Answer Key

F.Y.B.Sc. Life Sciences

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Q. 1

A) Fill in the blanks: (06)

1. Dihybrid
2. Genotype
3. Allele
4. Filial
5. XY/XX
6. Female

B) Match the columns: (07)

a. – iii, b. – vi, c. – iv, d. – I, e. – ii, f. – vii, g. – v

C) Define / Explain the following terms: (06)

1. Food chain: A food chain is a linear network of links in a food web starting from producer organisms (such as grass or trees which use radiation from the Sun to make their food) and ending at apex predator species

2. Ecosystem: a biological community of interacting organisms and their physical environment.

3. Ammensalism: Ammensalism is the ecological interaction in which an individual species harms another without obtaining benefit.

4. Tropism: A tropism is a biological phenomenon, indicating growth or turning movement of a biological organism, usually a plant, in response to an environmental stimulus.

5. Mutualism: Mutualism describes the ecological interaction between two or more species where each species benefits.

6. Connectance: An ecological network is a representation of the biotic interactions in an ecosystem, in which species are connected by pairwise interactions. Or Interlinking of various food webs.

Q.2. A) Answer any one of the following: Dr. Shalini Rai (10)

1. The laws of inheritance were derived by Gregor Mendel, a 19th century monk conducting hybridization experiments in garden peas (*Pisum sativum*). Between 1856 and 1863, he cultivated and tested some 28,000 pea plants. From these experiments, he deduced two

generalizations that later became known as Mendel's Laws of Heredity or Mendelian inheritance. He described these laws in a two part paper, "Experiments on Plant Hybridization", which was published in 1866.

Mendel's Laws

Mendel discovered that by crossing true-breeding white flower and true-breeding purple flower plants, the result was a hybrid offspring. Rather than being a mix of the two colors, the offspring was purple flowered. He then conceived the idea of heredity units, which he called "factors", one of which is a recessive characteristic and the other dominant. Mendel said that factors, later called genes, normally occur in pairs in ordinary body cells, yet segregate during the formation of sex cells. Each member of the pair becomes part of the separate sex cell. The dominant gene, such as the purple flower in Mendel's plants, will hide the recessive gene, the white flower. After Mendel self-fertilized the F1 generation and obtained an F2 generation with a 3:1 ratio, he correctly theorized that genes can be paired in three different ways for each trait: AA, aa, and Aa. The capital A represents the dominant factor while the lowercase a represents the recessive.

Mendel stated that each individual has two alleles for each trait, one from each parent. Thus, he formed the "first rule", the Law of Segregation, which states individuals possess two alleles and a parent passes only one allele to his/her offspring. One allele is given by the female parent and the other is given by the male parent. The two factors may or may not contain the same information. If the two alleles are identical, the individual is called homozygous for the trait. If the two alleles are different, the individual is called heterozygous. The presence of an allele does not promise that the trait will be expressed in the individual that possesses it. In heterozygous individuals, the only allele that is expressed is the dominant. The recessive allele is present, but its expression is hidden. The genotype of an individual is made up of the many alleles it possesses. An individual's physical appearance, or phenotype, is determined by its alleles as well as by its environment.

Mendel also analyzed the pattern of inheritance of seven pairs of contrasting traits in the domestic pea plant. He did this by cross-breeding dihybrids; that is, plants that were heterozygous for the alleles controlling two different traits. Mendel then crossed these dihybrids. If it is inevitable that round seeds must always be yellow and wrinkled seeds must be green, then he would have expected that this would produce a typical monohybrid cross: 75 percent round-yellow; 25 percent wrinkled-green. But, in fact, his mating generated seeds that showed all possible combinations of the color and texture traits. He found 9/16 of the offspring were round-yellow, 3/16 were round-green, 3/16 were wrinkled-yellow, and 1/16 were wrinkled-green. Finding in every case that each of his seven traits was inherited independently of the others, he formed his "second rule", the Law of Independent Assortment, which states the inheritance of one pair of factors (genes) is independent of the inheritance of the other pair. Today we know that this rule holds only if the genes are on separate chromosomes

Mendel's Law of Dominance

In a heterozygote, the allele which masks the other is referred to as dominant, while the allele that is masked is referred to as recessive.

