MODULE-24: QUANTITATIVE INHERITANCE

Learning objectives

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

- distinguish between qualitative and quantitative traits
- understand the quantitative traits values and means of population

QUANTITATIVE TRAITS

- Continuously varying characters are called quantitative characters or metric characters (Example: economically important traits such as height, weight, milk yield, wool yield, egg production etc.) and variation in them is called quantitative variation or continuous variations.

Quantitative genetics is the study of continuous traits and their underlying mechanisms.

- Quantitative traits are controlled by multiple genes, each segregating according to Mendel's laws.
- The inheritance of quantitative traits or poly genes is called Quantitative inheritance, Multiple factor inheritance, Multiple gene inheritance or Polygenic inheritance.

PHENOTYPIC TRAITS	
Qualitative Traits	**Quantitative Traits**
Traits of kind	Traits of degree
Discrete phenotypic classes	A spectrum of phenotypic classes
Discontinuous variations	Continuous variations
Each trait is governed by two or many alleles of a single gene	Each trait is governed by many non-allelic genes or poly genes.
Single gene effects can be detected	Due to poly genetic control effects single gene effects can be detected too slightly
The phenotypic expression of a gene is not influenced by environment.	The phenotypic expression is affected by environmental conditions to varying degrees
Analysis is made by counts and ratios.	Analysis is made by statistical methods.

VALUES AND MEANS

- Genetic properties of a population are expressed in terms of gene frequencies and genotype frequencies.
- To understand the connection between gene frequencies and the quantitative differences exhibited in a quantitative/metric character, the concept of value is introduced.
- A given quantitative trait is characterized by a mean value and a standard deviation expressed in metric units by which the character is measured.

Phenotypic value (*P*)

- The phenotypic value of a given quantitative trait is the yield of the individual with respect to the trait.
- The phenotypic value symbol is *P*.
- The phenotypic value can be measured and is evaluated in relation to the population mean value.
- The phenotypic value (*P*) of an individual is determined by the combined effect of the genotypic value (*G*) and the environmental deviation (*E*)

P = G + E

Genotypic value (G)

- Genotype is the sum total of genes possessed by an individual in pairs and environment is all the non-genetic circumstances that influence the phenotypic value.
- For any individual the genotypic value (G) is determined by the combined effect of all genes in all the loci which influence the trait.
- The genotypic value symbol is G.

Environmental deviation (E)

- The environmental deviation represents the combined effect of all non-genetic factors that have influenced the phenotypic values.
- The environmental deviation symbol is E.
- The genotype will confer certain value on the individual whereas the environment causes a deviation from this in one direction or the other.
- For a single locus, the mean environmental deviation in the whole population is taken to be zero. So the mean phenotypic value is equal to the mean genotypic value.

GENOTYPIC VALUE

- Genotypic value may be calculated by taking a mean of a large population with same genotype raised under similar conditions.
- Here mean environmental deviation in the whole population is taken as zero.
- The genotypic value is partitioned into additive gene action, dominance and epistatis.
  - $G = A + D + I$

where

- G - Genotypic value
- A - Additive value
- D - Dominance deviation and
- I - Interaction or epistatic value

  - Considering a single locus with two alleles, A_1 and A_2.
    - The genotypic value of
      - $A_1 A_1$ homozygote = $+a$
      - $A_2 A_2$ homozygote = $-a$ and
      - $A_1 A_2$ heterozygote = d
    - The value of d of the heterozygote depends on the degree of dominance.
    - The degree of dominance may be expressed as d/a .

Genotype A_1A_1 A_1A_2 A

Genotypic value $-a$ 0 d +

POPULATION MEAN

- Consider the following assumption:
  - Diploid organism
  - Diallelic autosomal locus
  - Random mating population
- The mean phenotype is obtained by summing the frequency weighted genotypic values (assuming that the environmental deviation is zero for each genotype).
- Let the gene frequency of A_1 and A_2 be p and q

Genotype	Frequency	Genotypic value	Frequency-weighted genotypic value
$A_1 A_1$	p^2	$+a$	$p^2 a$
$A_1 A_2$	$2pq$	d	$2pqd$
$A_2 A_2$	q^2	$-a$	$-q^2 a$
Total			**$a(p-q)+2pqd$**

- The contribution of any locus to the population mean has two terms: *a (p-q)* attributable to the homozygote and *2pqd* attributable to heterozygote.
- With additive combinations the population mean value resulting from the joint effects of several loci is the sum of the contributions of each locus.
  - *Population mean (M) = Σ a (p - q) + 2 Σ pqd*
- Population Mean Genotypic Value is a function allele frequency. This Population Mean Genotypic Value is identical to the population mean phenotypic value if the mean environmental deviation is zero.

