

## **MODULE-29: HERITABILITY**

### **Learning objectives**

After completing this module, the learner should be able to:

- understand the various definition, importance, features and uses of heritability
- understand the approximate heritability value of some important economical traits of livestock
- understand the relationship between breeding value and progeny difference

## **DEFINITION**

### **Narrow sense**

- Breeding value is of prime importance in selection programme since breeding values are passed on from parent to offspring and not the genotype. Therefore we are interested in the proportion of phenotypic variance attributable to breeding values. This is represented by the fraction of  $V_A/V_P$ , which is called the heritability in the narrow sense ( $h^2$ ).
- Heritability is defined as the ratio of additive genetic variance to phenotypic variance.

Heritability in narrow sense is used to refer per cent or proportion of the phenotypic variation between individuals for a particular trait that is due to differences in the additive genetic effects of the trait.

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$$h^2 = V_A/V_P$$

- The ratio  $V_A/V_P$  expresses the extent to which phenotypes are determined by the genes transmitted from parents. It represents the percentage of genetic progress made in the next generation when superior individuals are selected as parents.

### Broad sense

- The ratio  $V_G/V_P$  is called the heritability in the broad sense or the degree of genetic determination.
- It expresses the extent to which individual's phenotypes are determined by the genotypes. Heritability in broad sense includes variation due to additive gene action ( $V_A$ ), dominance ( $V_D$ ) and epistasis ( $V_I$ ).
- In the selection programme it is the heritability in the narrow sense or simply heritability, which is very important. Unless otherwise specified, heritability means heritability in the narrow sense ( $h^2$ ).

### Symbol

- The customary symbol  $h^2$  stands for the heritability itself and not for its square.
- The symbol derives from Wright's (1921) terminology where "h" stands for the corresponding ratio of standard deviations.

### Mathematically heritability

- Mathematically heritability is the regression of breeding value on phenotypic value.  $h^2 = b_{AP}$ . Therefore  $h^2$  can be taken as the change in breeding value expected per unit change in phenotypic value.

## IMPORTANCE AND FEATURES OF HERITABILITY

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### Importance of heritability

- If the breeder chooses individuals to be parents according to their phenotypic values, his success in changing the characteristics of the population can be predicted only from knowledge of the degree of relationship between phenotypic values and breeding values. This degree of correspondence is measured by the heritability.
- Heritability in narrow sense is a measure of the strength of the relationship between phenotypic values and breeding values for a trait in a population.
- Heritability in the broad sense is a measure of the strength of the relationship between phenotypic values and genotypic values.

### Features of Heritability

- Heritability is a population measure, not a value to be associated with an individual animal.
- Heritability is a property of the character and also of the population and the environment in which it is measured.
- The value of the heritability depends on the magnitude of all the components of variance ( $V_P = V_A + V_D + V_I + V_E$ ), so change in any one of these will affect it.
- All the genetic components are influenced by gene frequencies and may therefore differ from one population to another. More variable environment reduces the heritability and more uniform condition increases. Therefore heritability of a trait is not fixed. It varies from population to population and from environment to environment.
- Heritability ranges from 0 to 1.
- If heritability is high, selection tends to be effective and vice versa.

## HERITABILITY OF SOME IMPORTANT TRAITS

- Approximate heritability value of various traits in various animal species

Species	Trait	$h^2$
Cattle (dairy)	Calving interval	0.10
	Milk yield	0.25
	Fat %	0.55
	Protein %	0.50
Cattle (beef)	Calving interval	0.05
	Birth weight	0.40
	Weaning weight	0.30
	Yearling weight	0.40
	Mature weight	0.65
	Feed conversion	0.40
Pigs	Litter size (number born alive)	0.05
	Little size (number weaned)	0.10
	Weaning weight	0.10
	Feed conversion	0.50
	Loin eye area	0.50
	Back fat thickness	0.70
Sheep	Litter size	0.15
	Birth weight	0.30
	Weaning weight (60-day)	0.20
	Yearling weight	0.40
	Grease fleece weight	0.40
	Staple length	0.50
Horses	Wither height	0.40
	Cannon bone circumference	0.45
	Temperament	0.25

