

# Chapter VII

## SOME GENETIC PARAMETERS OF POPULATIONS

### I. HERITABILITY

#### Definition:

1. This term used to describe **the strength of inheritance of a trait,**  
**i.e. whether it is likely to be passed on to the next generation or not.**

## **2. A precise definition would be:**

**For a given trait heritability is the amount of the superiority of the parent above their contemporaries which on average is passed on to the offspring.**

**3. Heritability measures the degree to which offspring resemble their parents in performance for a trait.**

**If offspring resemble their parents closely for a trait, we would say that the trait is highly heritable. If, however, offspring don't resemble their parents closely for a trait, the trait is lowly heritable.**

# Types of heritability:

## a. Heritability of broad sense:

$$h^2b = \frac{\sigma^2G}{\sigma^2p} = \frac{\text{Genetic variation}}{\text{Total phenotypic variation}}$$

It is total genetic variation as a proportion of total phenotypic variation.

## b. Heritability in the narrow sense:

$$h^2n = \frac{\sigma^2A}{\sigma^2p} = \frac{\text{Additive genetic variation}}{\text{Total phenotypic variation}}$$

It is the proportion of total phenotypic variance attributable to additive genetic variance.

## E. Realized heritability:

$$h^2 = \frac{R}{S} = \frac{\text{Response from selection}}{\text{Selection differential}}$$

It is the proportion of **superiority of selected parents** that is **expected to be realized in their progeny**.

- The notation  $h^2$  is given to heritability and is ranged from **0 to 1** or **0 to 100%**.
- You cannot have **a negative heritability**.

# Uses and the importance of heritability:

**1. To estimate breeding value (BV) from phenotype (P) for each individual in a population as :**

$$BV = P + h^2 (P - \bar{P})$$

**That is breeding value for a single trait is estimated as phenotypic superiority (inferiority) times heritability, added to the original population mean.**

**2. To predict response to selection:**

$$h^2 = \frac{R}{S}$$

**Where:**

**$h^2$  = is realized heritability.**

**R = is response to selection.**

**S = Selection differential.**

**3. Used in estimating the genetic correlation which is very important in selection experiment.**

**4. Indicate the possibility of genetic improvement by selection of individuals phenotypically.**

**5. To formulate effective breeding plans.**

## **Heritability divisions:**

**The heritability of a given trait may be any fraction from zero to one or to 100% and the traits can be divided into three categories:**



## **a. Low or weak heritability (less than 0.2):**

**A low heritability estimate tells us that there is low correlation between genotype and phenotype.**

**Low heritability estimates also tell us that variations due to additive gene action are probably small. Moreover, non additive gene action such as dominance, overdominance and epistasis may be important.**

**To make progress in selection when the heritability of a trait is low, much more attention must be paid to the performance of the collateral relatives and the progeny.**

**Example: Fitness traits (fertility and reproductive characters).**

## **b. Medium or intermediate heritability (0.2 - 0.4):**

**Example: Most of the productive traits (milk yield, fat yield, wool yield).**

## **c. High or strong heritability (above 0.4):**

**A high heritability estimate tells us that the correlation between the phenotype and the genotype of the individuals, on the average, should be high.**

**High heritability estimates also indicate that additive gene action is important for that trait and the mating of the best to the best should produce desirable offspring i.e. selection on the basis of individual's own phenotype should be effective.**

**Example: Most of structural traits (body length, height, muscle measurements), carcass traits and fat percent.**

## II- Realized heritability:

From selection experiments.

Heritability estimate can be determined by expressing selection response as a proportion of the selection differential.

$$h^2 = \frac{R}{S}$$

Where:

**$h^2$ :** is the realized heritability

**R:** is selection response. (The amount of superiority or inferiority of the present generation over the previous generation)

**i.e.** (Average of the present generation – Average of population).

**S:** is selection differential. (The amount of superiority or inferiority of those individual selected for parents when compared to the average of the population from which they were selected).

**i.e.** ( Average of the parents – Average of population).

## II. REPEATABILITY

### Definition:

It is the correlation coefficient between **two different records or measurements** on **the same animals**.

**Or** It is the correlation coefficient between **repeated records or measurements** of **the same trait** in a population.

**Or** It is the proportion of **total phenotypic variance for a trait** attributable to **permanent differences among individuals**.

$$\text{Repeatability (R)} = \frac{V_G + V_{EP}}{V_P} = \frac{V_A + V_D + V_I + V_{EP}}{V_A + V_D + V_I + V_{EP} + V_{ET}}$$

N.B.:

- Repeatability should be **greater than or equal to broad sense heritability** which should be **greater than or equal to narrow sense heritability** of the same trait in a population.

$$R > h^2_b > h^2_n$$

- Like  $h^2$ , repeatability is **not a biological constant**. It may vary **for different traits, for the same traits among populations and for the same trait within a population over time**.

