to emphasize the importance of accurate breeding records, introduced the concept of progeny testing to evaluate the genetic potentials of young sires, and applied inbreeding to stabilize desired qualitative traits. He focused his work in the performances of his cattle and sheep, hiring rams, recording the offspring and keeping the sons of the best males. He fixed few and clear breeding objectives mating the best females with the best males. He was a proponent of the concepts such as "like begets like, prepotency is associated with inbreeding" and "breed the best to the best." Bakewell and his contemporaries in Europe pioneered the development of diverse breeds of beef cattle, dairy cattle, sheep, hogs and horses. Most livestock breeds with pedigree herd books and breed associations were established between the late 18th century and the second half of the 19th century. However, he disregarded the damaging effects of inbreeding and due to this, he had fertility troubles with his new breeds, but he is still considered as the first farmer practicing modern animal breeding.

3.2. Reasons why Bakewell is considered the founder of modern systematic Animal breeding

1. He fixed few and clear breeding objectives
2. He kept and used accurate breeding records to help him in making breeding decision
3. He used progeny testing to evaluate the genetic potentials of young sires
4. He applied inbreeding to stabilize desired qualitative traits

Students Assignment Exercise (SAE) Module 1 unit 2

1. Who first introduced the concept of progeny testing in animal breeding?

2. Bakewell was a proponent of 3 concepts list them
3. What was the limitation of Bakewell breeding programme?

4.0 CONCLUSION

Robert Bakewell, an English animal breeder, is considered the founder of modern systematic animal breeding.

5.0 SUMMARY

The principles of animal genetics were applied to change animal populations thousands of years before the sciences of genetics were formally established. This came with the self-taught work of Robert Bakewell (1725-1795), who produced new breeds and had a high reputation as a breeder. He was a proponent of the following concepts such as "like begets like, prepotency is associated with inbreeding" and "breed the best to the best."

6.0 TUTOR MARKED ASSIGNMENT

1. Who is the founder of systematic modern breeding?
2. State 3 reasons why Robert Bakewell is considered the founder of systematic modern breeding

7.0 REFERENCES / FURTHER READING

Austin Blasco. Animal Breeding: Institute of Animal Science and Technology, Universidad Politecnica de Valencia, Spain
ablasco@dca.upv.es

J.E Legate and E.J. Warwick (1990). Breeding and Improvement of Farm Animals. McGraw-Hill Publishing Company Singapore

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MODULE 2 PRINCIPLES AND PROBLEMS IN BREEDING ANIMALS FOR DISEASE RESISTANCE AND PRODUCTIVITY

- Unit 1 Principles and problems in breeding animals for increase productivity
- Unit 2 Principles and Problems in breeding animals for disease resistance

UNIT 1 PRINCIPLES AND PROBLEMS IN BREEDING ANIMALS FOR INCREASE PRODUCTIVITY

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- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main content
 - 3.1 Principles in breeding animals for increase productivity
 - 3.2 Problems in breeding animals for increase productivity
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References/Further Reading

1.0 INTRODUCTION

The techniques for the improvement of animals involve principles of selection based on quantitative variations. It is not possible for all of the desirable traits to be obtained in one individual. The successful product must contain maximum number of desirable traits and a minimum number of undesirable traits.

2.0 OBJECTIVES

At the end of this unit it you will be able to

- Explain principles that are involves in breeding animals for increase productivity
- List some problems associated with breeding animals for increase productivity

3.0 MAIN CONTENT

3.1 Principle of animal breeding for increase productivity

A major principle of animal breeding is to select those animals to become parents that will improve the genetic level in the next generation the most. For this purpose there is need to identify animals with the best genes that can influence the performance of the offspring. In most situations, this involves finding animals with the best additive genetic effects.

The animal breeder is not seeking to alter the nature of the normal population, but to increase the frequency of the desired genes and reduced the frequency of the undesired ones. The improvement in the desirable traits due to selection stems directly from changes in the frequency genes influencing the traits. Most of the traits of economic importance in farm animals are quantitative in nature, and they possesses the following characteristics

1. They are influenced by many genes (multiple gene effect), most of which probably have small effects individually.
2. They expression of the quantitative genes is conditioned by environmental effects, as such they have a continues distribution with no sharp demarcation between 'good' and 'bad'

The genetic change that can be attained depends on a number of factors. First of all, the traits that are to be improved must show additive genetic variation, and we need to be able to identify the best animals. It also matters how many traits we include in the breeding goal, what proportion of animals that are selected, how intensively they are used, how long the generation interval will be, etc.

Moreover, we need to be aware of the potential existence of genotype-environment interactions, and that a specific genotype is not always the best one in all environments. A good knowledge and understanding of various factors influencing genetic progress and how they can be optimized is crucial in designing a successful breeding programme.

The initial task in estimating the progress which can be expected from selection for any trait is to obtain an accurate estimate of the average or additive breeding values of the animals available for selection. The breeding values of the individual are predicted from available information, such as their own performance and their relatives' performance.

Breeders are aware that certain characters, especially the quantitative characters seem to be related to each other, whereby selection for improvement in one trait may affect other traits either positively or negatively. For example selection for increased wither height would likely lead to increase body weight. Also, selection for increase milk yield is likely to reduce the milk fat content.

Generally, the genetic progress per generation from selection depends upon the genetic superiority of the animals selected to be parents of the next generation, as compared to the average of all animals in the population from which they are selected. Mathematically

$$\Delta G = \bar{G}s - \bar{G}$$

Where: ΔG = genetic superiority of the selected individuals

$\bar{G}s$ = average breeding values of selected individual

\bar{G} = average breeding value of the population from which the selected individuals were drawn.

Since we do not know exactly the breeding or genetic values of the animals for quantitative traits, we must use their phenotype measures for selection. Hence, only the heritable fraction (heritability) of the phenotypic superiority can be expected to be transmitted to the next generation:

$$\Delta G = h^2 \times \bar{P}s - \bar{P}$$

Where ΔG = expected genetic change

h^2 = heritability of trait under selection

$\bar{P}s - \bar{P}$ = selection differential or difference between the mean of the selected parents ($\bar{P}s$) and average of the population (\bar{P}) for their generation

The rate of improvement in performance or genetic gain from selection during a generation is dependent on three components these are heritability, selection differential and generation interval. They are combined to measure progress due to selection as thus:

Genetic gain/generation = heritability x selection differential

$$\text{Genetic gain /year} = \frac{\text{heritability} \times \text{selection differentials}}{\text{generation interval}}$$

$$\text{Genetic gain} = \frac{h^2 \times SD}{GI}$$

These equations are the core of all animal improvement. Maximum gain will result when the h^2 and SD are high and GI is low. Therefore, any factor that will increase the heritability and selection differential or reduce the generation interval will improve the genetic gain of the trait under selection.

Heritability (h^2) expresses the part of the superiority of the parents which on an average is passed to the offspring

The Selection differential (SD) is define as the superiority of the animals selected to be parents over of the mean of the population from which they are selected

Generation interval (GI) is defined as the average age of the parents when their progeny are born.

3.2 Problems in breeding animal for increase productivity

The major problem in breeding animals for increase productivity is that many traits of economic importance in animals are dependent on the interaction of multiple genes. When attempts are made only to increase in one of these traits the other traits may depreciate or at worst the animal may die. That is if only one character is taken for improvement in the animals; the other characters will degenerate or result in harmful effects. Hence at the time of selection all the desirable characters are to be taken into consideration. For example, selection for increase in egg size in fowls resulted in the progeny that produced few numbers of eggs or even they die sometimes.

Unlike qualitative traits, it is almost impossible to identify individual gene effect on quantitative or metric trait. Thus, the seeming inability to discretely identify the genes involve in a quantitative traits brings a lot of frustration to animal breeders.

Genes at individual loci may have differing magnitude of influence, and environmental effect may further obscure the differences between the phenotypic expressions of the different genotypes, because most of the economic traits are highly influenced by environmental factors

Another major problem with animal breeding is that of genetic – environment interaction whereby animal selected in a particular environment may not perform well in another different environment. For example, would the dairy cattle selected under temperate conditions be more useful in tropical conditions than dairy cattle actually selected in the tropics?

4.0 CONCLUSION

The major tool to achieve genetic improvement is to select the best animals as parents to produce the next generation. However, the major problem in breeding animals for increase productivity is that many traits of economic importance in animals are dependent on the interaction of multiple genes

5.0 SUMMARY

The ultimate goal of a breeding program is genetic improvement of traits defined in the breeding objective for the animal population. The major tool to achieve this is to select the best animals as parents to produce the next generation, and among those parents also decide which ones should have the largest number of offspring. With successful selection, the progeny generation will on average be better than the average of the population from which the parents were chosen – a genetic progress is obtained.

6.0 TUTOR MARKED ASSIGNMENT

1. List the three component that determine the level of genetic gain that can be achieved from selection during a generation
2. Briefly highlight problems associated with breeding animal for increase production

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UNIT 2 PRINCIPLES AND PROBLEMS IN BREEDING ANIMALS FOR DISEASE RESISTANCE

CONTENTS

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Principles of Breeding animals for disease resistance
 - 3.2 Problems in Breeding animals for disease resistance
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References / Further Reading

1.0 INTRODUCTION

Improved animal health is one of the major objectives in animal breeding strategies. Selection for genetic disease resistance provides a potential avenue for improving the health status of farm animals, increasing productivity and reducing the need for pharmaceutical intervention, in this way reducing costs and delaying the appearance of resistant pathogens. Understanding the biological principles of disease heredity and resistance to disease is a prerequisite for the incorporation of these factors into multi-trait breeding programmes.