	Walking speed	0.40
	Time to trot one mile	0.45
	Time to run one mile	0.35
	Pulling power	0.25
Poultry	Egg production (to 72 wks)	0.10
	Egg size	0.45
	Egg weight (at 32 wks)	0.50
	Hatchability	0.10
	Viability	0.10
	Body weight (at 32 wks)	0.55

- On the whole, the characters with the lowest heritability are those most closely connected with reproductive fitness.
- Characters with the highest heritability are those that have least importance with regard to natural fitness.
- Heritability can be expressed as percentage from 0 to 100 or in decimal ranging from 0 to 1.
- According to Turner and Young (1969) the estimates of  $h^2$  values was grouped as
  - 0.3 or more - high
  - 0.3 - 0.1 - intermediate / medium
  - below 0.1 - low
- When we say heritability of a trait is 0.25, it mean that 25 per cent of the differences in performance for the trait in the population are heritable.
  - For example the heritability of milk yield in cattle is 25 % and average of the herd is 2000 kg. This does not mean that 500 kg (25%) is due to heredity and the remaining 1500 kg to environment. It means that of the difference between individual in the herd in milk yield approximately 25 % is due to heredity and 75 % is due to environment.

## USES

### Uses of heritability estimates

- To understand the relative contribution of heredity and environment in a trait in the population.
- To predict the breeding values and genetic gain of a trait under selection programme.
- To formulate suitable breeding plans for genetic improvement.

## BREEDING VALUE AND PROGENY DIFFERENCE

### Breeding value

The value of an individual judged by the mean value of its progeny is called breeding value of the individual.

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- All of genotypic value is not heritable. Breeding value is the part of an individual's genotypic value that is due to independent gene effects that can be transmitted from parents to offspring.
  - If an individual is mated to a number of individuals taken at random from the population, then its breeding value is twice the mean deviation of the progeny from the population mean.

### **Estimated breeding value (EBV)**

- Prediction of breeding value using performance data is known as estimated breeding value or EBV.

### **Progeny Difference (PD) or Transmitting ability (TA)**

- A parent passes on a sample half of its genes and therefore a sample half of the independent effects of those genes to its offspring. Because breeding value is the sum of the independent effects of all of an individual's genes affecting a trait, a parent passes on, *on average*, half its breeding value to its offspring. Half the parent's breeding value for a trait is our expectation of what is inherited from the parent and is called *progeny difference or transmitting ability*.

$$\text{PD} = \frac{1}{2} \text{ BV}$$

- Like breeding values, progeny differences are not directly measurable, but can be predicted from performance data. Such predictions are called *expected progeny difference (EPDs)*, *predicted difference (PDs)*, or *estimated transmitting abilities (ETAs)* and are commonly used to make genetic comparisons among animals during selection.

## **MODULE-30: ESTIMATION OF HERITABILITY**

### **Learning objectives**

After completing this module, the learner should be able to:

- understand the different methods of estimating heritability and advantages of each method

## **INTRODUCTION**

### **Causal components of variance**

- All heritability estimates are based on how much more relatives resemble each other for certain traits than non-relatives.

- Relatives resemble each other more than non-relatives because they have more genes in common.
- The degree of resemblance provides the means of estimating the amount of additive genetic variance ( $V_A$ ) and other components of variance.
- The  $V_P$  can be partitioned into components attributable to different causes as  $V_P = V_A + V_D + V_I + V_E$ . These components are called *causal components* of variance. These components cannot be estimated directly.

### Observational components of variance

- The measurement of degree of resemblance between relatives rests on the partitioning of the phenotypic variance in a different way, into components corresponding to the grouping of the individual into families like half sib, full sib.
- After grouping we can measure the phenotypic values between and within groups.
- Hence these components are estimated directly from phenotypic values. We shall call them as *observational components* of phenotypic variance and denote them by symbol  $\sigma^2$ .