This variation may be a function of differences in genetic components, **in permanent environmental components, in temporary environmental components or in any combinations**.

## Importance and usefulness of repeatability;

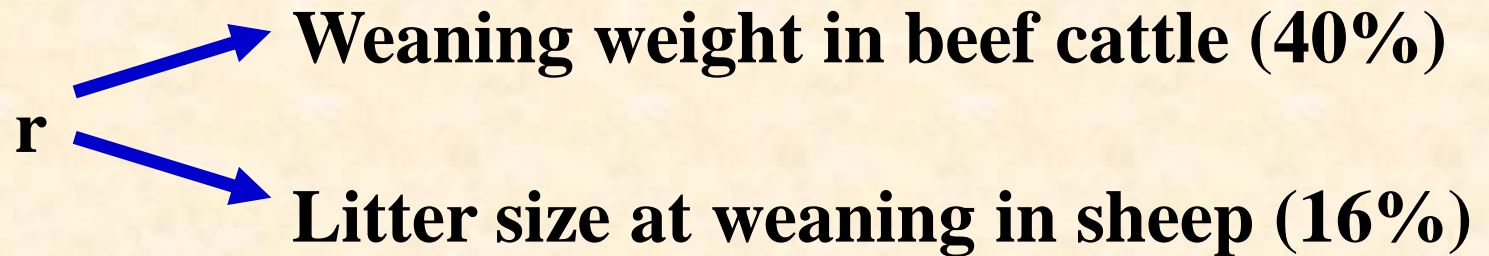
### 1. Repeatability and culling on the basis of first record:

- Repeatability estimates ( $r$ ) can be useful in making culling.

When  $r$  is high, cull poor producing individuals on the basis of their first records. When  $r$  is low, wait for more records before culling an animal.

For example, suppose we make a list of dairy cows on the basis of their first lactation milk yield to cull poor producers. Noting that the repeatability of milk yield is quite high ( $r =$  about 0.55), cows with poor first lactation indicate that their future production will also be poor.

Moreover, repeatability estimates also give an indication of **how many records** should be obtained on an individual before it may be culled from the herd or flock.



Obviously it would take **more records to cull for litter in sheep** than it would **for weaning weight in beef cattle**.

## 2. Repeatability and prediction of producing ability

Lifetime averages which show the ability of certain individuals to repeat performance over a long period of time are more useful in culling (or selection for future performance).

These estimates are called producing abilities of most probable producing abilities (MPPA).



## A. From a single record per individual:

$$\text{MPPA} = \text{herd average} + r (\text{own average} - \text{herd average})$$

**Where:**

**r (own average–herd average) estimates that part of an individual's deviation of a trait, from the population mean, that is likely to be retained in future records.**

## B. From number of records per individual:

$$\text{MPPA} = \text{herd average} + \frac{nr}{1 + (n - 1)r} (\text{own average} - \text{herd average})$$

**Where n is the number of records for each individual and r is the repeatability of the trait.**

## Common misconceptions about repeatability:

1. Like heritability, repeatability is a population measure, a characteristic of a trait in a population. It is not a value to be associated with an individual animal.
2. Like heritability, repeatability is not fixed. It varies from population to population and from environment to environment. Factors that affect heritability tend to affect repeatability in a similar manner.

### **III. CORRELATIONS**

- **Breeders are aware for example that increasing milk yield affects a quality such as fat percentage.**
- **Increasing live-weight gain may increase carcass fat deposition,**
- **Increasing body weight could increase fertility and increase mortality at birth.**

**Relationships in statistical terms are expressed by correlation with a scale from ranged from (-1--- 0 -- +1).**

**Correlation between two factors shows how one factor changes as another variable changes.**

- **Positive correlations** show that as one trait goes up then so does the other,
- While **negative correlations** show that as one trait goes up then the other goes down.