MODULE-25: AVERAGE EFFECT AND BREEDING VALUE

Learning objectives

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

- understand the concept of average effect and breeding value and its properties

AVERAGE EFFECT

- Parents pass on their genes and not their genotypes to the next generation.
- Thus genotypic value cannot be transmitted from parents to offspring.
- A new measure of value is therefore needed which will refer to genes.
- The new measure is the *average effect* .

- The average effect of a gene depends on the gene frequency. The average effect is therefore a property of the population as well as of the gene.
- Consider a locus with two alleles A_1 and A_2 at frequencies p and q respectively.
  - Let us first take the average effect of the gene A_1 , for which we shall use the symbol α_1.
  - If A_1 gametes unite at random with gametes from the population
    - $A_1 A_1$ genotype produced frequency = p of and
    - $A_1 A_2$ genotype produced frequency = q
    - The genotypic value of $A_1 A_1$ = $+a$ and that of $A_1 A_2$ = d
    - The mean of these = pa + qd (taking of the proportions in which they occur)
  - Average effect of the A_1 gene (α_1) = pa + qd - M
    - $\alpha_1 = pa + qd - \{ a (p - q) + 2pqd \}$
    - $\alpha_1 = q [a + d (q - p)]$
  - Similary for the A_2 gene
    - $\alpha_2 = -p [a + d (q - p)]$
  - Now consider the average effect of the gene substitution. This is the difference which would be caused by changing one allele in an average individual into the other allele, so that $\alpha = p (a - d) + q (d + a) = a + d (q - p)$
    - The relation of α to α_1 and α_2 can be seen as
      - $\alpha_1 - \alpha_2 = a + d (q - p) = \alpha$
  - Therefore $\alpha_1 = q \alpha ; \alpha_2 = -p \alpha$

BREEDING VALUE (BV)

- The value of an individual, as measured by the average value of its progeny is called the breeding value of the individual .
- This is also the sum of the average effects alleles (α - *alpha*) of the individual.

  - Breeding value = the value of genes to progeny
  - Genetic value = the value of genes to self

- It includes non-additive effects (such as dominance) which cannot be passed on to progeny

Genotype	Breeding value
$A_1 A_1$	$2\alpha_1 = 2q\alpha$
$A_1 A_2$	$\alpha_1 + \alpha_2 = (q - p)\alpha$
$A_1 A_2$	$2\alpha_2 = -2p\alpha$

- The mean breeding value = $2p^2q\,\alpha + 2pq\,(q-p)\,\alpha - q^2p\,\alpha = 2pq\,\alpha\,(p + q - p - q) = 0$.
  - With random mating, the mean breeding value is zero.
- A (additive genetic effect) is also sometimes referred to as breeding value.

DOMINANCE DEVIATION

- When a single locus only is under consideration, the difference between the genotypic value (G) and the breeding value (A) of particular genotype is known as dominance deviation. (Deviations of the genotypic value from the breeding value are dominance deviations).
- The genetic effects (G) can be further partitioned, ignoring interactions among loci,

$G = A + D$

Where

- A - Additive effects (sum of the breeding values) and
- D - Dominance deviations

- The dominance deviation arises from the property of dominance between alleles at the same locus .

INTERACTION DEVIATION

- When only a single locus is under consideration, the genotypic value is made up of breeding value and dominance deviation only.
  - $G = A + D$
- Metric traits are polygenic in inheritance and the genotype refers to more than one locus, the genotypic value may contain an additional deviation due to non-additive combination.
  - $G = A + D + I$
  - The deviation I is called the interaction deviation or epistatic deviation.