## HERITABILITY ESTIMATION METHODS

- The degree of resemblance between offspring and parent is measured by **regression coefficient** and that between full or half sib is measured by **correlation**.
- Coefficients of the causal component (variance components) in the Covariance (COV) with two factor interactions of relatives

Relatives	Variance components and their contribution				
	$V_A$	$V_D$	$V_{AA}$	$V_{AD}$	$V_{DD}$
Offspring – parent : $\text{cov}_{op}$	1/2	-	1/4	-	-
Half sibs : $\text{cov}_{(HS)}$	1/4	-	1/16	-	-
Full sibs : $\text{cov}_{(FS)}$	1/2	1/4	1/4	1/8	1/16

- In case of full sib the COV includes  $V_{Ec}$  (common environmental circumstances that cause differences between unrelated individual are not a cause of differences between members of the same family).
- Therefore, by observing the phenotypic covariance of different sorts of relationship the amount  $V_A$  obtained is

Relatives	Amount of $V_A$ provided by COV
Offspring and one parent	$1/2 V_A$

Offspring and mid-parent	$\frac{1}{2} V_A$
Half sib	$\frac{1}{4} V_A$
Full sib	$\frac{1}{2} V_A + \frac{1}{4} V_D + V_{Ec}$

## Heritability estimation methods

- Regression method Regression of offspring on one parent
  - Regression of offspring on mid parent
  - Intra sire regression of offspring on dam
- Correlation method:
  - Half sib correlation
  - Full sib correlation
- Using twin data in human [Dizygotic (fraternal) and Monozygotic (identical) twins]
  - The genetic covariance of twins is very simple. In case of Dizygotic twins the genetic COV are related as full sibs. The monozygotic twins have identical genotypes, so there is no genetic variance within pairs and the whole of the genetic variance appears in the between pair component. The genetic COV is therefore COV<sub>(MZ)</sub>:  $V_G$
- Heritability can also be estimated from selection experiment data

i.e.  $R = h^2 S$

$h^2 = R/S$

Where  $R$  = Response to selection and  $S$  = Selection differential

The heritability estimated by this way is called Realized heritability.

## ESTIMATION OF HERITABILITY BY REGRESSION METHOD

- In this method the resemblance between offspring and parents, the grouping of the observations is into pairs rather than groups. That is one parent (or) mean of two parents – paired with their one offspring (or) mean of several offsprings.
- The degree of resemblance is expressed as the regression of offspring on parents (Here correlation is often inappropriate).
- The regression is given by

$$b_{OP} = \frac{\text{cov}_{OP}}{\sigma_p^2}$$

Where  $\text{cov}_{OP}$  is the cov of offspring and parents

$\sigma_p^2$  is the variance of parents

- In general, for regression method the data of both parent and offspring are required.

### REGRESSION OF OFFSPRING ON ONE PARENT

- The *cov* between parent and offspring is  $1/2V_A + 1/4 V_{AA}$ .
- Ignoring  $1/4V_{AA}$  which is negligible, then the regression is

$$b_{OP} = \frac{1/2 V_A}{V_P}$$

$$b_{OP} = \frac{1/2 V_A}{V_P}$$

$$b = \frac{1}{2} h^2$$

$$\therefore h^2 = 2b$$

### REGRESSION OF OFFSPRING ON MID-PARENT

- The covariance of offspring with mean of both parents is the same as the *cov* with a single parent i.e  $1/2 V_A$ .
- But the total variance is  $1/2 V_P$  because in general, the variance of the mean of 'n' individuals is one  $n^{th}$  of the variance of single individual.

$$b_{OP} = \frac{1/2 V_A}{1/2 V_P} = \frac{V_A}{V_P} = h^2$$

### INTRA SIRE REGRESSION OF OFFSPRING ON DAM

- In farm animals a male is mated to several females and therefore the regression of offspring on mid parent is inappropriate.
- Since there are usually a few male parents and the mating is not random the simple regression on one or other parents are both unsuitable.
- The  $h^2$  can however be satisfactorily estimated from the average regression of offspring on dams calculated within sire groups. That is to say, the regression of offspring on dam is calculated separately for each set of dams mated to one sire and the regression in each set is pooled in a weighted average.
- The ISD estimates half the  $h^2$  as

$$b_{OP(IST)} = \frac{1/2 V_A}{V_P} = 1/2 h^2 ; \therefore h^2 = 2b$$

- This method eliminates the environmental cov that arises if sire groups have been in different environment / herds. This method also helps to overcome the differences among herds / breeds / sires.