2.0 OBJECTIVES

It is expected that at the end of this unit you will be able to

- Explain the principle that is involved in breeding animals for disease resistance
- Highlight some problems associated with breeding for disease resistance

3.0 MAIN CONTENT

3.1 Principle of Breeding Animals for disease resistance

Breeding for disease resistance (rather than controlling disease with expensive drugs) continues to be topical with a growing interest in sustainable livestock farming. Animal breeders have become increasingly interested in breeding strategies aimed at improving disease resistance in farm animals, as this lessens farmers dependent on the use

of drugs at a time when there is concern about their high usage in animal to be used for food products. There has also been concern at the level of drugs resistance by many disease organisms and the cost of veterinary drugs in developing countries

There are basically two approaches to achieve this

1. **Phenotypic selection approaches for genetic disease resistance:**

Improvement in disease resistance by artificial selection has been demonstrated in experimental work as well as in domestic animal species. Conventional selection for disease resistance results mostly in quantitative improvement in resistance without major changes in the mechanisms. Disease resistance traits fulfill the criteria used for incorporation of a trait into a breeding programme. Since selection is an evolutionary process, the incorporation of health criteria into breeding programmes must be based on an understanding of the evolutionary aspects of inherited disease as well as of resistance to disease. However, low heritability of disease traits and correlations with resistance to other diseases and production traits are the major limiting disadvantages of conventional breeding methods.

2. **Genomic approaches to the improvement of disease resistance;** the criterion for selection is shifted from phenotypically expressed disease status to allele status at the DNA level. This mode of selection is termed 'marker-assisted selection (MAS). In principle, MAS can enable selection for disease resistance without exposure to disease challenge and allows highly accurate selection which is unaffected by environmental factors. Thus, MAS provides an ostensibly feasible approach to selection for genetic disease resistance in farm animals. The realization of this potential in practice requires the following:

- a. Comprehensive genome maps of the various farm animal species
- b. Genomic analysis of the resistance trait, leading to mapping and identification of disease resistance loci (DRL)
- c. Incorporation of genomic information on DRL which are identified and mapped in this way within the framework of an MAS genetic improvement programme.

3.2 Problems in Breeding Animal for disease Resistance

Some of the challenges involved in conventional breeding for disease resistance include:

1. Deliberate and concerted selection for disease resistance requires deliberate exposure of the animals to the disease causing organism, a practice that presents many practical and ethical challenges in animal welfare
2. A system of challenging animals of every generation through the use of a live, virulent organism would be necessary, as a result, high death or debility rates would be almost certain until resistant animals are located, or unless indirect or preferable direct markers for genes contributing to genetic variation in resistance are identified.
2. Breeding for disease resistance would likely be very expensive, unless physiological indicators of resistance could be used in selection.
3. An indirect consequence may be the fact that selection for disease resistance would reduce or eliminate possibilities of selecting for other desirable traits due to genes interaction
4. The implication of selection for disease resistance can be wider than just its effect on the trait and population undergoing selection
5. Some school of thought argued that resistance that has evolved naturally during the course of evolution of a breed is likely to present greater challenges to a pathogen than resistance that has been created by artificial selection within a population during a relatively few generations
6. The more successful selection for increasing the level of disease resistance in a population, the greater will be the natural selection imposed on the pathogens to evolve in such a way as to overcome the resistance

4.0 CONCLUSION

Breeding for disease resistance is possible through the use of both the conventional selection and genomic approaches depending on the species of animal, however there are many challenges associated with breeding animals for disease resistance. This includes ethical challenges, cost, genes interaction, etc

5.0 SUMMARY

Selection for genetic disease resistance provides a potential avenue for improving the health status of farm animals, increasing productivity and reducing the need for pharmaceutical intervention. Therefore, improved animal health is a major objective in current animal breeding strategies. Understanding the biological principles of disease heredity and resistance to disease is a prerequisite for the incorporation of these factors into multi-trait breeding programmes. Conventional selection

and genomic selection are the major approaches in achieving the goal of breeding for disease resistance. The problems in breeding animals for disease resistance range from ethical challenges to cost and polygenic gene effect.

6.0 TUTOR MARKED ASSIGNMENT

1. Highlight two major approaches of breeding animals for disease resistance
2. List 4 challenges in breeding animals for disease resistance

7.0 REFERENCES / FURTHER READING

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MODULE 3 FUNDAMENTAL PRINCIPLES OF INHERITANCE

- | | |
|--------|--|
| Unit 1 | Historical Perspectives of Principles of Heredity |
| Unit 2 | Mendel's laws and Principles of Inheritance |
| Unit 3 | Types of Gene action and Exceptions to Mendelian ratio |
| Unit 4 | Sex Determination Mechanism |

UNIT 1 HISTORICAL PERSPECTIVES OF HEREDITY

CONTENTS

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Historical Background of Heredity
 - 3.2 Mendelian Perspective of Heredity

3.2.1 Mendel's Conclusions

3.2.2. Implications of Mendel's work

- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor-Marked Assignment
- 7.0 References / Further Reading

1.0 INTRODUCTION

The lack of a theory explaining inheritance slowed down animal breeding for many years, but the rediscovery of Mendel's rules at the beginning of the 20th century and the development of quantitative genetics in the 1920s and 1930s animal breeding had the tools needed for its development. Characters or traits are transmitted from parents to offspring or from one generation to another without much change by inheritance. In this unit, we shall examine underlying principles of inheritance as well as the various Laws of inheritance.

2.0 OBJECTIVES

At the end of this unit, you will be able to

- Explain some early theories about heredity
- Name the early proponent of heredity studies
- State two laws of Mendel
- State some implications of Mendelian genetics
- Highlight the major significant findings of Mendel research

3.0 MAIN CONTENT

3.1 Historical Background of Heredity

For much of human history people were unaware of the scientific details of how animals conceived and give birth to young ones and how heredity worked. Clearly they were conceived, and clearly there were some hereditary connection between parents and offspring, but the mechanisms were not readily apparent. Different ideas were put forward at different times about the mode of transmission of character from one generation to another by philosophers:

1. Hippocrates speculated that "seeds" were produced by various body parts and transmitted to offspring at the time of conception
2. Aristotle postulated that the male and female contributions are not equal, and that, while the female contributed the matter, the male contributed the emotion
3. Aeschylus, in 458 BC, proposed the male as the parent, with the female as a "nurse for the young life sown within her".
4. During the 1700s, Dutch Microscopist [Anton van Leeuwenhoek](#) (1632-1723) discovered what he called "animalcules" in the [sperm](#) of humans and other animals.
5. Some scientists speculated that they saw a "little man" (homunculus) inside each sperm. These scientists formed a school of thought known as the "Spermists". They contended that the only contributions of the female to the next generation were the womb in which the homunculus grew, and prenatal influences of the womb.

6. An opposing school of thought, the “Ovists”, believed that the future human was in the egg, and that sperm merely stimulated the growth of the egg. Ovists thought women carried eggs containing boy and girl children, and that the gender of the offspring was determined well before conception.
7. Pangenesis was an idea that males and females formed "pangenes" in every organ. These pangenes subsequently moved through their blood to the genitals and then to the children. The concept originated with the ancient Greeks and influenced biology until little over 100 years ago. The terms "blood relative", "full-blooded", and "royal blood" are relicts of pangenesis. Francis Galton, Charles Darwin's cousin, experimentally tested and disproved pangenesis during the 1870s.
8. Blending theories of inheritance supplanted the Spermists and Ovists during the 19th century. The blending theory proposed that the mixture of sperm and egg resulted in progeny that were "blend" of two parents' characteristics. Sex cells are known collectively as [gametes](#) (*gamos*, Greek, meaning marriage). According to the blenders, when a black furred animal mates with white furred animal, you would expect all resulting progeny would be gray (a color intermediate between black and white). This is often not the case. Blending theories ignore characteristics skipping a generation.
9. Charles Darwin had to deal with the implications of blending in his theory of [evolution](#). He was forced to recognize blending as not important (or at least not the major principle), and suggested that science of the mid-1800s had not yet got the correct answer. That answer came from a contemporary, Gregor Mendel, although Darwin apparently never knew of Mendel's work.

3.2 Mendelian Perspective on Heredity

While we are discussing Mendel, we need to understand the context of his times as well as how his work fits into the modern science of genetics.

An Austrian monk, Gregory Mendel, developed the fundamental principles that became the modern science of [genetics](#). Mendel demonstrated that heritable properties are parceled out in discrete units, independently inherited. These eventually were termed [genes](#). Mendel's

experimental organism was a common garden pea (*Pisum sativum*), which has a [flower](#) that lends itself to self-pollination. Mendel tested all 34 varieties of peas available to him through seed dealers. The garden peas were planted and studied for eight years. Each character studied had two distinct forms, such as tall or short plant height, smooth or wrinkled seeds. Mendel's experiments used some 28,000 pea plants. Some of Mendel's traits as expressed in garden peas can be found in *The Science of Biology*, 4th Edition, by Sinauer Associates (www.sinauer.com) and WH Freeman (www.whfreeman.com).

Mendel's contribution was unique because of

- i. His methodical or empirical approach to a definite problem,
- ii. Use of clear-cut variables
- iii. Application of mathematics (statistics) to the problem.

Using pea plants and statistical methods, Mendel was able to demonstrate that traits were passed from each parent to their offspring through the inheritance of genes.

Mendel made three major and lasting contributions to the science of genetics:

1. He discovered that character or traits are transmitted from parents to offspring through hereditary material called particulate which was later called gene
2. He gave us his principle of inheritance
3. He gave us the experimental method by which he established his principles by which you could test and perhaps improve them



Gregor Mendel, the Austrian monk who figured out the rules of heredity. The above photo is from <http://www.open.cz/project/tourist/person/photo.htm>.