- We know that
  - $P = G + E$
- So now the phenotypic value can be partitioned as
  - $P = A + D + I + E$
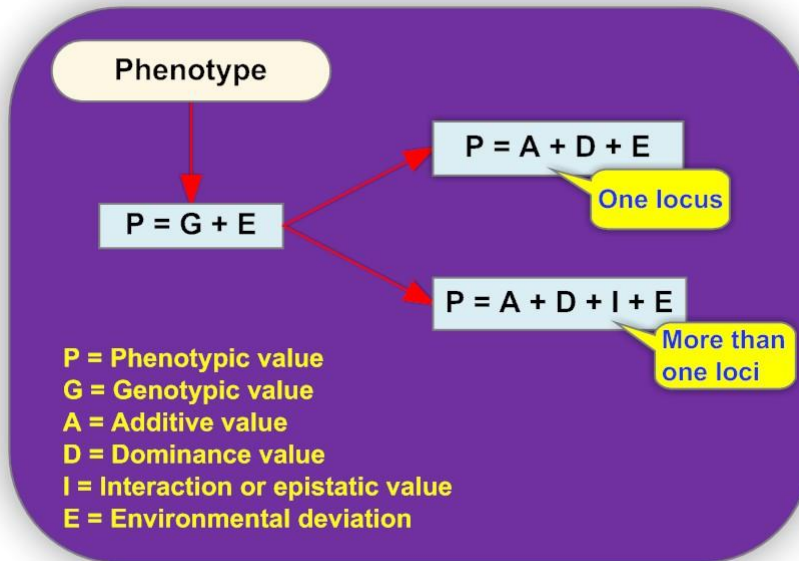
MODULE-26: COMPONENTS OF VARIANCE

Learning objectives

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

- understand the concept of genetic variance
- understand the different components of the phenotypic variance; the components of values and corresponding variance
- understand the properties of genotypic variance and environmental variance

VARIANCE

- The differences in phenotypic values of quantitative traits among individuals of a population are referred to as variation.
- The amount of variation is measured and expressed as variance. Variance measures the variability from an average or mean.
- The basic idea in the study of variance is its partitioning into components attributable to different causes.
- If there is no genetic variation then there is no scope for improvement.
- The components into which the phenotypic variance is partitioned are the same

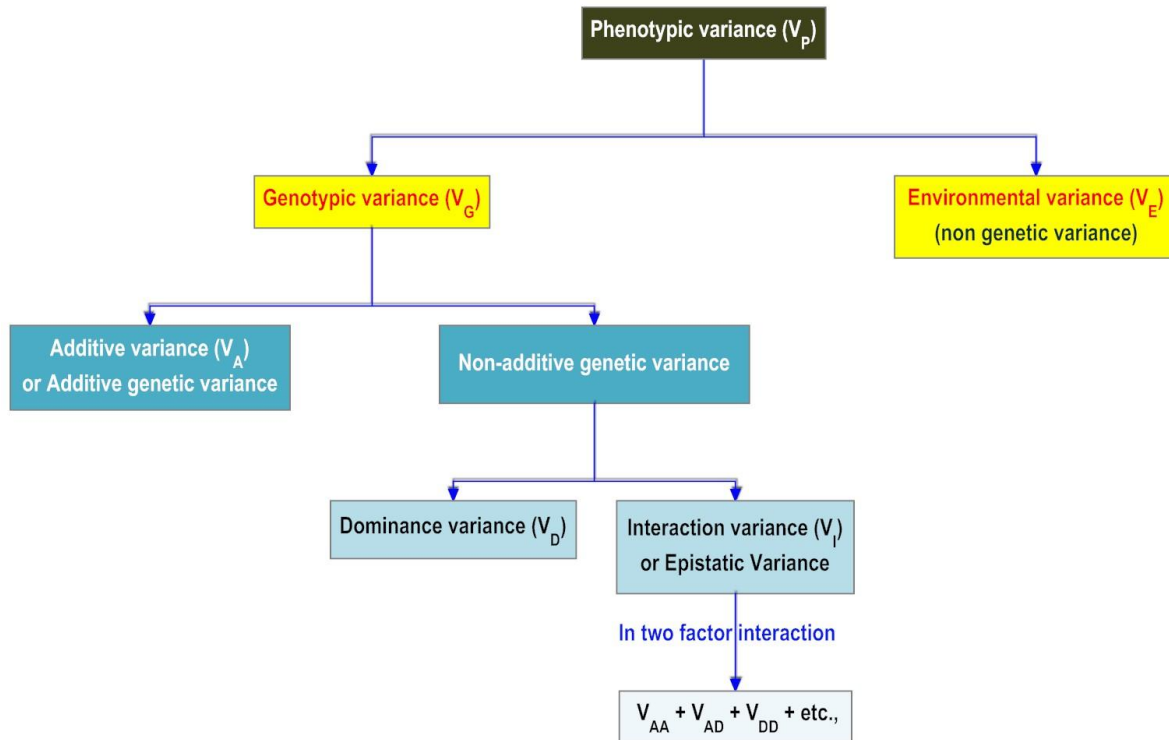as the components of phenotypic value described earlier.