## ESTIMATION OF HERITABILITY BY CORRELATION

- This method is used when data of progeny but not of parents are averaged.
- Here the individuals are grouped as half sib or full sib families.
- By analysis of variance the total observed variance can be partitioned into between groups and within groups.
- The ratio of between group component to total variance is called the **intraclass correlation coefficient** and is given by

$$t = \frac{\sigma_B^2}{\sigma_B^2 + \sigma_W^2}$$

Where  $\sigma_B^2$  = is the between group component

$\sigma_W^2$  = is the within – group component

$t$  = symbol for intraclass correlation

- The between group component expresses the amount of variation that is common to members of the same group and it can be referred as cov of members of the groups.
- The intra class correlation (t) among half sib or full sib is used to estimate  $h^2$ .

## HALF SIB CORRELATION

- Half sibs are relatives, which have one parent common.
- The coefficient of relationship between half sib is 0.25.
- The cov between half sib is due to  $1/4 V_A + 1/16 V_{AA}$ .
- Ignoring  $1/16 V_{AA}$ , which is negligible, the  $h^2$  estimate in half sib correlation is

$$t = \frac{1/4 V_A}{V_P}$$

$$t_{(HS)} = 1/4 h^2 ; \therefore h^2 = 4t_{(HS)}$$

- The intraclass correlation (t) between half sibs is multiplied by 4 to get heritability

## FULL SIB CORRELATION

- Full sibs are relatives who have both parents in common.
- The coefficient of relationship between full sibs is 0.50.
- The  $cov$  between full sibs is due to  $\frac{1}{2} V_A + \frac{1}{4} V_D + V_{Ec}$ .

$$t = \frac{\frac{1}{2} V_A + \frac{1}{4} V_D + \frac{1}{4} V_{Ec}}{V_P}$$

$$t_{(FS)} = \frac{1}{2} h^2 ; \therefore h^2 = 2t_{(FS)}$$

- The heritability based upon full sib correlation is therefore often over estimated since it includes  $\frac{1}{4} V_D + V_{Ec}$ .
- Therefore, the intraclass correlation among full sibs can therefore be used to estimate heritability of those character in which the effects of  $V_{Ec}$  and  $V_D$  are negligible.

## **CHOICE OF METHOD FOR DETERMINING HERITABILITY AND PRECISION OF HERITABILITY ESTIMATE**

- The choice of what sort of relatives to be used for estimation of heritability depends on the circumstances and for sorts of relationship the data available.
- There are two points to consider in estimation of heritability
  - Bias
  - Precision

### **Bias**

- It is introduced by environmental source of  $cov$  and non-additive genetic causes.
- Absence of non-additive genetic causes of resemblance in relationship (i.e.  $V_D$  and  $V_I$ ) and maternal environmental variance ( $V_{Ec}$ ) are the most important criteria in choosing method.
  - Example, in full sib,  $cov$  includes the  $\frac{1}{4} V_D + V_{Ec}$  and in regression of offspring on dam, it includes  $V_{Ec}$ .
- Therefore, the estimate of heritability from full sib or regression of offspring-dam is valid or reliable only in the absence of  $V_D$  and  $V_{Ec}$ .
- Generally the half sib correlation and regression of offspring on sire are the most reliable from this point of view.

### **Precision**

- The precision of an estimate of heritability is indicated by its standard error (S.E.). Generally standard error of heritability are uncomfortably large unless the regression ( $b$ ) is based on large number of pairs and the correlation is based on more number of sire groups and large number of progenies per sire group. But there are many limitations to achieve these objectives. They are

space, labour, cost and etc. Normally the estimate of heritability is valid or reliable only when it has very low standard error.

- In general, the closer the relationship the more precise is the estimate. The reason for this is that the observed  $b$  or  $t$  must be multiplied by a larger factor ( $1/r$ ) in distant relatives compared to closer relationship. That is in case of half sib, ' $t$ ' is multiplied by 4 and in case regression of offspring on one parent or intrasire regression of offspring on dam, the ' $b$ ' is multiplied by 2. In this point of view, regression of offspring on mid parent gives better precision than the other methods.

In general low heritability are more efficiently estimated by the half-sib correlation and heritability higher than about 0.25 are more efficiently estimated by offspring-parent regressions. However the difficulty in the latter method is that we need data of both parent and offspring.

## MODULE-31: REPEATABILITY

### Learning objectives

After completing this module, the learner should be able to:

- understand the concept of repeatability
- understand methods of estimation of repeatability
- understand the uses of repeatability
- understand the repeatability value of some important economic traits

## REPEATABILITY

Repeatability is defined as the correlation between measurements on the same animal for traits, which are measured more than once.