Student's Assessment Exercise (SAE) Module 3 Unit 1

1. Among the ancient theories of inheritance, who were the proponent of the terms "blood relative", "full-blooded", and "royal blood"?
2. What was the postulate of Aristotle about heredity?
3. List 3 ancient theories of inheritance prior to the discovery of Mendel's work in 1900
4. State 3 reasons that made Mendel's research work unique compare to the other early theories

3.2.2 Mendel's Conclusions

From his experiment Mendel arrived at the following conclusions

1. Factors are carried in reproductive cells such as pollen grains, ova, sperm cells. These factors are now called germinal unit or genes
2. Mendel suggested that these factors are always there even though they may not be apparent in appearance in some generations or progeny
3. Any character in an organism is control by two factors or genes, these are separated during gamete formation and pass into different gametes
4. Each factor is transmitted from parents to offspring intact or unchanged

3.2.2. Implications of Mendel's work

- a. Each parent contributes one factor of each trait shown in offspring.
- b. The two members of each pair of factors segregate from each other during gametes formation.
- c. The blending theory of inheritance was debunked.

- d. Males and females contribute equally to the traits in their offspring.
- e. Acquired traits are not inherited.

4.0 CONCLUSION

The discovery of Mendel, debunked many theories of ancient Philosophers about heredity and established the underlying principles on which the modern genetics is based. This is so because he was able to demonstrate empirically, that traits were passed from each parent to their offspring through the inheritance of genes

5.0 SUMMARY

Different theories were proposed at different times by many philosophers about mode of transmission of character from one generation to another. However, the first empirical study which gave rise to our present day understanding of the principles of inheritance was carried out by Gregor Mendel.

6.0 TUTOR MARKED ASSIGNMENT

1. Explain the perception of blending theory of inheritance
2. State the differences between Ovist and Spermist theory of heredity
3. Who is the father of modern genetic?
4. State the implications of Mendel's work

7.0 REFERENCES / FURTHER READING

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UNIT 2 MENDEL'S LAWS OF INHERITANCE

CONTENTS

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Laws of Mendel
 - 3.2 Mendelian crosses
 - 3.3 Application of Mendelian genetics to animal Improvement
 - 3.4 Application of principle of Genetics in livestock improvement
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References /Further Reading

1.0 INTRODUCTION

Our basic laws of inheritance were derived from a simple series of experiments with garden peas more than a century ago. Gregor Mendel crossed various pure lines of garden peas and, by following their hybrid progeny, observed that traits are inherited as alternate states of independent units of inheritance or genes (which Mendel called “factors”), and that these units come in pairs. Each unit of inheritance can have alternate states (alleles) that segregate at meiosis, with each gamete receiving only one allele (the principle of segregation, Mendel's first law); and that different alleles assort independently into the gametes (the principle of independent assortment, Mendel's second law). These principles became the fundamental principles of modern genetics

2.0 OBJECTIVES

At the end of this unit you should be able to

- States the laws of Mendel
- Explain the meaning of Monohybrid and Dihybrid crosses
- Write the genetic and phenotypic ratio of Monohybrid and Dihybrid crosses

- Explain the application of Mendelian genetics to animal Improvement
- List the application of genetic principles in animal improvement

3.0 MAIN CONTENT

3.1 Laws of Mendel

The observations of Mendel led him to formulate the following laws:

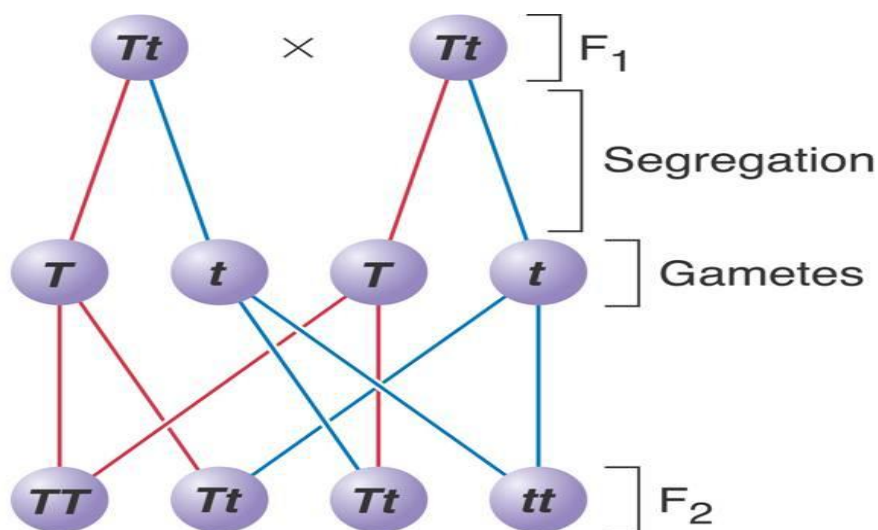
1. **Law of Segregation of genes:** the law state that two genes separator segregate from one another unchanged and unblended as they pass from parents to offspring or from generation to generation. Mendel observed that when red-flowered plant was crossed with a white flowered plant, all the F_1 plants were red-colour, but when the F_1 progeny were crossed, the red and white colours appeared in the F_2 generation in a ratio of 3red:1white. The results of Mendel's experiment formed the basis of his first law 'the law of segregation of genes'. This law debunked the Blending theory, which postulated that factors responsible for character transmission were fluid in nature and that the mixture of the two factors (sperm and egg) resulted in progeny that were intermediate or "blend" of the two parents' characteristics.
2. **Law of independent assortment of genes:** this law state that two pairs of genes in the same cross assort independently of each other. This law came about when Mendel started considering two pairs of characters (Dihybrid cross) e.g. round yellow and wrinkled green seed. He crossed a round yellow with a wrinkled green seed plants and found that the F_1 offspring produced all round yellow seeds (Round and yellow were dominant). When the F_2 generation was raised from these seeds, he observed that four types of plants were produced in a definite ratio of 9:3:3:1. Thus Mendel concluded that the factors determining the two differences of each pair were independent in how they are inherited. This form the basis of the second law "law of independent assortment of genes"(this is discussed in detailed under Dihybrid cross)

3.2 Mendelian crosses

Monohybrids cross.

In his research work, Mendel crosses individual plants that differ in only one trait, such as height of the pea plant (tall vs. short). The F_1 generation showed only one of the two parental traits. The F_2 generation showed a 3:1 ratio of the two parental traits. Mendel postulated the following:

1. A pea plant contains two discrete hereditary factors, one from each parent
2. The two factors may be identical or different
3. When the two factors of a single trait are different, one is dominant and its effect can be seen, the other is recessive and is masked by the dominant factor
4. During gameteogenesis (meiosis), the paired factors segregate randomly so that half of the gametes received one factor and half of the gametes received the other. This is Mendel's Law of Segregation



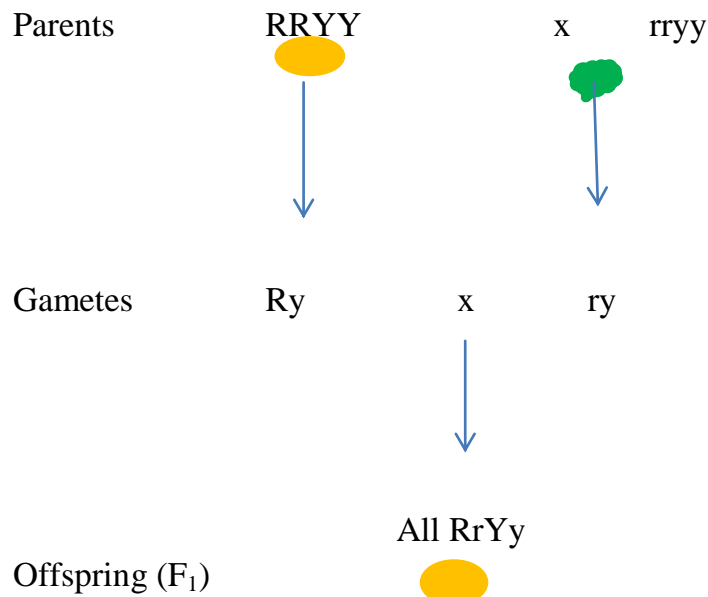
The phenotypic ratio of the F_2 was 3:1 that is 3 tall plants and 1 short plant

Dihybrid Cross

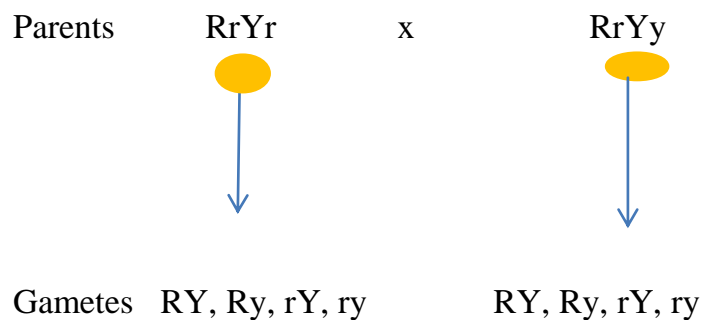
Mendel also performed Dihybrid crosses by crossing individual plants that differ in two traits

For example; Seed texture (round vs. wrinkled) and Seed colour (yellow vs. green).

The homozygote round yellow seed (RRYY) was dominant while the homozygote wrinkle green (rryy) was recessive. The gametes produce were RY and ry as shown in the figure below. The F₁ generation progeny were all heterozygote round yellow seed (RrYy)



When the F₁ progeny were crossed, the F₂ progeny were of 4 types



To find all the possible genetic combinations a Punnett square can be used

Punnett squares

It is a graphical method used in genetics to calculate the results of all possible fertilization. Punnett squares can be used to predict the genetic variations that will result from a cross.

They help predict the chances an offspring will be homozygous or heterozygous for a trait

- A capital letter represent the dominant allele; R= round
- A lowercase letter represent the recessive allele; r= wrinkle
- The gametes produced by each parent are written along the top and left
- Possible gene combinations are written in the boxes
- Punnett squares give you probabilities or predictions, not absolute numbers
- the larger the number of offspring, the closer the resulting numbers will get to expected values

From each there are 4 possible kinds of male and female gametes, namely RY, Ry, rY, ry. The law of chance dictates that any one of the male gametes may unite with any one of the female gametes making altogether 16 generation which will appear in a proportion of 9:3:3:1 That is, the phenotypic ratios of the F₂ was

9 round yellow: 3 round green: 3 wrinkle yellow: 1 wrinkle green.