- The relative magnitude of variance components is determined by the degree of resemblance between relatives
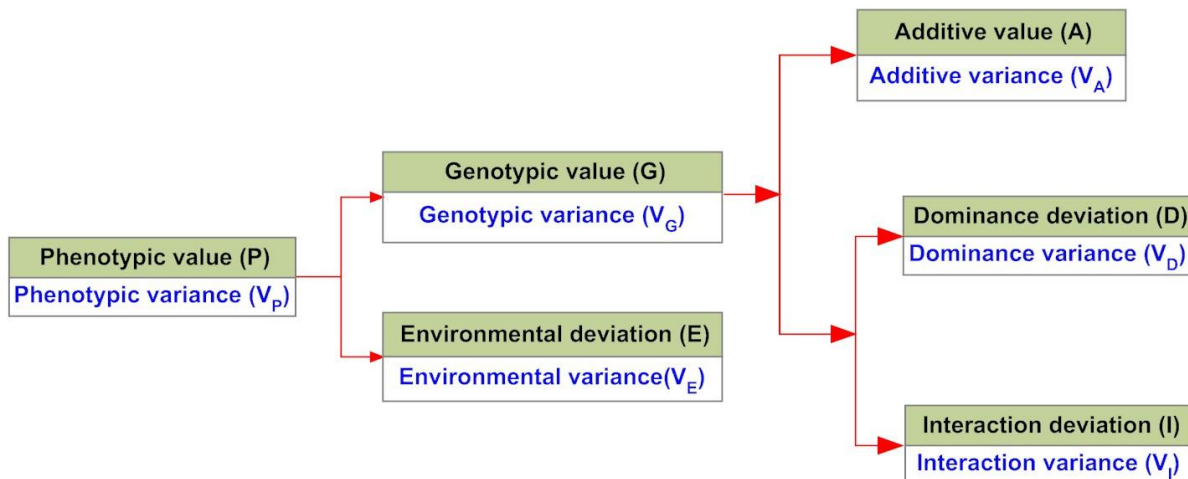
COMPONENTS OF VARIANCE

- The different components of variance are the same as the components of the phenotypic value.

Phenotypic variance (V_P)

Genotypic variance (V_G)

Environmental variance (V_E)
(non genetic variance)

Additive variance (V_A)
or Additive genetic variance

Non-additive genetic variance

Dominance variance (V_D)

Interaction variance (V_I)
or Epistatic Variance

In two factor interaction

$V_{AA} + V_{AD} + V_{DD}$ + etc.,

- The components of values and corresponding variance

Additive value (A)
Additive variance (V_A)

Genotypic value (G)
Genotypic variance (V_G)

Dominance deviation (D)
Dominance variance (V_D)

Phenotypic value (P)
Phenotypic variance (V_P)

Environmental deviation (E)
Environmental variance(V_E)

Interaction deviation (I)
Interaction variance (V_I)

- The important difference between components of value and variance is that in case of phenotypic value, each component can have positive or negative values on the other hand phenotypic variance are always positive.
- There is usually a substantial amount of non genetic variation whose cause is unknown and which cannot be eliminated by experimental design. This is referred to as "*intangible variation*".

GENOTYPE VARIANCE

- The variances are obtained by squaring the values multiplying by the frequency of the genotypes concerned and summing over the all genotypes.
- Genotypic variance is due to additive effects of genes and non-additive effects of genes.
- Additive effects are connected with breeding values of the individual because parents pass their genes to their offspring not their genotype.

Additive and Dominace variance

- Variance is obtained by squaring the values then multiplying by the frequency of the genotype concerned, and summing the three genotypes.