**Correlations are broadly classified follows:**

**Positive correlation:**

**0 ---- 0.3 low; 0.4 ---- 0.5 medium; 0.6 and above high**

**Different types of correlations:**

**In animal breeding it is important to recognize three different correlations and to describe them we need to go back to the basic equation of:**

$$\begin{aligned}
 \mathbf{P} &= \mathbf{G} + \mathbf{E} \\
 \text{Phenotype} &= \text{Genotype} + \text{Environment} \\
 \text{For trait } \mathbf{X} \quad \mathbf{X(p)} &= \mathbf{X(G)} + \mathbf{X(E)}
 \end{aligned}$$

$$\begin{aligned}
 \boxed{\text{Phenotypic correlation}} &= \boxed{\text{Genetic correlation}} + \boxed{\text{environmental correlation}} \\
 \text{For trait } \mathbf{Y} \quad \mathbf{Y(p)} &= \mathbf{Y(G)} + \mathbf{Y(E)}
 \end{aligned}$$

The above equations highlight the fact that if the two traits appear to be related (there is a phenotypic correlation between them), then this could be for two reasons:

1. Some of the genes affecting one trait also affect the other i.e. the genetic correlation between  $X(G)$  and  $Y(G)$ . This is **pleiotropy**.

**2. Some non–genetic or environmental factors affecting one trait also affect the other, i.e. the environmental correlation between X (E) and Y (E).**

### **A. Phenotypic correlation ( $r_p$ ):**

**The phenotypic correlation ( $r_p$ ) between two quantitative characteristics describes the extent to which individuals above average for one trait tend to be above, below or near average for the other trait.**

**The estimation of phenotypic correlations is straight forward. When traits X and Y have been measured on a number of individual from a population:**

$$r_p = \frac{\sum XY - \frac{(\sum X)(\sum Y)}{n}}{(\sum X^2 - \frac{(\sum X)^2}{n}) \times (\sum Y^2 - \frac{(\sum Y)^2}{n})}$$

## B. Genetic correlation ( $r_g$ ):

The genetic correlation is a measure of the extent to which the same genes or closely linked genes, cause simultaneous variation in two different traits.

It describes the extent to which individuals genetically have average for one trait are genetically above, equal or below average for a second quantitative trait.

## **Positive genetic correlations:**

**Indicates that physiologically, as well as genetically, the two traits are correlated or influenced by the same genes and selection for the improvement of one will also result in the improvement in the other.**

**Ex. Yearling body weight & fertility in sheep.**

## **Negative genetic correlations:**

**This means that selection for the improvement of one trait, results in a decline in the other to which it is genetically correlated.**

**Ex. Butterfat percentage & milk yield in dairy cattle.**



## Causes of genetic correlations:

**A.** Some of the genes affecting one trait also affect the other "**Pleiotropy**". **Pleiotropy** is the process where by one gene may affect two or more trait.

**B.** Some genes may be **closely linked together on the same chromosome** that they seldom, if ever, separate by crossing over during synapsis in meiosis.

Closely linked genes would tend to stay together over several generations and the association of the traits determined by them would persist.

## Importance of genetic correlation:

a. They can indicate how things are likely to change in the next generation.

**Ex.** Selecting for growth rate in this generation by picking the heaviest bulls at 400 days of age, the birth weight of their calves (the next generation) will also increase and could result in calving difficulty.

b. They can be used to plan counter selection measures to prevent any correlated changes that are not wanted.

**Ex.** in the above example where birth weights were increased by increasing 400-day weight, the breeder should look for individual sires (by progeny testing) whose calves were produced without calving difficulty despite their being heavier at birth.

c. They can be used in situations where **one trait may be difficult to improve and another correlated trait can be used to help improve it.** The difficult trait may be difficult because of practical problems in measuring it accurately and it has low heritability.

**Ex.** in sheep, **fertility has low heritability** direct selection would bring slow improvement. This could be assisted by selecting for **yearling body weight** that is both phenotypically and genetically correlated with fertility (lambs born).

## **Estimation of genetic correlation:**

The estimation of the genetic correlations resets on the resemblance between relatives.

**We compute the components of covariance of the two characters from an analysis of covariance which takes exactly the same form as the analysis of variance therefore:**

**The genetic correlation can be estimated as the following:**

$$r_g = \frac{\text{Cov. XY}}{\sigma^2 X \cdot \sigma^2 Y}$$

$$= \frac{\text{Cov. XY}}{\sigma X \cdot \sigma Y}$$

## **C- Environmental correlation ( $r_E$ ):**

**An environmental correlation ( $r_E$ ) between traits arises from the same environmental effect causing simultaneous variation in both the traits.**

**The environmental correlation can be estimated as the following:**

$$r_E = \frac{r_P - r_G \cdot h_X \cdot h_Y}{e_X e_Y}$$

**Where :-**

**$r_E$  is the environmental correlation**

**$r_p$  is the phenotypic correlation**

**$r_g$  is the genetic correlation**

$$\mathbf{h_x} = \mathbf{h_x^2}$$

$$\mathbf{h_y} =$$

$$\mathbf{e_x} =$$

$$\mathbf{e_y} =$$