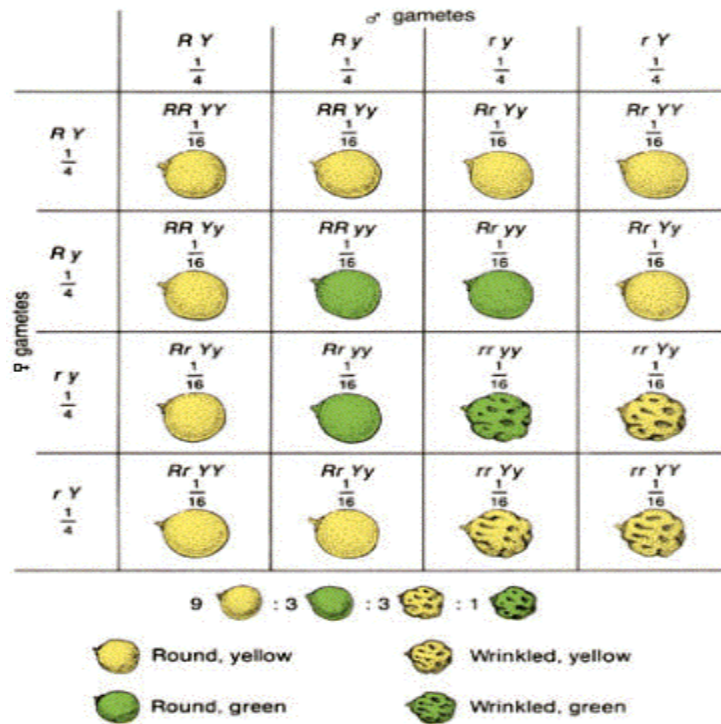


Figure 1: Inheritance of two traits simultaneously (Dihybrid cross). The above graphic is from the Genetics pages at McGill University (<http://www.mcgill.ca/nrs/dihyb2.gif>).

Data From one of Mendel’s Dihybrid Crosses

If the genes, assort independently the predicted phenotypic ratio in the F₂ generation would be 9:3:3:1. Mendel’s data was very close to segregation expectations, thus, he proposed the law of Independent assortment of genes. During gamete formation, the segregation of any pair of hereditary determinants is independent of the segregation of other pairs

P-cross	F1-generation	F2-generation	Ratio
Round, Yellow seeds X Wrinkled, Green seed	All round, yellow	<ul style="list-style-type: none"> • 315 round yellow seed • 101 wrinkled, yellow seed • 108 round, green seed • 32 green wrinkled seed 	<ul style="list-style-type: none"> • 9.8 • 3.2 • 3.4 • 1.0

3.3 Application of Mendelian genetics to animal Improvement

Although Mendel worked on plant, the basic principles of heredity discovered by him apply to animal breeding. This is because the mechanisms of heredity are essentially the same in both plants and animals. The application of Mendelian principles can be seen in the inheritance of many qualitative traits in farm animals.

The first law (law of segregation of genes), for example, in cattle the polled or absence-of-horns trait is dominant over the horned trait. Thus when homozygous horned cattle are mated with homozygous polled cattle, the offspring possess one gene for the presence of horned and another for the absence of horns i.e. they are heterozygous for the character. Since the polled gene is dominant, all offspring are polled. If the heterozygous offspring are mated, then, as both parents produce equal numbers of germ cell carrying either allele, the chances of any sperm cell from the male fusing with any egg of the same type or of a different type are equal and so four combinations of the genes are possible. The phenotype grouping is therefore three polled to one horned animal, but since fertilization is at random, it must not be expected in practice that among every four progeny of such mating the result will be 3 polled and one horned animal. This will occur only when a very large number of mating are evaluated.

The second law, that of independent assortment can be demonstrated in an example where the inheritance of two pairs of genes are consider at the same time. For example we can consider two dominant traits polledness and dwarfism in Hereford cattle. If a homozygous polled, non – dwarf individual is mated to a homozygous horned-dwarf individual the F_1 progeny will all be phenotypically polled and non-dwarf cattle. If the F_1 progeny are then mated, the resulting offspring (F_2) will exhibit four different phenotypes in the ratio of nine polled non-dwarf, to three polled dwarf, to 3 horned non dwarf, to 1 one horned dwarf individuals (9:3:3:1).

Students Assessment exercise (SAE) Module 3 Unit 2

1. With the aid of diagram, write the genetic and phenotypic ratios of monohybrid cross between two heterozygote tall plants (Tt)

3.4 Application of principle of Genetics in livestock

The knowledge of the principle of genetics has enabled us to develop scientific selection and breeding of animals. Through this selection and breeding, it has been possible to do the following:

- i. Increase production of animals such as milk, eggs, meat etc
- ii. Improved quality of animals and animal products
- iii. Improved resistance of animals to diseases, insects and climatic factors

4.0 CONCLUSION

Although Mendel used plants in his research, however, our understanding and application of Mendel's Laws are extremely importance in animals breeding.

5.0 SUMMARY

The observations of Mendel led him to formulate two basic laws of inheritance. These are Law of Independent Assortment of genes and Law of Segregation of Genes

6.0 TUTOR MARKED ASSIGNMENTS

1. State two laws of Mendel
2. State the differences between Monohybrid and Dihybrid crosses
3. List three application of principle of genetics in agriculture

7.0 REFERENCES/ FURTHER READING

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UNIT 3 TYPES OF GENE ACTION AND EXCEPTIONS TO MEDELIAN RATIO

CONTENTS

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Complete dominance
 - 3.2 Incomplete dominance
 - 3.3 Codominance
 - 3.4 Over dominance
 - 3.5 Epistasis
 - 3.6 Pleiotropy
 - 3.7 sex-influenced
 - 3.8 sex-limited genes
 - 3.9 Sex-linked traits
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References / Further Reading

1.0 INTRODUCTION

As advances in genetics have confirmed and illuminated the mechanisms underlying Mendel's observations, we have also discovered the need to adapt and modify his principles. Gene's interaction and exceptions to Mendel's laws of inheritance are described in this unit.

2.0 OBJECTIVES

At the end of this unit you should be able to define the following

- Complete dominance
- Incomplete dominance
- Co dominance
- Over dominance
- Epistasis

- Pleiotropy
- Linkage
- sex-influenced
- sex-limited genes
- Sex-linked traits

3.0 MAIN CONTENT

3.1 Complete Dominance

This is a type of gene action in which one allele at locus completely masks the effect of another allele at the same locus. All the allelic pairs that Mendel studied showed complete dominance relationships i.e. one allele at a locus is dominant to the other allele, so that the phenotype of the homozygous dominant and heterozygous genotypes are the same. The recessive genotype is phenotypically expressed only when the organism is homozygous.

3.2 Incomplete Dominance

Incomplete (partial) dominance is shown when the dominant allele is not completely dominant to the recessive allele and the heterozygote's phenotype is closer to the dominant phenotype than to the recessive phenotype, but is not identical to the dominant phenotype. In other word, incomplete dominance is a form of intermediate inheritance in which one allele for a specific trait is not completely dominant over the other allele. This results in a combined phenotype. Examples: In cross-pollination experiments between red and white snapdragon plants, the resulting offspring are pink. The dominant allele that produces the red colour is not completely expressed over the recessive allele that produces the white colour

3.3 Co dominance

In co dominance both alleles of a pair are fully expressed in a heterozygote individual, thus the F_1 heterozygote exhibits the phenotypes of both homozygote parents. There is no dominant or recessive allele. Both alleles contribute equally to the production of the phenotypes, so the heterozygous genotype produces a phenotype that is intermediate between those produced by the two homozygous

genotypes. The ABO blood system provides a good example of co dominance

3.4 Over Dominance

is a type of gene action in which the performance of heterozygous animals is more extreme than that of both homozygous parents.

3.5 Epistasis

it is a form of gene interaction in which an allele at one locus interferes or masks the effect of another allele at a different locus. A gene that masks another gene's expression is said to be Epistatic and the gene whose expression is masked by a non-allelic gene is said to be hypostatic.

3.6 Pleiotropy

Pleiotropy is shown when an allele at a single locus has an influence on more than one characteristic. A gene which affects several characteristics is said to have pleiotropic effect.

3.7 Linkage

An exception to Mendelian law of independent assortment of genes, linkage occurs when particular genes are at different loci but are carried on the same chromosome. Because chromosomes tend to be transmitted in their entirety, the different genes are transmitted together, thus, segregation rule may not hold. Different genes situated close together on a particular chromosome tend to be linked more than those situated at opposite ends of the chromosome.

3.8 Sex-limited genes

Sex-limited genes are autosomal genes (body cell) that affect traits which appear only in one sex, but not in the other sex. Traits of this kind are called sex-limited traits e.g. milk production in dairy cattle, the formation 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.

3.9 Sex-influenced Traits

These are also autosomal genes however, the traits controlled by these autosomal genes appear in either sexes, but the frequency of occurrence is higher in one sex than the other. An example is pattern baldness in humans.

3.10 Sex-linked genes

Genes whose inheritance pattern is different in males and females are said to be sex linked. The sex linked genes are located on the sex chromosomes and have different patterns of inheritance.

4.0 CONCLUSION

Different alleles can exert different phenotypic effects; Gene's interaction leads to modification of normal Mendelian ratios.

5.0 SUMMARY

The interaction within alleles of gene controlling a single character may be dominant, incomplete dominance and co-dominance and are called intra allele interaction. When an interaction occurs between different pairs of alleles influencing a character of an individual is said to be interallelic interaction or Epistatic. The gene that has masking effect is called Epistatic gene, and the gene whose effect is masked is known as hypostatic gene.