Genotype	$A_1 A_1$	$A_1 A_2$	$A_2 A_2$
Frequencies	p^2	$2pq$	q^2
Assigned values	a	d	-a
Breeding values	2q a	(q-p) a	-2p a
Dominance deviation	$-2q^2$ d	2pqd	$-2p^2$ d

- The additive variance which is the variance of breeding value is obtained as follows
  - $V_A = (2q\ a\ )^2 p^2 + [(q-p)\ a\ ]^2 2pq + (-2p\ a\ )q^2$
  - $V_A = 4p^2q^2\ a^2 + (q^2-2pq+p^2)\ a^2\ 2pq + 4p^2q^2\ a^2$
  - $V_A = 2pq\ a^2\ (2pq + q^2 - 2pq + p^2 + 2pq)$
  - $V_A = 2pq\ a^2\ (1)$
  - $V_A = 2pq\ [a + d\ (q-p)]^2$
- The variance of dominance deviation is
  - $V_D = (-2q^2 d)^2 + (2pqd)^2 + (-2p^2 d)^2$
  - $V_D = (2pqd)^2$
- Total genetic variance
  - $V_G = V_A + V_D$
  - $V_G = 2pq\ [a + d\ (q-p)]^2 + (2pqd)^2$
  - $V_G = 2pq\ a^2 + (2pqd)^2$
- In general the genes contribute much more variance when at intermediate frequencies than when at high or low frequencies, recessives at low frequency, in particular, contribute very little variance.
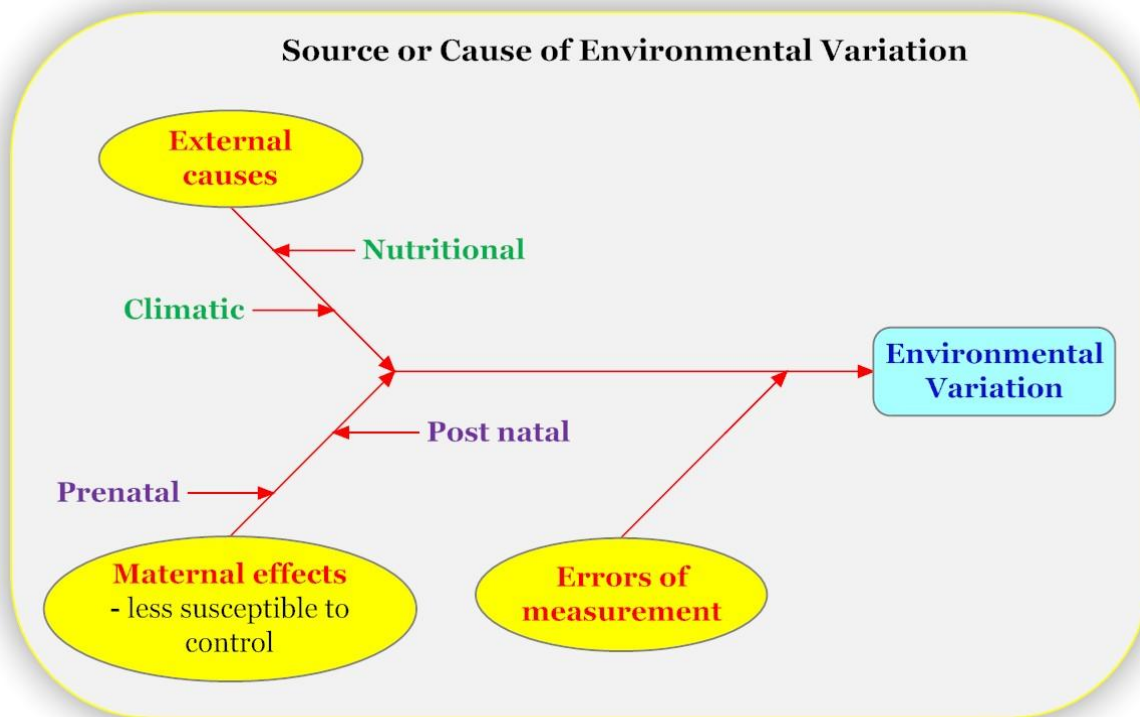
Interaction variance

- When more than one locus is under consideration then the interaction deviations give rise to the interaction variance.
- It is the variation of the interaction deviations brought about by the epistatic interactions at different loci.

- Two factor interactions arise from interaction of two loci three factor from three loci etc.
- In two factor interaction
  - $V_I = V_{AA} + V_{AD} + V_{DD}$ + etc

ENVIRONMENTAL VARIANCE

- It includes all variations of non genetic origin environmental variance is a source of error that reduces precision in genetic studies.

