## AS-2319

## M.Sc (III Semester) Examination, 2013

## Forestry, Wildlife and Environmental Sciences

## Guru Ghasidas Vishwavidyalaya University, Bilaspure (C.G)

# Quantitative Genetics in Forest Tree Breeding

**Time allowed: Three hours**

**Maximum Marks: 60**

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### I. Answer the following questions (20 X 1 = 20)

### Multiple choice questions

1. Mendel’s law includes
   a) Law of dominance    b) Law of segregation
   c) Law of independent assortment    d) All
   **Answer: d) All**

2. The phenotypic ratio of F2 population in monohybrid cross is
   a) 4:1    b) 1:3
   c) 3:1    d) 3:2
   **Answer: c) 3:1**

3. The genotypic ratio of F2 population in monohybrid cross is
   a) 1:2:1    b) 1:4:1
   c) 2:1:2    d) 1:2:3
   **Answer: a) 1:2:1**

4. Heterosis includes
   a) Average heterosis    b) Economic heterosis
   c) Heterobeltosis    d) All
   **Answer: d) All**

5. Luxuriance is the increased vigour and size of
   a) Inter-specific hybrids    b) Inbreds
   c) Cybrids    d) All
   **Answer: a) Inter-specific hybrids**

**True or false**

6. In luxuriance, the progenies are generally sterile
   **Answer: True**
7. Polyploidy means changes in chromosome number
   **Answer: True**
8. Gene mutation also called as point mutation
   **Answer: True**
9. Genetic components includes additive and non additive components of variance
   **Answer: True**
10. Population is generally described by mean and standard deviation
    **Answer: True**
11. The F2 ratio in masking gene action is 1:1
    **Answer: False**
12. Total number of individual in a population less than one (n-1) is called as degrees of freedom
    **Answer: True**
13. The highest and lowest value of observations is called as variance
    **Answer: False**
14. Disease resistant is a qualitative character
    **Answer: True**
15. Seed size is a quantitative character
    **Answer: True**

**Fill in the blanks**

16. Estimation of heterosis in relation to the best commercial variety of the crop is --------
    **Answer: Economic or useful heterosis**
17. Quantitative (GXE) interaction is also called as --------------------
    **Answer: non cross over GXE interaction**
18. The sum total of all genes present in a population is -------------
    **Answer: gene pool**
19. Hardy-Weinberg equilibrium is -------------------------
    **Answer:** $(p + q)^2 = p^2 + 2pq + q^2 = 1$
20. The selection used in natural stands where tree parentage is unknown is ----------------
    **Answer: Mass selection**

**II. Answer any four of the following questions (4 X 10 = 40)**

**Q.1. What is gene interaction and write different types of gene interaction? Explain the biochemical pathway of gene interaction?**

The various relationships of two or more olegogenes in producing the concerned characters are known as gene interaction

**Types of gene interaction**

**a) Complementary gene action (9:7)**

In rice, two dominant genes (Rc and Rd) are needed to produce red pericarp. When one of the two genes or both the genes are in the recessive state, the pericarp is white. This is known as Complementary gene action. The F2 ratio is 9:7.

**b) Supplementary gene action (9:3:4)**

In maize, a gene Pr has no effects of its own. But Pr gene modifies the action of gene R which produce red colour. In the presence of R, Pr changes the red colour to purple. This type of gene interaction is called Supplementary gene action. The F2 ratio is 9:3:4.

**c) Inhibitory gene action (13:3)**

The inhibitory gene I has no effect of its own. But gene I stops the action of gene R which produces red colour in maize. When the inhibitory gene is recessive (i) it is not inhibitory. The F2 ratio is 13:3.

**d) Masking gene action (12:3:1)**

In barley, a dominant gene Y produces yellow seed coat, while another gene B produces black seed coat. When genes B and Y are present together the effect of Y cannot be seen due to the masking effect of gene B. The F2 ratio is 12:3:1

**e) Duplicate gene action (15:1)**

Some characters are governed by two genes that produce identical effects, irrespective of whether they are present together or alone. The alternative form of the character results only when both the genes are in the recessive state. The F2 ratio is 15:1.