6.0 TUTOR MARKED ASSIGNMENT

1. Differentiate between the following
2. Complete and incomplete dominance
3. Codominance and Over dominance
4. Epistasis and Pleiotropy
5. Sex limited and sex-linked genes

7.0 REFERENCES / FURTHER READING

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UNIT 4 SEX DETERMINATION MECHANISM

CONTENTS

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Sex determination Mechanism
 - 3.1.1 X-Y system of sex determination
 - 3.1.2 X-0 system
 - 3.1.3 Z-W system
 - 3.2. SRY System of Sex Determination in Mammals
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignments
- 7.0 References/ Further Readings

1.0 INTRODUCTION

Within a population, sexual reproduction enhances genetic diversity because the genetic material of offspring comes from two sources. For most species of animals and some species of plants, sexual reproduction is carried out by individuals of the opposite sex—females and males. The underlying mechanism by which an individual develops into a female or a male is called **sex determination**. As we will see, a variety of mechanisms promote this process.

For some species, females and males differ in their genomes. For example, you are probably already familiar with the idea that people differ with regard to X and Y chromosomes. Females are XX and males are XY, which means that females have two copies of the X chromosome, whereas males have one X and one Y chromosome. Because these chromosomes carry different genes, chromosomal differences between the sexes also result in unique phenotypes and inheritance patterns

2.0 OBJECTIVES

At the end of this unit you will be able to

- explain sex determination mechanism in different species of animals
- explain SRY Mammalian Sex Determination mechanism

3.0 MAIN CONTENT

3.1 Sex Determination Mechanism

Researchers have studied the process of sex determination in a wide range of species and discovered that several different mechanisms exist. In this section, we will explore some common mechanisms of sex determination in animals and plants. Sex determination in some species is due to the presence of particular chromosomes a pair of chromosomes, called the **sex chromosomes determines** sex in many different species. Some examples are described

3.1.1 X-Y system of sex determination

In the X-Y system of sex determination, which operates in mammals, the male contains one X chromosome and one Y chromosome, whereas the female contains two X chromosomes. In this case, the male is called the **heterogametic sex**. Two types of sperm are produced: one that carries only the X chromosome and another that carries the Y. In contrast, the female is the **homogametic sex** because all eggs carry a single X chromosome. The sex of the offspring is determined by whether the sperm that fertilizes the egg carries an X or a Y chromosome. What causes an offspring to develop into a male or female? One possibility is that two X chromosomes are required for female development. A second possibility is that the Y chromosome promotes male development. In the case of mammals, the second possibility is correct. Chromosomal basis for sex determination: the chromosomal basis for sex determination in mammals is rooted in the location of a particular gene on the Y chromosome. The presence of a gene on the Y chromosome called the *Sry* gene causes maleness.

3.1.2 X-0 system

Another mechanism of sex determination that involves sex chromosomes is the X-0 system that operates in many insects. In some insect species, the male has only one sex chromosome (the X) and is designated X0, whereas the female has a pair (two X's). In other insect species, such as *Drosophila melanogaster*, the male is XY. For types of insect species (i.e., X0 or XY males, and XX females), the ratio between X chromosomes and the number of autosomal sets determines sex.

3.1.3 Z-W system

this determines sex in birds and some fish, the male is ZZ and the female is ZW. The letters Z and W are used to distinguish these types of sex chromosomes from those found in the X-Y pattern of sex determination of other species. In the Z-W system, the male is the homogametic sex, and the female is heterogametic.

3.2 SRY System of Sex Determination in Mammals

It is often stated that sex determination in humans is based on the presence or absence of the Y chromosome. However, the situation is more complex. Sex determination in humans and other mammals is actually due to a **single gene** that is normally located on the Y chromosome. Near one of the pseudoautosomal regions called "sexdetermining region" (**SRY**). The SRY produces a gene product, **Testis determining factor (TDF)** that stimulates undifferentiated gonadal tissue in embryos to form testes. The gene functions early in the developmental stages of the embryo that ultimately causes tissue that is developing into ovaries to 'switch' their development, so that they develop as testes. Individuals without this gene develop as females. Sometimes, the SRY gene becomes associated with a chromosome other than the Y. In these cases, an individual can have the chromosome complement XY, and be a perfectly normal female (or be XX and be a normal male). Therefore it is not the Y chromosome that determines maleness, or the presence of two X chromosomes that determines femaleness, it is the presence or absence

of the protein coded for by the SRY gene that determines gender in mammals.

4.0 CONCLUSION

The earlier perception of sex determination in mammals using XY system was discontended by the SRY system which shows that Sex determination in humans and other mammals is actually due to a **single gene** that is normally located on the Y chromosome regions called “sex determining region”(SRY). The SRY produces a gene product, **Testis determining factor (TDF)** that stimulates undifferentiated gonadal tissue in embryos to form testes.

5.0 SUMMARY

The underlying mechanism by which an individual develops into a female or a male is called **sex determination**. There are different mechanisms of sex determination in different species of animals; these include XY mechanism in mammals, XO mechanism in insect and ZW mechanism in avian species. However, studies on mechanism of sex determination in mammals' shows that it is not the Y chromosome that determines maleness, or the presence of two X chromosomes that determines femaleness, it is the presence or absence of the protein coded for by the SRY gene that determines gender in mammals.

6.0 TUTOR MARKED ASSIGNMENT

1. What is sex determination
2. List the systems of sex determination in mammals, insect and avian
3. Briefly explain SRY system of sex determination
4. What is the difference between the X-Y and X-0 systems of sex determination?

7.0 REFERENCES / FURTHER READING

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MODULE 4 TYPES OF TRAITS AND THEIR INHERITANCE IN ANIMALS

- Unit 1 Qualitative and Quantitative characters and their inheritance
 Unit 2 Gene and Gene types

UNIT 1 QUALITATIVE AND QUANTITATIVE TRAITS AND THEIR INHERITANCE

CONTENTS

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Quantitative traits and their inheritance
 - 3.2 Qualitative traits and their inheritance
 - 3.3 Differences between quantitative and qualitative traits
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignments
- 7.0 References/ Further Readings

1.0 INTRODUCTION

In genetics, traits can be divided into two groups based on their mode of inheritance and their effects on the organism’s phenotype; these are qualitative and quantitative traits. All genetic traits an organism has fit neatly into one of these two categories.

2.0 OBJECTIVES

At the end of this unit you will be able to

- Explain the meaning of quantitative and qualitative traits

- Explain the inheritance pattern of quantitative and qualitative traits
- Differentiate between quantitative and qualitative traits
- List the characteristics of quantitative and qualitative traits
- List some examples of quantitative and qualitative traits

3.0 MAIN CONTENT

3.1 Quantitative Characters and their inheritance

Quantitative traits are those traits with continuous range of variation and do not fit into natural categories. They are economically important measurable phenotypic traits of degree such as body weight, height, susceptibility to pathological diseases or intelligence in man; milk yield, meat or egg production in poultry etc. The quantitative traits are also called metric traits. Generally, quantitative traits are under the influence of large number of genes or multiple genes effect. They can also be describing as "polygenic traits." Quantitative traits are easily influence by environmental factors, thus may be modified variously by the environmental conditions.

The inheritance of poly genes or quantitative traits is variously called quantitative inheritance, multiple factor inheritance, multiple gene inheritance or polygenic inheritance which means that the traits are influence by many genes. The quantitative inheritances have the following characteristics:

1. The segregation phenomenon occurs at an indefinitely large number of gene loci.
2. The genes for a multiple trait have different biochemical functions but similar phenotypic effects,
3. Blocks of genes are bound together by inversions and transmitted as units from inversion heterozygotes to their progeny, but such blocks are broken up by crossing over in insertion homozygotes.
4. The polygenes have pleiotropic effects; that is, one gene may modify or suppress more than one phenotypic trait.
5. The environmental conditions have considerable effect on the phenotypic expression of poly genes for the quantitative traits.

3.2 Qualitative traits and their inheritance

Qualitative traits are those traits that are easily classified into distinct or discrete categories. This means that you can neatly categorize these traits. For example, if a breed of animal had either black or white coat colour or nothing in between, this would be a discrete trait, also, traits of which an organism either has it or not, also fit into this category e.g present or absent of horn in cattle, present or absent of beard in goats. Inherited diseases caused by single mutations are good examples of qualitative traits. The ABO human blood groups illustrate this concept well. Except for some rare special cases, the humans can only fit into one of four categories for the ABO part of their blood type: A, B, AB, or O. Since the ABO part of your blood type fits neatly into four categories, it is a qualitative trait.

The pattern of inheritance for a qualitative trait is typically monogenetic, which means that the trait is only influenced by a single gene or small group of genes. The environment has very little influence on the phenotype of these traits, thus there is little or no environmental modifications to obscure the gene effects.

3.3 Differences between Quantitative and Qualitative traits

The basic differences between quantitative and qualitative traits involves a number of genes contributing to the phenotypic variability and the degree to which the phenotype can be modified by environmental factors

	Quantitative traits	Qualitative traits
1	Control by many genes (polygenic)	Control by one or few genes (monogenic)
2	Easily influence or modify by environmental factors	Not easily influence or modify by environmental factors
3	Exhibit continues variation, i.e they phenotype forms spectrum	Exhibit discontinues variation
4	They are metric traits or character of degree thus have to be measured	They are discrete character or character of final
5	They are concerned with a population of organism consisting of all possible mating	They are concerned with individual mating
6	The pattern of inheritance is polygenic	The pattern of inheritance in monogenic
7	They are mostly economic traits	They are mostly fancier or aesthetic traits

4.0 CONCLUSION

Quantitative traits are largely control by many genes or multiple genes, they are easily influence by environmental factors, thus may be modified variously by the environmental conditions. While qualitative traits are control by one or few genes and they are not easily influence by environmental factors, thus can hardly be modified by environmental conditions. Therefore, the knowledge of quantitative and qualitative traits is necessary to enable the breeder design appropriate breeding techniques for livestock improvement.