- It is represented by the symbol ' $r$ '.
- It ranges from 0 to 1 or 0 to 100 per cent.
- Example: Lactation milk yield, Fleece weight in sheep, and Litter size in swine.

### Repeatability Vs Heritability

- The meaning of repeatability becomes clearer when it is compared with heritability.
- Repeatability is an indicator of the extent to which an animal's superiority in one measurement will be seen in subsequent measurements of the same animal.
- But heritability indicates the extent to which the superiority of parents will be seen in their offspring.

### Repeatability Vs Environmental Variance

- To understand repeatability and to calculate it, a different division of environmental variance is required.
- Some environmental effects are permanent and therefore influence permanently in all periods and affect all measurements.
- Other environmental effects are temporary and vary from one period to the next. Since the temporary effects are independent from period to period, they are likely to be positive and negative and tend to be zero over several periods.
- *Permanent environmental factors*
  - Repeatability is concerned with the extent to which differences between individuals are permanent. i.e remain throughout their lives. Those permanent differences must be due to factors that remain permanent throughout the individuals' lifetime. These include the individuals genotype ( $G=A+D+I$ ) and a deviation due to any permanent environmental factors  $E_p$ . i.e. a deviation due to environmental factors that exert the same effect on all measure of performances throughout the individuals life time.
    - Example: permanent defects like udder damage in cows.
  - $E_p$  is also referred to as general environmental effect.
- *Temporary environmental factors*
  - This is due to temporary environmental factors  $E_t$ , which affect one measurement but not the rest and vary from one period to next.
    - Example, quality / quantity of feed, climate etc.
  - $E_t$  is also referred to as special environmental effect.
  - Using the distinction between  $E_p$  and  $E_t$  we can say that permanent differences between the performances of individuals are due to differences in  $G + E_p$ .
- *Environmental variances*
  - The respective environmental variances are referred as  $V_{Ep}$  or  $V_{Eg}$  and  $V_{Et}$  or  $V_{Es}$ .
    - Where
      - $V_{Ep}$  or  $V_{Eg}$  refers to permanent or general environmental variance contributing to the between-individual component and
      - $V_{Et}$  or  $V_{Es}$  refers to temporary or special environment variance arising from temporary or special circumstances within individual.
  - Heritability indicates the relative contribution of  $V_A$  to  $V_P$ .
  - In a similar manner, repeatability indicates the relative contribution of  $V_G + V_{Ep}$  to  $V_P$ .
  - In terms of causal components of variance, repeatability is expressed as

$$\text{Repeatability } (r) = \frac{V_G + V_{Ep}}{V_P}$$

- Because of this, we can conclude that for repeatable character, heritability is never greater than repeatability

## ESTIMATION OF REPEATABILITY

- Repeatability can be estimated by Intraclass correlation method.
- The ratio of the between individual component to the total phenotypic variance is the intraclass correlation ( $r$ ).
- When more than one measurement of the character can be made on each individual the phenotypic variance can be partitioned into:
  - Variance within animals, which is equal to  $V_{Et}$
  - Variance between animals, which is equal to  $V_G + V_{Ep}$

$$r = \frac{\text{Between animal variance}}{\text{Between animal variance} + \text{Within animal variance}} = \frac{V_G + V_{Ep}}{V_P}$$

- It is the correlation between repeated measurements on the same individual and is known as the repeatability of the character. By analysis of variance the variance components are estimated and repeatability is estimated.
- Like heritability, repeatability is a population measure and is not a value associated with an individual animal. Like heritability, repeatability is not fixed, and varies from population to population and from environment to environment.

## USES OF REPEATABILITY

- Repeatability estimate sets upper limits to heritability in broad sense. Since repeatability is easier to estimate than heritability we can reasonably guess the probable value of heritability from the estimate of repeatability.
- Repeatability estimates are used to predict future performance from past records. When the repeatability for a trait is high, selection for the trait on the basis of the first record itself would be effective in improving the over-all performance of the herd in the next year.
- Repeatability indicates gain in accuracy expected from multiple measurements. If repeatability is high multiple measurements are not going to improve the accuracy of selection. If repeatability is low then two or more measurements will improve the accuracy of selection because increase in number of measurements reduces  $V_{Et}$  or  $V_{Es}$  that appears in the phenotype variance ( $V_P$ ), and thus the reduction of  $V_P$  represents the gain in accuracy.
- Used to estimate the future performance of animals or **Most probable Producing Ability (MPPA)**. Lush suggested the formula for estimating MPPA using repeatability estimate to adjust the records of cows with varying number of records / observations to uniform basis for comparison during selection programme.