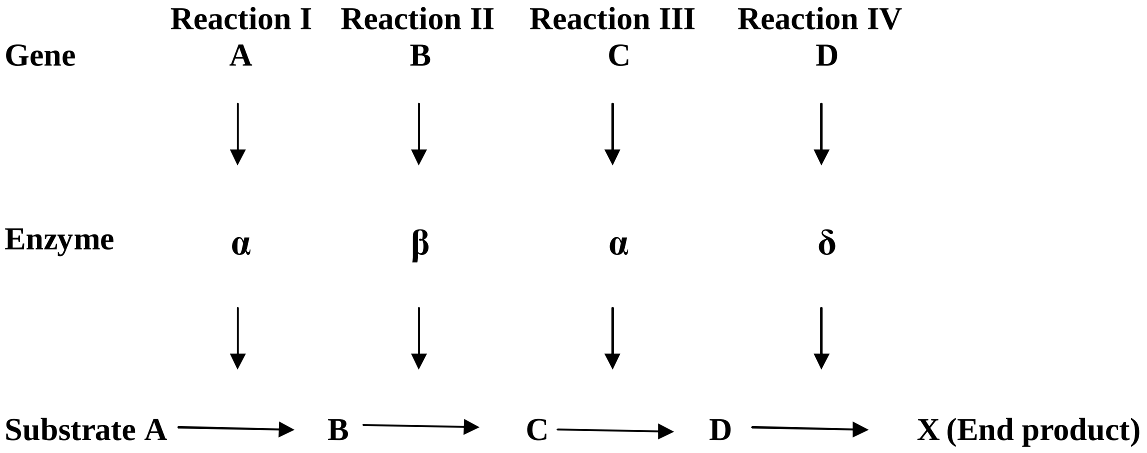
For example, the non floating character in rice is governed by 2 genes namely DW1 and DW2 either alone or together. The floating habit results only when both the genes are in the recessive form (ie., dw1dw1 dw2dw2)

**f) Polymeric gene action (9:6:1)**

The two genes produce identical effects individually but their effect is increased when both the genes are present together. In barley, gene A or B alone produces awns of medium length. But when genes A and B are present together long awns produced. The double recessive condition, aa, bb produces awnless lemma. The F2 ratio is 9:6:1.

**Biochemical basis of gene interaction.**

Gene interaction arises because each character is produced by a series of biochemical reactions. Each reaction provides the substrate for the next reaction. For example the substrate A is converted into the end product X by four reaction as follows.



- The first reaction is catalysed by the enzyme α and converts the substrate A into the product B.

- The product B serves as substrate for the second reaction which catalysed by the enzyme β and gives the product C.
- The product C serves as substrate for the third reaction which catalysed by the enzyme γ and gives the product D.
- Similarly the D is catalysed by the enzyme δ and convert the D into final product X. Thus each reaction is catalysed by a specific enzyme. In turn, each enzyme is encoded by a single gene.

**Q.2. Briefly describe the following question**

**a. What are the effects of inbreeding?**

Mating between individuals of more closely related descent or ancestry is called inbreeding. The reduction or loss in vigour and fertility as a result of inbreeding is known as inbreeding depression.

**Effects of inbreeding**

- Appearance of lethal and sub lethal alleles. It leads to death or reducing survival and reproduction rate.
- Reduction in vigour. Plants become shorter and weaker.
- Reduction in reproduction ability
- Reduction in yield
- Increase in homozygosity. The variation within line decreases rapidly. After 7 – 8 generations of selfing the lines become completely homozygous (99%). The lines which are almost homozygous due to continuous inbreeding and are maintained through close inbreeding are known as inbred lines.
- Separation of population into distinct lines. This leads to an increase in the variance of the population as a whole.

**b. What are the different categories of inbreeding depression?**

**High inbreeding depression**

- Great loss of vigour and yield
- Shows lethal characteristics and do not survive. (eg.) Alfalfa and Carrot

**Moderate inbreeding depression**

- Moderate loss of vigour and yield
- Shows sub lethal characteristics
- Production and maintenance of inbred lines are relatively easier
- Example are maize, jowar and bajra

**Low inbreeding depression**

- Shows a small degree of inbreeding depression
- Lines cannot be maintained due to poor fertility
- Examples are onion, sunflower and hemp.