5.0 SUMMARY

In animal breeding, traits can be grouped into qualitative and quantitative traits, based on their mode of inheritance and their effects on the organism's phenotype. Quantitative traits are those traits with a continuous range of variation and the pattern of their inheritance is polygenic, which means that the trait is under the influence of a large number of genes or multiple genes effect. They are easily influenced by environmental factors, thus may be modified variously by the environmental conditions. Qualitative traits are those traits that are easily classified into distinct or discrete categories. The pattern of inheritance for a qualitative trait is typically monogenetic, which means that the trait is only influenced by a single gene or small group of genes. The environment has very little influence on the phenotype of these traits, thus there is little or no environmental modifications to obscure the gene effects.

6.0 TUTOR MARKED ASSIGNMENTS

1. List 2 quantitative and 2 qualitative traits in livestock
2. Explain the type of inheritance of quantitative and qualitative traits
3. List 4 differences between quantitative and qualitative traits
4. Group the following traits into either quantitative or qualitative; litter size in goats, milk fat, body weight, presence of horn in cattle, coat colour, egg production in chicken, presence of beard in goats, milk yield

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UNIT 2 GENE AND GENE TYPES

CONTENTS

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 What is a gene
 - 3.2 Types of genes
 - 3.2.1 Lethal or Detrimental genes
 - 3.2.2 Dominant and Recessive genes
 - 3.2.3 Additive genes Complimentary Gene
 - 3.2.4 Penetrance
 - 3.2.5 Expressivity
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References / Further Reading

1.0 INTRODUCTION

Genes hold the information to build and maintain an organism's cells and pass genetic traits to offspring, however some genes are incompatible with life and could be detrimental to the organism that have them. Different alleles can exert different phenotypic effects; some their effect can easily be seen while other may be hidden and may expressed themselves phenotypically only when the condition is favourable for them. In this unit we shall consider some types of genes and their expression

2.0 OBJECTIVES

At the end of this unit you should be able to

- Define gene
- Explain the meaning of lethal or detrimental genes
- Explain how lethal genes can be control in animals population
- List the differences between dominant and recessive gene

3.0 MAIN CONTENT

3.1 What is gene?

Gene is a unit of heredity in a living organism. Genes hold the information to build and maintain an organism's cells and pass genetic traits to offspring, the genes are located in the chromosomes. Chromosomes are found in the nucleus of the cell. The region of the chromosome at which a particular gene is located is called locus. The genes are molecules of chemical substance called Deoxyribonucleic acid (DNA). The number of DNA is equal to the number of chromosomes in a cell. In human being, body cells have 46 chromosomes called diploid condition ($2n$) while gamete has 23 chromosomes called haploid condition (n). A chromosome consists of a single, very long DNA helix on which thousands of genes are encoded.

3.2 Types of genes expression

3.2.1 Lethal or Detrimental genes

Gene changes which are incompatible with development or survival are known as lethal genes. In other words, genes which results in the death of an individual at any stage of development in life are called lethal genes. It can be immediately following fertilization, during embryonic differentiation, at parturition or postnatal. Lethal genes may be dominant and exert their effect in heterozygotes. Such genes are rare and difficult to study since they are rapidly eliminated from a population unless their effect occurs late in life after the affected individual have produced offspring that carries the genes. Most lethal genes are recessive and exert their effect only when homozygous. Some genes are deleterious to the organism that have them but are not lethal, (i.e they do not cause death) provided the environmental factors are favourable. However, they can cause deformation of the individual at any stage in life. Such genes are called semi-lethal genes.

Control of lethal or detrimental genes

The action to be taken if lethal or detrimental genes are discovered in a herd depends on the type of the herd and the seriousness of the abnormality. In a commercial herd, the action that is usually necessary is to cull the sire or sires which produced the defective offspring and replaced them with unrelated males.

For seed stock, correction measures need to be drastic, since there obligation is to provide stocks which will perform well for future customers.

Therefore, the following should be considered as possible measures for elimination of lethal or detrimental genes or for reducing its frequency in the herd

1. Cull all sires which have produced defective offspring
2. Remove all females which have produced defective offspring from the seed stock herd.
3. Cull other closed relatives of affected individuals including normal offspring of sires and dams which have produced defective individuals
4. If the affected individuals are viable and fertile, retain them for progeny-testing of prospective breeding animals
5. Progeny-test all prospective herd sires before using them extensively in the herd

3.2.2 Dominant and Recessive genes

Dominant genes are genes with observable effect when present in homozygote or heterozygote form. The degree of dominance can vary widely. In some cases it is complete and the outward effect is the same as if the dominant genes were present in both of the members of the chromosome pair. In other cases dominant is incomplete with some level of intermediate expression. The recessive genes have no apparent effect on the organism when present in only one member of the chromosome pair of an individual. To determine the genotype of unknown individual test cross or back cross is used.

- i. **Test cross:** The cross of an individual of unknown genotype to a completely recessive individual is known as a test cross. In this case, the type of progeny will depend on the types and frequencies of gametes produced by the parent of unknown genotype
- ii. **Back cross:** Back cross involves crossing a progeny to one of their parents

3.2.3 Additive genes

Additive genes are also known as polymeric genes. This is a situation where two pairs of genes determine a character. For example, in *Cucurbitapeoplants*, crossing two plants with spherical fruits yielded only discoid-fruited progeny (F_1). When F_1 are crossed, discoid, spherical and long progeny are produced. In this example, the F_1

progeny are not like any of the parents, and in F_2 , a third phenotype appears. In pigs, coat colour also follows the same inheritance pattern.

3.2.4 Complimentary Gene

Complimentary genes are dominant alleles which are located at two different loci and segregate independently of each other. Their presence or activities produces complimentary phenotypic effect

Penetrance

The frequency with which a gene produces a phenotypic or visible effect in the individuals, which carry it, is known as penetrance. In other words penetrance refers to the proportion of individuals which exhibit phenotypic effect of a specific gene carried by them. In general genes express themselves in all the individuals in which they are present in the appropriate genotype is known as penetrance. It indicates the number of individuals that give the expected phenotype to any degree.

2.2.5 Expressivity

The degree of phenotypic expression of a penetrant gene is called expressivity. In other words, the ability of a gene to produce identical phenotypes in all the individuals carrying it in the appropriate genotype is known as expressivity.

4.0 CONCLUSION

Our knowledge of genes as well as the various types of genes and their effect on phenotypic variations is necessary to enable the breeder select appropriate breeding techniques.

5.0 SUMMARY

Gene is a unit of heredity in a living organism. It holds the information to build and maintain an organism's cells and pass genetic traits to offspring. However, some of these genes could result in the death of an individual at any stage of development in life and are called lethal genes while some could be deleterious to the organism that have them but are not lethal, provided the environmental factors are favourable. Such genes are called detrimental or semi-lethal genes.

6.0 TUTOR MARKED ASSIGNMENT

1. What is a gene?
2. Define additive genes
3. Explain the difference between lethal and semi lethal genes

4. Explain the differences between dominant and recessive genes
5. Briefly explain how you can control lethal genes in a dairy herd
6. Define penetrance and expressivity

7.0 REFERENCES/ FURTHER READING

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MODULE 5 VARIATION AND ITS STATISTICAL MEASUREMENTS

- Unit 1 Variations in Animal population
Unit 2 Measurements of variation

UNIT 1 VARIATIONS IN ANIMAL POPULATION

CONTENTS

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Definition of Variation in Animal
 - 3.2 Types of Variations
 - 3.3 Causes of Variation
 - 3.3.1 Genetic Source of Variation
 - 3.3.2 Environment Source
 - 3.3.3 Interactions between heredity and Environment

- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References / Further Reading

1.0 INTRODUCTION

The assessment of most animal species reveals the existence of phenotypic differences between individuals, for example in cattle there are obvious difference in coat colours and the presence and absence of horns. If cattle are weighed or if milk production is recorded there will be differences in performance between individuals. These differences between individuals of the same species or breed for the same trait or character are called Variation. Variation among animals in weight, growth rate, efficiency of feed utilization, carcass characteristics, disease resistance etc has been observed.

The basic idea in this study of variation is the partitioning of total phenotypic variation into the components attributable to different causes. The relative magnitudes of these components determine the genetic proportion of the population and the degree of resemblance between relatives.

2.0 OBJECTIVES

At the end of this unit you will be able to

- Define variation
- State types of variations in animal population
- List the causes of variation in animal population

3.0 MAIN CONTENT

3.1 Definition of Variation in Animal

The differences between individuals of the same species or breed for the same trait or character are called Variation. The assessment of most animal species reveals the existence of phenotypic differences between individuals. For example variation exist among animals in size, rate of growth, efficiency of feed utilization, carcass characteristics, disease resistance etc

3.2 Types of variation

Variation can be classified into two categories depending on the character examined and upon the unit of measurement used.

- Discrete or discontinuous variation:** These character for which there are two or only relatively distinct categories are described as showing discrete or discontinues variation. The discontinues variation fall into a few clearly defined classes which is usually due to the fact that these traits are under the control of one or a few pairs of genes whose final expression is not greatly influenced by external environmental factors. Discrete variation is usually exhibited by qualitative traits, such as coat colour, presence or absence of horns in cattle
- Continues Variation:** For other characters where the number of categories is large and limited to the units and accuracy of measurement used for Classification, these characters are described as showing continuous variation. The continues variation does not falls into clearly defined classes which is usually due to the fact that these traits are under the control of many genes whose final expression is greatly influenced by external environmental factors. Continues variation is usually exhibited by quantitative traits such as milk yield in cattle, weight gain, birth weight etc

3.3 Causes of Variation

The causes of variation in animal can be group into three: First is the average difference between genotype, the second is the variation from environmental source and thirdly, the interactions between heredity and Environment. Phenotypic variation refers to the observable or measurable difference among individuals within a population for a particular trait.