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

Where n = number of records and  
r = repeatability of the trait

- Repeatability estimate also throw light on the nature of environmental variance affecting the trait.

### REPEATABILITY ESTIMATES OF IMPORTANT ECONOMIC TRAITS IN LIVESTOCK AND POULTRY

Species	Trait	Repeatability
Cattle (dairy)	Services per conception	0.15
	Calving interval	0.15
	Milk yield	0.50
	Fat %	0.60
Cattle (beef)	Birth weight	0.20
	Weaning weight	0.40
	Body measurements	0.80
Sheep	Birth weight	0.35
	Weaning weight (60-day)	0.25
	Grease fleece weight	0.40
Swine	Litter size (number born alive)	0.15
	Litter size (number weaned)	0.10
	Birth weight	0.30
	Weaning weight	0.15
Horses	1-mile time (flat races)	0.57
	1-mile time (trotters)	0.39
	1-mile time (pacers)	0.45
	Cutting score	0.22
Poultry	Egg weight	0.90
	Egg shape	0.95
	Shell thickness	0.65

- The estimates of repeatability values are grouped as:
  - 0.0 - 0.3 : Low

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- 0.3 - 0.6 : Medium
  - 0.6 and above : High

## MODULE-32: GENETIC AND PHENOTYPIC CORRELATIONS

### Learning objectives

After completing this module, the learner should be able to:

- understand the concept, classification and uses of correlations
- predict the phenotypic, genetic and environmental correlation between important economic traits in farm animals

## CORRELATIONS

- The correlation or correlation coefficient is a measure of the strength of the relationship between two variables or two metric characters.
- The notation for the correlation between characters X and Y is  $r_{XY}$ .
- Correlations are used to describe the relationship between two traits in a population
  - Example: correlation between daily weight gain and feed conversion efficiency in swine.
- The values for a correlation coefficient range from  $-1$  to  $+1$ .
- The correlation can either be positive or negative.

### Types of correlation

- There are three types of correlation:
  - Phenotypic correlation ( $r_P$ )
  - Genetic correlation ( $r_G$ ) or ( $r_A$ )
  - Environmental correlation ( $r_E$ )

## PHENOTYPIC CORRELATION

- The association between two characters that can be directly observed is the correlation of phenotypic values or phenotypic correlation ( $r_P$ ).
- It measures the strength of the relationship between phenotypic value in one trait and phenotypic value in another trait.
- In genetic studies the phenotypic correlation is partitioned into genetic ( $r_A$ ) and environmental ( $r_E$ ) correlations.
- The phenotypic correlation is determined from measurements of the two characters in a number of individuals from the population.
- A correlation, whatever its nature is the ratio of the appropriate covariance to the product of the two standard deviations.
- Therefore the phenotypic correlation between two traits X and Y is

$$\text{Phenotypic correlation } (r_p) = \frac{\text{COV}_{P(XY)}}{\sqrt{\text{VAR}_{P(X)} \text{VAR}_{P(Y)}}} = \frac{\text{COV}_{P(XY)}}{\sigma_{P(X)} \sigma_{P(Y)}}$$

Where

- $\text{COV}_{P(XY)}$  is the phenotypic covariance between X and Y traits,
- $\sigma_{P(X)}$  and  $\sigma_{P(Y)}$  are the phenotypic standard deviations of X and Y traits.
- Here the phenotypic COV is the sum of the genetic and environmental covariance i.e.  $\text{COV}_P = \text{COV}_A + \text{COV}_E$

## GENETIC CORRELATIONS

- The genetic correlation ( $r_A$ ) is the correlation of breeding values between two characters.
- It is caused by the association between the breeding values of the two traits. The reason why genetic correlations are so important is that if two traits are genetically correlated, selection for one will cause genetic change in the other.
- The genetic correlations are mostly caused by genes with pleiotropic action.  
**Pleiotropy** is the property of a gene whereby it affects two or more characters, so that if the gene is segregating it causes simultaneous variation in the character it affects.
  - For example, genes that increase growth rate also increase both stature (height) and weight, so that they cause correlation between these two characters.
- **Linkage** is another cause of correlation and may persist for a few generations until linkage is broken down due to recombination.