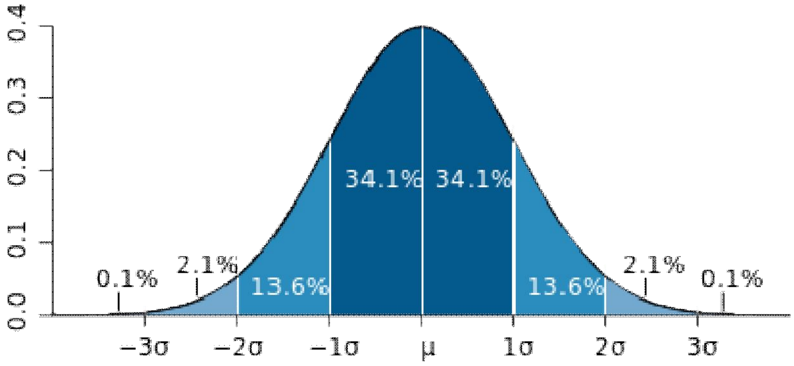
**No inbreeding depression**

The self pollinated species do not show inbreeding depression. They do show heterosis because these species reproduce by self fertilization is called homozygous balance. The cross pollinated species exhibits heterozygous balance.

## Q.3. Discuss the following

### a. Standard deviation in normal population

The population is generally described by mean and standard deviation



**Standard deviation** ( **σ**) shows how much variation or dispersion from the average exists. A low standard deviation indicates that the data points tend to be very close to the mean (also called expected value); a high standard deviation indicates that the data points are spread out over a large range of values.

The standard deviation of a random variable, statistical population, data set, or probability distribution is the square root of its variance. It is algebraically simpler though in practice less robust than the average absolute deviation. A useful property of the standard deviation is that, unlike the variance, it is expressed in the same units as the data. Note, however, that for measurements with percentage as the unit, the standard deviation will have percentage points as the unit.

In addition to expressing the variability of a population, the standard deviation is commonly used to measure confidence in statistical conclusions. For example, the margin of error in polling data is determined by calculating the expected standard deviation in the results if the same poll were to be conducted multiple times. The reported margin of error is typically about twice the standard deviation – the half-width of a 95 percent confidence interval. In science, researchers commonly report the standard deviation of experimental data, and only effects that fall much farther than one standard deviation away from what would have been expected are considered statistically significant – normal random error or variation in the measurements is in this way distinguished from causal variation. When only a sample of data from a population is available, the term standard deviation of the sample or sample standard deviation can refer to either the above-mentioned quantity as applied to those data or to a modified quantity that is a better estimate of the population standard deviation (the standard deviation of the entire population).

## b. Progeny test and its significance in tree improvement

Determination of genotype of a plant / tree by studying the progeny produced by it is called as progeny test.

### Significance of progeny test

- It is an essential part of all modern plant breeding programme.
- Heterozygous plants and homozygous plants are easily differentiated by progeny test
- Progeny testing of selected tree is essential to assess its genotypic worth and breeding values
- It is a test to compare the offspring of different parents.

### Kinds of progeny test.

### Half-sib selection with progeny testing

Selections are made based on progeny test performance instead of phenotypic appearance of the parental plants. Seed from selected half-sibs, which have been pollinated by random pollen from the population (meaning that only the female parent is known and selected, hence the term "half-sib") is grown in unreplicated progeny rows for the purpose of selection. A part of the seed is planted to determine the yielding ability, or breeding value, for any character of each plant. The seed from the most productive rows or remnant seed from the outstanding half-sibs is bulked to complete one cycle of selection.

### Full-sib selection with progeny testing

A number of full-sib families, each produced by making crosses between the two plants from the base population are evaluated in replicated trials. A part of each full-sib family is saved for recombination. Based on evaluation the remnant seed of selected full-sib families is used to recombine the best families.

**Q.4. Differentiate the following question**

a) **Tree breeding and Tree improvement**

**Tree breeding** is the application of genetic, reproductive biology and economics principles to the genetic improvement and management of forest trees. A typical forest tree breeding program starts with selection of superior phenotypes (plus trees) in a natural or planted forest. This application of mass selection improves the mean performance of the forest. Offspring is obtained from selected trees and grown in test plantations that act as genetic trials. Based on such tests the best genotypes among the parents can be selected. Selected trees are typically multiplied by either seeds or grafting and seed orchards are established when the preferred output is improved seed. Alternatively, the best genotypes can be directly propagated by cuttings or in-vitro methods and used directly in clonal plantations.