3.3.1 Genetic Source of Variation

A measure of genetic variation is the amount of heterozygosity at a locus in a population which is given by the total frequency of heterozygotes at a locus. The genotype of an individual is fixed at conception and barring a mutation remains the same for the remainder of its life. Its genetic makeup is determined by the genes that it receives from both parents.

The individual as well as its parent possess thousands of genes. Members of inbred animals are more likely to be alike genetically than non-inbred individuals.

The degree of genetic similarity among individuals within an inbred linen increases as the amount of inbreeding increases especially if there is directional selection. Parent's homozygote for many pairs of genes will have more offspring that are more alike genetically than parents that are heterozygous for several of genes. In fact genetic variability within a species is almost unlimited.

3.3.2 Environment Source

Phenotypic variations in economic traits due to environment are also of great importance. Environment includes all such factors as disease, nutrient supply, temperature effects, accident and others which the individual may encounter from the time of conception until its death.

Phenotype variations due to environment are important because

1. They are not transmitted from parents to their offspring,
2. They overshadow variation due to heredity.
3. The proper environment is necessary for an individual to reach its genetic potential
4. Rapid improvement can be made in the efficiency of livestock production by supplying uniform and superior environmental conditions to breeding animals.

3.3.3 Interactions between heredity and Environment

The interaction between heredity and environment means that animals of a certain genotype may perform more satisfactorily in some environment than in another. In other words one environment permits the expression of the genetic characters in a breed or strain another does not.

4.0 CONCLUSION

Variation in animal population can be group into two, that is continues and discontinues or discrete variation. Our knowledge of variation as well as the various types of variations and their effect on phenotypic variations is necessary to enable the breeder select appropriate breeding techniques.

5.0 SUMMARY

Traits generally are grouped into those which show qualitative differences and those which show quantitative differences. Those which show qualitative differences are term as showing discrete or discontinue variation while those which show quantitative differences are term as showing continues variation. The causes of variation could either be genetic or environmental or the combined effect of both the genetic and environmental factors

6.0 TUTOR MARKED ASSIGNMENT

1. Define variation
2. List two types of variation
3. state two differences between the two types of variation listed in question ii above
4. List 5 factors that controls variation in animal population

7.0 REFERENCES /FURTHER READING

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UNIT 2 MEASUREMENTS OF VARIATION

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Normal curve and Means
 - 3.2 Variance
 - 3.3 Standard deviation
 - 3.4 Coefficient of variation
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References / Further Reading

1.0 INTRODUCTION

We have discussed in the preceding module that majority of the economic traits are influence by large number of genes (polygenic) and by many environmental factors. As a consequence most of these traits are measured quantitatively, and they exhibit what we already described as continues variation. A number of special procedures and techniques have been devised to characterizing and summarizing such continues variations.

To study animal population, a statistical description of the population is required. This description in its simplest form consists of a measure of central tendency and a measure of the variability of the population. Ordinarily we do not have measurements on the entire population. However, by studying a sample of observations from the population, a statistic can be derived which are descriptive of the sample and which provide estimates of the corresponding population.

2.0 OBJECTIVES

At the end of this unit you will be able to

- Define and state the uses of variance, standard deviation and coefficient of variation
- list the components of variance
- Calculate mean, variance, standard deviation and coefficient of variation

3.0 MAIN CONTENT

3.1 Normal curve and Means

Most of biological measurements can be considered to be normally distributed. A distinctive feature of this normal distribution is that the values are clustered at a mid-point, thinning out symmetrically toward both extremes. Figure 1 shows a theoretical normal distribution. The height of the curve at a particular point represents the frequency of individual having that particular value.

There are at least three common measures of central tendency; mean, median and mode. The mean represents the average of all measurements in a population; the media represents the class value half way between the two extreme values; and the mode represents the class with the highest frequency. For a true normal distribution, the mean, median and the mode will coincide. However, the most useful statistics in estimating central tendency in most population is the mean, since samples from a normally distributed population may show departure from normality.

The population mean is merely the arithmetic average of all the values included in the population. It is conventionally represented by a symbol μ for a population mean and \bar{X} for sample mean. Individual measurements in a sample can be symbolized by $X_1, X_2, X_3 \dots, X_n$, and the mean can be computed as follows

$$\bar{X} = \frac{(X_1 + X_2 + X_3 + \dots + X_n)}{n}$$

Where n is the number of observations included in the samples

3.2 Variance

The measurement of the variation in a trait or character is called variance, which can be divided into different components. The amount of variation is measured and expressed as the variance when values are expressed as deviation from the population mean. The variance is usually denoted by σ^2 for population and S^2 for sample variance, and is defined as the average of the squared deviations from the mean. It is the most useful measure of variation for studying the variability of population.

The total phenotypic variance of a population (σ^2_p), i.e. the measure of the observable variation, can be broken into two portions; genetic

variance (σ_G^2) that is the variance among genotypic means and environmental variance (σ_E^2) that is the remaining variance often classified as the variance due to environmental deviations

If the phenotype is the sum of genetic and an environmental effect, then $P = G + E$.

If the genotypes are not distributed randomly across environment, there will be some covariance between genotype and environmental values and the covariance will be hidden in the genetics and environment variance. All measures of importance of genes are framed in terms of the proportion of variance ascribable to their variations.

Actually since in reality we deal with a sample from the population we can compute estimates from the population variance according to the following formula

$$s^2 = \frac{(X_1 - \bar{X})^2 + (X_2 - \bar{X})^2 + \dots + (X_n - \bar{X})^2}{n - 1}$$

Since the deviations are squared, variance is a positive value with zero as a lower limit. The sum of the squared deviations from the mean is divided by n-1 rather than n to compute the sample variance. Dividing n-1 provides unbiased estimates.

3.3 Standard deviation

The standard deviation is the square root of the variance; it is symbolized by σ for population and s for sample. While variance is expressed in kilogram or centimeter square, the standard deviation is expressed in kilograms or centimeters just as the original items measured. Since the standard deviation is the square root of the variance, it can be computed as follows:

$$s = \sqrt{\frac{(X_1 - \bar{X})^2 + (X_2 - \bar{X})^2 + (X_3 - \bar{X})^2 + \dots + (X_n - \bar{X})^2}{n - 1}}$$

3.4 Coefficient of Variation

The standard deviation as a percentage of the mean is termed coefficient of variation (CV). It is used to compare the variability of traits measured in different units. The formula for computing CV is

$$CV = \frac{S \times 100}{\bar{X}}$$

4.0 CONCLUSION

Variation is the raw material the breeders need to make appropriate selection for herd improvement. Therefore, without variation there cannot be selection.

5.0 SUMMARY

Variation among animals in a population is the raw material available for breeders to make selection for herd improvement. The variation which is observed in a population arises from both genetic and environmental influences. Genetic variations results from differences in genes, while environmental variations results from environmental factors, both of which act together to determine the phenotype of an individual in the population.

The mean or average of observations and a measure of variability around the mean are needed to describe the distribution of values for a particular trait.

6.0 TUTOR MARKED ASSIGNMENT

1. Define the following terms; mean, variance and standard deviation
2. What is the relationship between variance and standard deviation?

7.0 REFERENCES/ FURTHER READING

Malcolm B Willis (1998). Dalton's Introduction to Practical Animal Breeding. Blackwell Scientific Publication, 2nd edition ,London Edinburgh Boston

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MODULE 6 HERITABILITY AND REPEATABILITY

Unit 1	Heritability
Unit 2	Repeatability

UNIT 1 HERITABILITY

CONTENTS

1.0	Introduction
2.0	Objectives
3.0	Main Content
3.1	Heritability
3.2	Properties of heritability
3.3	Methods of Estimating heritability
4.0	Conclusion
5.0	Summary
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1.0 INTRODUCTION

This module deals with the general question of how we quantify the action of genes on the phenotype. We observe the phenotype directly and we can easily measure various aspects of it. We also come to believe that hereditary factors are involved in the phenotype when we observe that offspring resemble their parents. And even though it is, in principle, possible to know an animal's entire genotype, the fact is that we have no way of directly relating this to most phenotypic traits due to their highly polygenic nature. One feature that is often introduced into the discussion of parent- offspring resemblance is heritability. Most people use this concept in attempt to be more sophisticated in their understanding of the determination of the phenotype. However, all too often, heritability turns into a formula for determining the extent to which a trait is "genetic" vs. "environmental". We will learn what heritability is, its estimation and where it is useful. It is expected that every student in this class would have a good understanding of this important genetic concept heritability. The guiding features of our discussion on heritability will be the following principles:

1. Heritability is a function of both the genetic and environmental variances;
2. Heritability is strictly a property of a population.
3. Different populations, even if closely related, can have very different heritability.

2.0 OBJECTIVES

At the end of this unit, you will be able to

- Define heritability
- Explain methods of estimating heritability
- State the importance of heritability

3.0 MAIN CONTENT

3.1 Heritability

One of the most important factors in the formation of effective breeding plans for improving the genetic quality of both plants and animals is the knowledge of relative contribution made by genes to the variability of a trait under consideration. Heritability expresses that part of the superiority of the parents which on an average is passed on to the offspring. Heritability can be expressed as a percentage (from 0 to 100%) or proportion (0.0 to 1.0). these extremes values are rarely encounter in practice. The reason for our focus on heritability is that it determines the degree of resemblance between parents and offspring, which in turn determines the response to selection. That is heritability determines the improvement that can be achieved through selection; traits with high heritability such as body weight, birth weight etc, can easily be improved through selection than traits with low heritability (e.g. fertility traits).

The term h^2 is used to signify heritability.