$$\text{Genetic correlation } (r_A) = \frac{\text{COV}_{A(XY)}}{\sqrt{\text{VAR}_{A(X)} \text{VAR}_{A(Y)}}} = \frac{\text{COV}_{A(XY)}}{\sigma_{A(X)} \sigma_{A(Y)}}$$

Where

- $\text{COV}_{A(XY)}$  is the genetic covariance of the additive deviations between X and Y traits and
- $\sigma_{A(X)}$  and  $\sigma_{A(Y)}$  are the standard deviations of the additive genetic value of the traits X and Y.

## USES / APPLICATIONS

- From the animal breeder's point of view, genetic correlation is important, because of the change brought by selection. It is important to know how the improvement of one character will cause simultaneous changes in other characters. This is called **correlated response** brought in the character not selected for (may be positive or negative). Selection for a character affects favourably or adversely the other characters if they are genetically correlated.

- Example:
  - Milk yield and butter fat % are genetically negatively correlated
  - Egg production and egg size are genetically negatively correlated
  - Here selection for milk yield in dairy cattle reduces the fat percentage. Likewise selection for egg yield in poultry reduces egg size. Therefore the reductions in other economically important traits through genetic antagonism need to be taken note in designing selection programmes.
- Uses of genetic correlation are
  - To predict the direction and magnitude of response of correlated character during selection. The knowledge of genetic correlation is useful to forecast reduction in the correlated traits in single trait selection if they are negatively correlated.
  - **Indirect selection:** Sometimes certain traits are difficult and costly to measure. So these traits can be improved by selecting easily measurable trait by correlated response.
  - The  $r_p$  and  $r_A$  are used in the construction of selection indices .

## METHODS OF ESTIMATING GENETIC CORRELATION

- The genetic correlation can be estimated by
  - Parent - offspring analysis and
  - Sib-analysis

## PARENT-OFFSPRING ANALYSIS

- The parent-offspring relationship can be used for estimating the genetic correlation.
- To estimate heritability of one character from the resemblance between offspring and parents, we compute the COV of offspring and parent for the one character by taking the product of the parent or mid parent value and mean value of the offspring.
- To estimate the genetic correlation between two characters we compute what might be called the **cross-covariance** obtained from the product of the value of trait X in parents and value of trait Y in offspring or vice versa.
- This cross covariance is half the genetic covariance of the two characters that is  $\frac{1}{2} \text{COV}_{A(XY)}$ .
- In addition, the covariance of offspring and parents for each of the trait are also needed separately for the estimation of genetic correlation and the genetic correlation is given by

$$\text{Genetic correlation } (r_A) = \frac{\frac{1}{2} \text{COV}_{A(XY)}}{\sqrt{\frac{1}{2} \text{COV}_{A(XX)} \frac{1}{2} \text{COV}_{A(YY)}}} = \frac{\text{COV}_{A(XY)}}{\sigma_{A(XX)} \sigma_{A(YY)}}$$

## SIB-ANALYSIS

- **Half-sib analysis:** The causal components of covariance are exactly similar to those of components of variance. Thus analysis of half-sib families the components of COV between sires estimates  $\frac{1}{4} \text{COV}_{A(XY)}$  i.e. one-quarter of the COV of breeding values of two characters.
- For the estimation of correlation the components of variance of each character are also needed.
- Thus the between sire components of variance,  $\sigma^2_{S(X)}$  and  $\sigma^2_{S(Y)}$  estimate  $\frac{1}{4} \text{VAR}_{A(X)}$  and  $\frac{1}{4} \text{VAR}_{A(Y)}$  respectively for the trait-X and trait-Y. Therefore the  $r_A$  is obtained as  $\frac{1}{4} \text{VAR}_{A(Y)}$  respectively for the trait-X and trait-Y. Therefore the  $r_A$  is obtained as

$$\text{Genetic correlation } (r_A) = \frac{\frac{1}{4} \text{COV}_{A(XY)}}{\sqrt{\frac{1}{4} \text{COV}_{A(X)} \frac{1}{4} \text{COV}_{A(Y)}}} = \frac{\text{COV}_{A(XY)}}{\sigma_{A(X)} \sigma_{A(Y)}}$$