**Tree improvement** refers to the application of forest genetics principles within a given silvicultural system for the purpose of improving the genetic quality of the forest. Its goal is to improve the genetic value of the population while maintaining genetic diversity. Meeting this goal means that genetic improvement is aimed at the population level, rather than improvement of breeds or inbred lines. Tree improvement programs provide a known source of seed, seedlings or propagules for forest establishment. Worldwide, tree improvement programs are linked to a range of silvicultural systems but they are most commonly integrated with plantation silviculture (Zobel and Talbert 1984).

b) **Variation and variability**

Variation is the differences among the individuals belonging to single species or different species

Variability is the amount of variation present among the members of a population or species may have reference to one or more characters and at genotypic and or phenotypic levels.

c) **Monoecious and dioecious**

Plants having the stamens and the pistils in separate flowers on the same plant is called as monoecious plants.
Example: *Pinus roxburgii, Pinus wallichiana*

Dioecious plants have both the male and female reproductive organs on separate
Example:
Date palm, Coconut, Papaya.

d) **Dominant allele and recessive allele**

Dominance in genetics is a relationship between alleles of a single gene, in which one allele masks the phenotypic expression of another allele at the same gene locus. In the simplest case, where a gene exists in two allelic versions (designated *A* and *B*), three combinations of alleles (genotypes) are possible: *AA*, *AB*, and *BB*. If *AA* and *BB* individuals (homozygotes) show different forms of some trait (phenotypes), and *AB* individuals (heterozygotes) show the *same* phenotype as *AA* individuals, then allele *A* is said to *dominate* or*be dominant to* or *show dominance to* allele *B*, and *B* is said to *be recessive to A*. If instead *AB* has the same phenotype as *BB*, *B* is said to be dominant to *A*.

In other words in heterozygous (Ab) state, the allele A mask the effect of the allele b so A is said to be dominant allele and the allele b is said to be recessive. The dominant alles are expressed by capital letter (A) while the recessive alleles are expressed by small letters (b).

## Q.5. Discuss the following

### a) Estimation techniques of heritability

The ratio of genetic variance to the total variance ie., phenotypic variance is known an heritability

It is the ratio which indicating the degree to which parents passes their characteristics along to their off-springs

Heritability can be measured by two ways
1. Broad sense heritability
2. Narrow sense heritability

Broad sense heritability

It is defined as the ratio of total genetic variance in a population to the phenotypic variance.

Phenotype (*P*) = Genotype (*G*) + Environment (*E*).

Likewise the variance in the trait – Var (P) – is the sum of genetic effects as follows:

$$\mathrm{Var}(P) = \mathrm{Var}(G) + \mathrm{Var}(E) + 2\,\mathrm{Cov}(G,E).$$

In a planned experiment Cov(*G*,*E*) can be controlled and held at 0. In this case, heritability is defined as:

$$H^2 = \frac{\mathrm{Var}\ (G)}{\mathrm{Var}\ (P)}$$

.

$H^2$ is the broad-sense heritability. This reflects all the genetic contributions to a population's phenotypic variance including additive, dominant, nd epistatic (multi-genic interactions), as well as maternal and paternal effects, where individuals are directly affected by their parents' phenotype (such as with milk production in mammals).

A particularly important component of the genetic variance is the additive variance, Var(A), which is the variance due to the average effects (additive effects) of the alleles. Since each parent passes a single allele per locus to each offspring, parent-offspring resemblance depends upon the average effect of single alleles. Additive variance represents the genetic component of variance responsible for parent-offspring resemblance. The additive genetic portion of the phenotypic variance is known as Narrow-sense heritability and is defined as

$$h^2 = \frac{\text{Var (A)}}{\text{Var (P)}}$$

.

An upper case $H^2$ is used to denote broad sense, and lower case $h^2$ for narrow sense.