The phenotypic variation seen in a population is as a result of combined effect of genetic and environmental variation. If σ^2 is used to signify variance and P, G and E are used to indicate phenotypic, genetic and environmental variation then

$$\sigma_p^2 = \sigma_G^2 + \sigma_E^2$$

However, genetic variation can be broken down into three components:

additive (A), dominant (D) and Epistatic (I). Likewise, the environmental variation can be divided into general or permanent effect (E_g) and specific or common effects that is common to all members of a particular litter or to individual of the same dam (E_s).

This means that the above equation can be written as

$$\sigma_p^2 = \sigma_A^2 + \sigma_D^2 + \sigma_I^2 + \sigma_{Eg}^2 + \sigma_{Es}^2$$

The additive variance is the most important part in animal breeding because it is the portion or part of the variance that is transferable from parents to offspring or from generation to generation.

Heritability is a ratio rather than an absolute figure such that decrease in any of the other source of variance will increase the h^2 .

Mathematically, heritability can be define in two ways

1. **Broad sense definition:** heritability is a proportion of genetic variance (σ_G^2) to total phenotypic variance (σ_P^2)

$$h^2 = \frac{\sigma_G^2}{\sigma_P^2}$$

2. **Narrow sense definition:** heritability in narrow sense is the ratio of additive variance (σ_A^2) to phenotypic variance (σ_P^2)

$$h^2 = \frac{\sigma_A^2}{\sigma_P^2}$$

The progress that can be expected in the improvement of a trait by selection depend on the ratio of the additive genetic variance to the total phenotypic variance

3.1 Properties of heritability

1. If all the phenotypic variability of a trait is genetic in nature as it is true for most classical Mendelian traits such as blood type, then environmental influence is absence, h^2 will be equal to 1. That is, if $\sigma_G^2 = \sigma_P^2$ then $h^2 = 1$
2. If all the phenotypic variability is environmental in nature as its true for any trait within a genetically homozygous line, then h^2 of the trait is zero

That is, if $\sigma_E^2 = \sigma_P^2$, then $\sigma_G^2 = 0$ and $h^2 = \frac{0}{\sigma_P^2} = 0$

3. If half of the phenotypic variability is due to genes effect, then the h^2 is 50%

i.e if $\sigma_G^2 = \frac{1}{2} \sigma_P^2$ then $h^2 = \frac{\sigma_G^2}{\sigma_P^2} = \frac{1}{2} = 50\%$

4. If the environmental variance (σ_E^2) is 3 times as large as the genetic variance (σ_G^2), then the h^2 is 25%

That is, if $\sigma_E^2 = 3\sigma_G^2$, then $h^2 = \frac{\sigma_G^2}{\sigma_P^2} = \frac{1}{4} = 25\%$

3.1.2 Methods of Estimating Heritability

Numerous procedures for estimating heritability are used in research studies, especially for the economically important traits in farm animals. The underlying basis for estimating h^2 depends on evaluating how much more alike individuals with similar genotypes are than unrelated or less closely related individuals

The parent-offspring and the paternal half-sib relationships are most widely used to determine h^2 in farm animals

1. Parents- Offspring Relationship:

If records for a particular trait (e.g growth rate) exist for parents and offspring then regression of offspring on either parents or offspring on mid-parents (i.e the average for dam and sire) can be used to estimate h^2 .

The regression of offspring on sire or offspring on dam gives a regression coefficient (b_{xy})

$$b_{xy} = \frac{\sigma_{xy}}{\sigma_x^2}$$

Where:

b = regression coefficient

y = record of offspring for a particular trait

σ^2 = variance

σ = covariance

x = records of either sire or dam

The sum of product of the xy for the paired observations or measurements x for parents and y for offspring is obtained

The measurement of a trait on both the parents and their offspring should be correlated for both influences as age or sex when these factors are likely to influence the measurements.

The regression of offspring on parent represent one-half of the h^2 , since the relationship to only one of the two parents is involve, the regression coefficient must be multiply by 2 to obtain h^2

i.e. $h^2 = 2b$.

But with offspring mid-parents regression, the coefficient is equal to heritability

i.e. $h^2 = b$

2. Half-sib correlation

The heritability of a trait can be estimated from the resemblance between full-sib (full brothers or full sisters) or between half-sib (half-brothers or half-sisters). However, of great value are half-sib correlations where the study involves progeny from different sires or dam and in which measurements are needed only on progeny but not on parents. This technique is preferable to parents-offspring technique because half-sib usually have similar environment to one another and measured at the same point in time. In contrast, parents may be measured at a different point in time from their offspring and may also have been assessed under somewhat different environmental conditions to those in which progeny were measured.

Half-sib have on the average $\frac{1}{4}$ of their genes in common rather than $\frac{1}{2}$ as with parent – offspring regression. That is, the correlation between half-sib is quadruped to give the heritability so that any error in estimation are also quadruped.

The paternal half-sib correlation is preferable to those of maternal half-sib largely because

- i. It is easier to get more of the paternal half-sib than the maternal half-sib
- ii. Maternal effects are eliminated when paternal half-sib are used
The h^2 could be estimated from intra-class correlation (t) between paternal half- sibs. This can be computed as ratio of variance components

$$t = \frac{\sigma_s^2}{\sigma_s^2 + \sigma_w^2}$$

Where: σ_s^2 = sire variance
 σ_w^2 = within sire variance.

The heritability is computed by multiplying the t by 4
i.e. $h^2 = 4t$

Full-sibs are rarely used for estimation of h^2 because maternal effect confounds the data and the same is true of identical twins data.

4.0 CONCLUSION

Heritability is an important concept in animal breeding, it express the fraction of the observed phenotype of the parents which on an average is passed from parents to their offspring. Heritability for a trait can be estimated by several methods; However, Parents- offspring and Paternal half-sib relationship are mostly used to determine the heritability of farm animals

5.0 SUMMARY

Heritability is defined as a proportion of genetic variance to total phenotypic variance; this is a broad sense definition. In a more restrictive or narrow sense, it is the proportion of additive variance to total phenotypic variance. It is a ratio rather than absolute figure and can be express as a percentage or proportion, but ranges from 0 to 100 or 0.0 to 1.0. There are several methods of estimating heritability; however, Parents- offspring and paternal half-sib relationship are mostly used to determine the heritability of farm animals

6.0 TUTOR MARKED ASSIGNMENT

1. What is repeatability?
2. Explain the broad sense and narrow sense definition of heritability
3. What is the implication of high and low heritability estimate in animal breeding?
4. Explain two methods of estimating heritability

7.0 REFERENCES / FURTHER READING

Malcolm B Willis (1998). Dalton's Introduction to Practical Animal Breeding. Blackwell Scientific Publication, 2nd edition ,London Edinburgh Boston

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UNIT 2 REPEATABILITY

- 1.0 Introduction
- 2.0 Objectives
- 3.0 Main Content
 - 3.1 Repeatability
 - 3.2 Estimation of repeatability
- 4.0 Conclusion
- 5.0 Summary
- 6.0 Tutor Marked Assignment
- 7.0 References / Further Reading

1.0 INTRODUCTION

Repeatability is a concept closely alike to heritability, since the same gene or genes combination influence the successive expressions of a trait, repeatability should be as large as heritability. It could be larger since certain permanent environmental influences may be included in the numerator of the repeatability fraction. It is usually term as the upper limit of heritability.

2.0 OBJECTIVES

At the end of this unit, you will be able to

- Define repeatability
- States the importance of repeatability in animal breeding
- Know the estimation of repeatability

3.0 MAIN CONTENT

3.1 Definition of repeatability

Repeatability is the tendency for successive records of the same animal to be more alike than those of different animals. It is the expression of the same trait at different times in the life of the same individual.

Repeatability is useful for those traits which can be measured several times during an animal's life time, such as lactation milk yield for dairy cows, number farrowed and litter weight for swine and weaned weight of calf for beef cattle.

A high repeatability means that one record is a good guide to future ones and therefore, waiting is hardly needed. In contrast, low repeatability characters benefit from additional records.

Mathematically Repeatability (r) is define as

$$r = \frac{\text{genetic variance} + \text{general environmental variances}}{\text{total phenotypic variance}}$$

3.2 Estimation of repeatability

Repeatability is also known as intra class correlation, which is the expected correlation between observations within the group or class. Now the ratio of between group variance (σ_B^2) to the sum of between group variance (σ_B^2) and within group variance (σ_w^2) is measured.

That is repeatability can be

$$r = \frac{\sigma_B^2}{\sigma_B^2 + \sigma_w^2}$$

If σ_w^2 is small then observations within a group are similar and highly repeatable (i.e. the repeatability will be high),

If σ_w^2 is large this indicates that there is a substantial variation within group and so the repeatability will be low

Importance of repeatability

Knowledge of repeatability estimate for various traits may be used in

- i. Predicting future performances of an animal that has one or more previous record
- ii. Selecting animals for breeding purpose
- iii. It also gives an indication of how long an individual animal could remain in the herd before it may be culled from the herd or flock.
- iv. When the repeatability estimate for a trait is high, culling on the basis of the first record should be effective in improving the overall record of the herd for next year.

4.0 CONCLUSION

A high repeatability estimate is an indication that one record for a particular trait is a good guide to future ones and therefore, waiting is hardly needed before culling decision could be taking. However, for low repeatability characters additional records are required before appropriate decision could be made.

5.0 SUMMARY

Repeatability is a concept closely alike to heritability; it is the upper limit of heritability. Repeatability is useful for those traits which can be measured several times during an animal's life time. It is used for prediction of future performance of an animals and it also gives an indication of how long an animal could remain in the herd before it could be culled. When repeatability is high culling decision can be taking on the first record of the animal, but if the repeatability is low more record may be required.

6.0 TUTOR MARKED ASSIGNMENT

1. What is repeatability?
2. list 3 importance of repeatability in animal breeding
3. What is the implication of high and low repeatability in animal breeding?

7.0 REFERENCES / FURTHER READING

- Malcolm B Willis (1998). Dalton's Introduction to Practical Animal Breeding. Blackwell Scientific Publication, 2nd edition ,London Edinburgh Boston
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