Source or Cause of Environmental Variation

- Environmental variance may partitioned into
  - Special environmental variance (V_{Es}) - within individual variance
  - General environmental variance (V_{Eg})

MODULE-27: GENOTYPE ENVIRONMENT CORRELATION AND INTERACTION

Learning objectives

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

- define and provide examples of genotype-environment correlation and interaction
- understand the properties and importance of genotype-environment correlation and interaction

GENOTYPE ENVIRONMENT CORRELATION AND INTERACTION

- So far we have assumed that phenotype is determined by Genotype and Environment. But besides $G + E$, the phenotype can also be influenced by two complications viz.
  - Genotype – Environment Correlation (G x E correlation)
  - Genotype – Environment Interaction (G x E interaction

GENOTYPE – ENVIRONMENT CORRELATION

- The correlation between genotype and environment arises when better genotypes are given better environment or vice versa.
  - Example: Milk yield in dairy cattle.
    - The normal practice of dairy husbandry is to feed cows according to their milk yield, the better genotypes being given more feed. This introduces correlation between phenotypic value and environmental deviation.
  - Since genotypic and phenotypic values are correlated there is a correlation between genotypic value and environmental deviation.
  - When G x E correlation is present, the phenotypic variance is increased by twice the covariance of genotypic values and environmental deviations and equation becomes $V_P = V_G + V_E + 2\ cov_{GE}$
  - If V_G and V_E are estimated, the G x E correlation component $2\ cov_{GE}$ can be estimated as $2\ cov_{GE} = V_P - (V_G + V_E)$.
  - The genotype environmental correlation is best regarded as part of the genetic variance (V_G).
  - The correlation between genotype and environment is seldom an important complication and normally neglected in experimental populations, where randomization is one of the main objectives of experimental design.
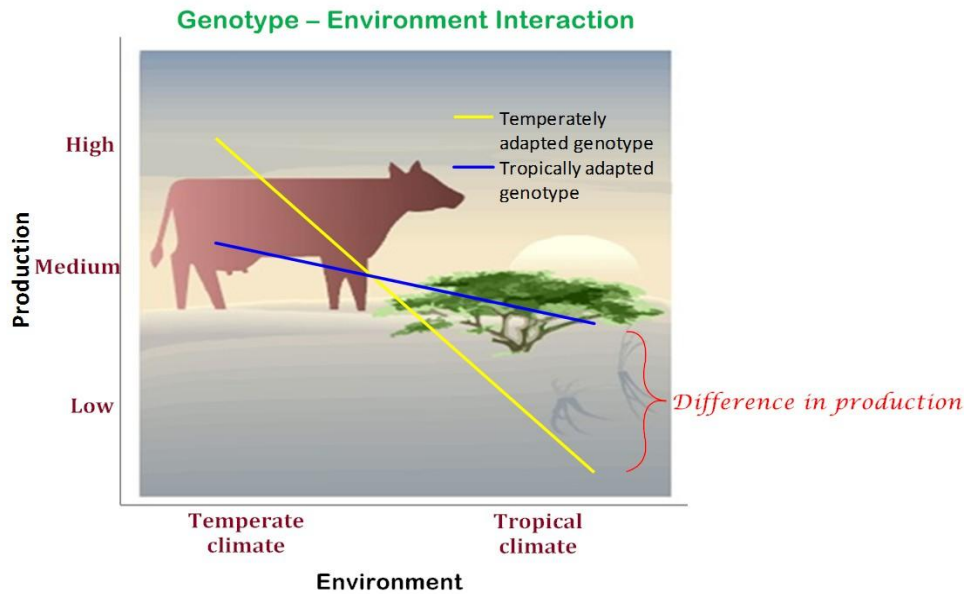
GENOTYPE – ENVIRONMENT INTERACTION

- Under certain combination of genotype and environment, the phenotype may not be equal to the sum of these two variables but rather be smaller or larger.
  - $P < or > (G + E)$
- When interaction is absent the phenotype equals the sum of genotype and environment.
  - $P = (G + E)$

- If the ranking order of two (or more) genotypes varies from environment to environment in which they are conducted then there is $G \times E$ interaction.
- The best genotype in one environment is not th e best in another environment.
- The $G \times E$ interaction is defined as the relative change in the performance of two or more genotypes in two or more environments. That is the phenomenon of genotype – environment interaction is reflected by the differential expression of different genotypes over environments (The genotype can be breeds, strains or lines. The environments can be nutrition, climate, housing and management etc.).
- For example the genotype A may be superior to genotype B in the environment - I, but inferior in environment – II, when $G \times E$ interaction is present.