Estimation techniques of heritabilities

1. Growing progeny from a group of parents or crosses together in the same genetic test plantation. Heritability estimates are then derived from the relative performance of the progenies within and between parent trees.
2. Parent – off-spring regression technique: the narrow-sense heritability estimates can be done for height, wood specific gravity and form traits. Wood specific gravity is strongly controlled by genetics while height growth is strongly influenced by the environment under which the trees are grown and lesser degree by the genetic. Heritability is not a fixed value of a given characteristic of a given species. Estimates of heritability are not estimated without error. Therefore the ratios obtained are only a relative indication of genetic control and should not be interpreted as absolute or invariant values.

   Types of heritability

   Low heritability = 0.3 and < 0.3

   Medium heritability = 0.3 – 0.6

   High heritability = 0.6 and > 0.6

   0.6 means 60% is heritable. In general, heritability cannot be > 1. If heritability is > 1 means > 100% heritable.

### b) Significance of heritability

Additive variance is important for selection. If a selective pressure such as improving livestock is exerted, the response of the trait is directly related to narrow-sense heritability. The mean of the trait will increase in the next generation as a function of how much the mean of the selected parents differs from the mean of the population from which the selected parents were chosen. The observed response to selection leads to an estimate of the narrow-sense heritability (called realized heritability). This is the principle underlying artificial selection or breeding

In selective breeding of plants, the expected response to selection can be estimated by the following equation:

$$R = h^2 S$$

In this equation, the Response to Selection (R) is defined as the realized average difference between the parent generation and the next generation. The Selection Differential (S) is defined as the average difference between the parent generation and the selected parents.

For example, imagine that a plant breeder is involved in a selective breeding project with the aim of increasing the number of kernels per ear of corn. For the sake of argument, let us assume that the average ear of corn in the parent generation has 100 kernels. Let us also assume that the selected parents produce corn with an average of 120 kernels per ear. If $h^2$ equals 0.5, then the next generation will produce corn with an average of 0.5(120-100) = 10 additional kernels per ear. Therefore, the total number of kernels per ear of corn will equal, on average, 110. Note that heritability in the above equation is equal to the ratio Var (A)/ Var (P) only if the genotype and the environmental noise follow Gaussian distributions .

**Q.6. Write short answer for the following questions**

a) **With in family selection**
In this selection, individuals are chosen on the basis of their deviation from the family mean. The family values per se are given no weight when selections are made. It is used along with family selection. Among all the selection methods it gives the slowest rate of inbreeding.

b) **Inbreeding coefficient**
Inbreeding coefficient (F) measures the probability that two genes at any locus in an individual are identical by descent from the common ancestor(s) of the two parents. This means the degree to which two alleles are more likely to be homozygous (AA or aa) rather than heterozygous (Aa) in an individual, because the parents are related.. F is a relative measure, in that there will be a certain level of homozygosity within the base population; F simply estimates the increase from that initial level as a result of recent inbreeding.

c) **Population and population mean**
In genetics, population means all the individuals which are mating at random. In statistics, population means indefinitely large number or observations of the same kind.

The mean is the arithmetic average of a set of observations

The population mean is the mean of the population.

Different symbols make the distinction between these two, although the formulas are exactly the same. It is calculated by the following formula

$$\text{Population mean } (\mu) = \frac{\Sigma x}{N}$$

$$\text{Sample mean } (\overline{x}) = \frac{\Sigma x}{n}$$

Where., $\Sigma x$ is sum of all data value

N is number of data items in population

n is number of data items in sample

The only difference between the two is that the sample mean is referred to as "x bar" whereas the population mean is referred to as "mew." Both are found by calculating the sum of all values you are given and dividing by "n," the number of total values. We can often use x bar, the sample mean, to draw conclusions about the mean of the entire population.

**d) Variance**

A measurement of the spread between numbers in a data set. The variance measures how far each number in the set is from the mean. Variance is calculated by taking the differences between each number in the set and the mean, squaring the differences (to make them positive) and dividing the sum of the squares by the number of values in the set.

$$\sigma^2 = \frac{\Sigma(X - \mu)^2}{N}$$

**e) Random mating**

A mating in which each female gamet is equally likely to unite with any male gamet and the rate of reproduction of each genotype is equal ie., there is no selection.

In random mating gene frequencies remain constant. Variance for the character remains constant. The correlation between relatives does not change.