## ENVIRONMENTAL CORRELATION

- The Environmental correlation is the correlation of environmental deviations together with non-additive genetic deviations between two characters.

$$\text{Environmental correlation } (r_E) = \frac{\text{COV}_{E(XY)}}{\sqrt{\text{VAR}_{E(X)} \text{VAR}_{E(Y)}}} = \frac{\text{COV}_{E(XY)}}{\sigma_{E(X)} \sigma_{E(Y)}}$$

Where

- $\text{COV}_{E(XY)}$  is the environmental covariance between X and Y traits and
- $\sigma_{E(X)}$  and  $\sigma_{E(Y)}$  are the standard deviations of the environmental values of the traits X and Y.
- In practice, the environmental covariance and variance are obtained by subtracting additive genetic covariance and variance from the phenotypic covariance and variance. For example, the phenotypic correlation is

$$\text{Phenotypic correlation } (r_P) = \frac{\text{COV}_{P(XY)}}{\sigma_{P(X)} \sigma_{P(Y)}}$$

and the phenotypic covariance can be written as

$$\text{Phenotypic correlation } (r_P) = \frac{\text{COV}_{P(XY)}}{\sigma_{P(X)} \sigma_{P(Y)}}$$

- The phenotypic covariance is the sum of the genetic and environmental covariances i.e.,  $\text{COV}_P = \text{COV}_A + \text{COV}_E$

- Writing these covariances in terms of the correlations and standard deviations as above gives:

$$r_P \sigma_{P(X)} \sigma_{P(Y)} = r_A \sigma_{A(X)} \sigma_{A(Y)} + r_E \sigma_{E(X)} \sigma_{E(Y)}$$

Substituting  $\sigma_A = h \sigma_P$  and  $\sigma_E = e \sigma_P$

$$r_P \sigma_{P(X)} \sigma_{P(Y)} = r_A h_X \sigma_{P(X)} h_Y \sigma_{P(Y)} + r_E e_X \sigma_{P(X)} e_Y \sigma_{P(Y)}$$

Dividing through by  $\sigma_{P(X)} \sigma_{P(Y)}$  on both sides leads to  
 $r_P = r_A h_X h_Y + r_E e_X e_Y$

- The above equation reveals how genetic and environmental causes of correlations combine together to give phenotypic correlation.
- If both characters have low heritability, the phenotypic correlation is chiefly determined by environmental correlation.
- If they have high heritability, then the  $r_P$  is almost entirely genetic.

### PHENOTYPIC ( $r_P$ ), GENETIC ( $r_A$ ) AND ENVIRONMENTAL CORRELATION ( $r_E$ ) BETWEEN IMPORTANT ECONOMIC TRAITS IN FARM ANIMALS

Traits	$r_P$	$r_A$	$r_E$
<b>Cattle</b>			
Milk yield: Butter fat yield	0.93	0.85	0.96
Milk yield: Butter fat per cent	- 0.26	- 0.38	- 0.18
<b>Pigs</b>			
Weight gain: Back fat thickness	0.0	0.13	- 0.18
Growth rate: Feed efficiency	- 0.84	- 0.96	- 0.50
Weight gain: Feed efficiency	0.66	0.69	0.64
<b>Sheep</b>			
Fleece weight: Staple length	0.35	0.35	0.40
Fleece weight: Crimps per inch	- 0.21	- 0.56	0.10
Fleece weight: Body weight	0.36	0.11	-
<b>Poultry</b>			
Body weight: Egg production	0.01	- 0.17	0.08
Body weight: Egg weight	0.33	0.42	0.23
Egg weight : Egg production	-0.05	-0.31	0.02

- The  $r_A$  and  $r_E$  are different in magnitude, or even in sign. A difference in sign between the two correlations indicates that the genetic and environmental sources affect the characters through different physiological mechanism.

Correlations	Negative	Positive
<b>Low</b>	- 0.2 to - 0.4	0.2 to 0.4
<b>Medium</b>	- 0.4 to - 0.6	0.4 to 0.6
<b>High</b>	- 0.6 and above	0.6 and above