Mendel's law of dominance states that in a heterozygote, one trait will conceal the presence of another trait for the same characteristic. Rather than both alleles contributing to a phenotype, the dominant allele will be expressed exclusively. The recessive allele will remain "latent," but will be transmitted to offspring by the same manner in which the dominant allele is transmitted. The recessive trait will only be expressed by offspring that have two copies of this allele; these offspring will breed true when self-crossed.

By definition, the terms dominant and recessive refer to the genotypic interaction of alleles in producing the phenotype of the heterozygote. The key concept is genetic: which of the two alleles present in the heterozygote is expressed, such that the organism is phenotypically identical to one of the two homozygotes. It is sometimes convenient to talk about the trait corresponding to the dominant allele as the dominant trait and the trait corresponding to the hidden allele as the recessive trait. However, this can easily lead to confusion in understanding the concept as phenotypic. For example, to say that "green peas" dominate "yellow peas" confuses inherited genotypes and expressed phenotypes. This will subsequently confuse discussion of the molecular basis of the phenotypic difference. Dominance is not inherent. One allele can be dominant to a second allele, recessive to a third allele, and codominant to a fourth. If a genetic trait is recessive, a person needs to inherit two copies of the gene for the trait to be expressed. Thus, both parents have to be carriers of a recessive trait in order for a child to express that trait.

Since Mendel's experiments with pea plants, other researchers have found that the law of dominance does not always hold true. Instead, several different patterns of inheritance have been found to exist.

Mendel's Law of Segregation

Mendel's Law of Segregation states that a diploid organism passes a randomly selected allele for a trait to its offspring, such that the offspring receives one allele from each parent.

Observing that true-breeding pea plants with contrasting traits gave rise to F_1 generations that all expressed the dominant trait and F_2generations that expressed the dominant and recessive traits in a 3:1 ratio, Mendel proposed the law of segregation. The law of segregation states that each individual that is a diploid has a pair of alleles (copy) for a particular trait. Each parent passes an allele at random to their offspring resulting in a diploid organism. The allele that contains the dominant trait determines the phenotype of the offspring. In essence, the law states that copies of genes separate or segregate so that each gamete receives only one allele.

For the F_2 generation of a monohybrid cross, the following three possible combinations of genotypes could result: homozygous dominant, heterozygous, or homozygous recessive. Because heterozygotes could arise from two different pathways (receiving one dominant and one recessive allele from either parent), and because heterozygotes and homozygous dominant individuals are phenotypically identical, the law supports Mendel's observed 3:1 phenotypic ratio. The equal segregation of alleles is the reason we can apply the Punnett square to accurately predict the offspring of parents with known genotypes.

The physical basis of Mendel's law of segregation is the first division of meiosis in which the homologous chromosomes with their different versions of each gene are segregated into daughter nuclei. The behavior of homologous chromosomes during meiosis can account for the segregation of the alleles at each genetic locus to different gametes. As chromosomes separate into different gametes during meiosis, the two different alleles for a particular gene also segregate so that each gamete acquires one of the two alleles. In Mendel's experiments, the segregation and the independent assortment during meiosis in the F1 generation give rise to the F2 phenotypic ratios observed by Mendel. The role of the meiotic segregation of chromosomes in sexual reproduction was not understood by the scientific community during Mendel's lifetime.

Mendel's Law of Independent Assortment

Independent assortment allows the calculation of genotypic and phenotypic ratios based on the probability of individual gene combinations.

Independent Assortment

Mendel's law of independent assortment states that genes do not influence each other with regard to the sorting of alleles into gametes: every possible combination of alleles for every gene is equally likely to occur. The independent assortment of genes can be illustrated by the dihybrid cross: a cross between two true-breeding parents that express different traits for two characteristics. Consider the characteristics of seed color and seed texture for two pea plants: one that has green, wrinkled seeds (yyrr) and another that has yellow, round seeds (YYRR). Because each parent is homozygous, the law of segregation indicates that the gametes for the green/wrinkled plant all are yr, while the gametes for the yellow/round plant are all YR. Therefore, the F_1 generation of offspring all are YyRr.

For the F2 generation, the law of segregation requires that each gamete receive either an R allele or an r allele along with either a Y allele or a y allele. The law of independent assortment states that a gamete into which an r allele sorted would be equally likely to contain either a Y allele or a y allele. Thus, there are four equally likely gametes that can be formed when the YyRr heterozygote is self-crossed as follows: YR, Yr, yR, and yr. Arranging these gametes along the top and left of a 4 × 4 Punnett square gives us 16 equally likely genotypic combinations. From these genotypes, we infer a phenotypic ratio of 9 round/yellow:3 round/green:3 wrinkled/yellow:1 wrinkled/green. These are the offspring ratios we would expect, assuming we performed the crosses with a large enough sample size.