Genotype	Environment - I	Environment - I
A	Superior	Inferior
B	Inferior	Superior

- Therefore each genotype has its specific *adaptability* for which the $G \times E$ interaction is responsible.
- When there is no interaction the best genotype in one environment will be the best in all.
- When the interaction between genotype and environment is present, the phenotypic value becomes $P = G + E + I_{GE}$.
- The interaction component also makes changes in the sources of variation for the phenotypic variance and result in $V_P = V_G + V_E + V_{GE}$.
- Since the variance occurring in genetically uniform groups is entirely due to environmental differences among the individual, the variance due to interaction is included with environment variance.
- In practical breeding, an important concept concerning $G \times E$ interaction is adaptability. In temperate climate, Zebu cattle (*Bos indicus*) are inferior to the various European breeds of cattle (*Bos taurus*). In tropical climate, Zebus are superior. The ranking of European breeds and Zebus depend upon the climate in which they are tested. For example the ranking of bulls may vary according to the country in which the performance of their daughters is measured.

Genotype – Environment Interaction

Importance of $G \times E$ interaction

- Genotype – Environmental ($G \times E$) Interaction are very important if individuals of a population are reared under different conditions, where environment cannot be controlled.
- Experimental evidences shows that the best dairy breed sires in the temperate countries were not the best in the tropical countries.
- The importance of I_{GE} was also found between countries with a high level of concentrate feeding versus pasture feeding base.
- The best sires in low environment level were not the best in the high environment level.
- Therefore the $G \times E$ interaction requires additional efforts in selection of breeding stock with a general adaptability to more than one environment condition or specifically suitable for desired environmental condition.

MODULE-28: RESEMBLANCE BETWEEN RELATIVES

Learning objectives

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

- understand the uses of resemblance between relatives
- understand how to estimate resemblance between relatives
- understand to estimate the intra class correlation coefficient and regression of offspring on parents

USES OF RESEMBLANCE BETWEEN RELATIVES

- The resemblance between relatives is one of the basic genetic phenomena displayed be metric characters.
- The degree of resemblance is a property of the character and can be determined by simple measurements made on the population and it provides the means of estimating the amount of additive genetic variance.
- It is the proportionate amount of additive genetic variance (i.e. the heritability) that chiefly determines the best breeding method to be used for improvement.
- The principle is that the relatives resemble each other due to the effects of common genes they have.
- So its degree provides the means to estimate the additive genetic variance which is heritable and is a fixed component of genotypic variance.
- Hence the knowledge on the causes of resemblance between relatives and the method of estimating the additive genetic variance from the observed degree of resemblance between relatives is useful in the study of metric characters.

ESTIMATION OF RESEMBLANCE BETWEEN RELATIVES

- The partitioning of phenotypic variance into components attributable to different causes (V_A, V_D, V_I) are called as *causal components* of variance denoted by V.
- The measurement of the degree of resemblance between relatives rests on the partitioning of the phenotypic variance into components corresponding to the grouping of the individuals into families (full sibs, half sibs).
- These components can be estimated directly from the observed phenotypic values and are known as *observational components* of phenotypic variance denoted by σ^2.
- For estimation of resemblance between relatives (full sibs, half sibs) the total observed variance is partitioned into two components namely between group components (σ^2_B) and within group components (σ^2_W).
- The greater the similarity within the groups, the greater in proportion will be the difference between the groups.
- The resemblance between relatives can be either similarity of individuals in the same group or the difference between individuals in different groups.

INTRA CLASS CORRELATION COEFFICIENT

- The degree of resemblance can therefore be expressed as the proportion of between group component to the total variance. This is known as intra class correlation (t) coefficient and is given by

$$t = \frac{\sigma^2_B}{\sigma^2_B + \sigma^2_W}$$

Where σ^2_B is the between group component and σ^2_W the within group component

- The between group component expresses the amount of variation that is common to members of the same group and it can be equally well referred to as the covariance of members of the groups.

DEGREE OF RESEMBLANCE BETWEEN OFFSPRING AND PARENTS

- For the estimation of degree of resemblance between offspring and parents, the grouping of the individuals into pairs rather than families is required.
- One parent or mean of the parents is paired with one offspring or mean of several offsprings.
- The degree of resemblance is therefore expressed as the regression (b_{OP}) of offspring on parents and is given by

$$b_{OP} = \frac{cov_{OP}}{\sigma_P^2}$$

Where cov_{OP} is the covariance of offspring and parents and σ_P^2 is variance of parents