Because of independent assortment and dominance, the 9:3:3:1 dihybrid phenotypic ratio can be collapsed into two 3:1 ratios, characteristic of any monohybrid cross that follows a dominant and recessive pattern. Ignoring seed color and considering only seed texture in the above dihybrid cross, we would expect that three-quarters of the F_2 generation offspring would be round and one-quarter would be wrinkled. Similarly, isolating only seed color, we would assume that three-quarters of the F_2 offspring would be yellow and one-quarter would be green. The sorting of alleles for texture and color are independent events, so we can apply the product rule. Therefore,

the proportion of round and yellow F_2 offspring is expected to be (3/4) × (3/4) = 9/16, and the proportion of wrinkled and green offspring is expected to be (1/4) × (1/4) = 1/16. These proportions are identical to those obtained using a Punnett square. Round/green and wrinkled/yellow offspring can also be calculated using the product rule as each of these genotypes includes one dominant and one recessive phenotype. Therefore, the proportion of each is calculated as (3/4) × (1/4) = 3/16.

2. Step to check Goodness of fit:

i. Set the null hypothesis

ii. Calculate the expected frequency (E)

iii. Calculate difference between Observed and expected frequency (O-E)

Square- $(O-E)^2$

iv. Summation of $(O-E)^2$

v. Compare calculated value of chi square with tabulated value at particular level of significance for specific degree of freedom.

vi. if chi calculated value is less that chi tabulated value then goodness of fit / null hypothesis is accepted otherwise rejected.

Q. 2. B) Answer any two of the following: (10)

1. X- linked inheritance.

Sex linkage or sex linked inheritance is the phenotypic expression of an allele related to the allosome (sex chromosome) of the individual. In autosomal chromosomes both sexes have the same probability of existing, but since humans have many more genes on the female X chromosome than on the male Y chromosome, these are much more common than Y-linked traits.

In mammals, the female is homogametic, with two X chromosomes (XX), while the male is the heterogametic sex, with one X and one Y chromosome (XY). Genes on the X or Y chromosome are called sex-linked. In ZW sex-determination system used by birds the opposite is true: the male is the homogametic sex (ZZ), and the female is heterogametic (ZW).

X-linked recessive traits are expressed in all heterogametics, but are only expressed in those homogametics that are homozygous for the recessive allele. For example, an X-linked recessive allele in humans causes haemophilia, which is much more common in males than females because they are hemizygous and therefore express the trait when they inherit one mutant allele. In contrast, a female must inherit two mutant alleles, a less frequent event since the mutant allele is rare in the population.

The incidence of recessive X-linked phenotypes in females is the square of that in males X-linked traits are maternally inherited from carrier mothers or from an affected father. Each son born to a carrier mother has a 50% probability of inheriting the X-chromosome carrying the mutant allele. There are a few Y-linked traits; these are inherited from father.

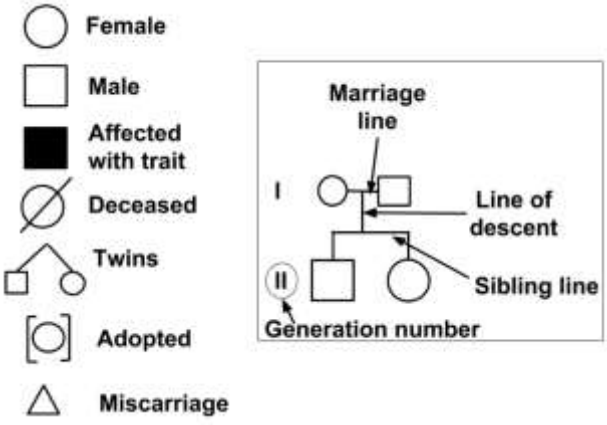
In classical genetics, a reciprocal cross is performed to test if a trait is sex-linked.

2. Sutton's Hypothesis.

Sutton and Boveri proposed the Chromosomal theory of Inheritance independently. Sutton developed this hypothesis in "The Chromosomes in Heredity" (1903) and concluded that chromosomes contain hereditary units and that their behaviour during meiosis is random. His work formed the basis for the chromosomal theory of heredity. Sutton did his observations using grasshopper cells. His paper, in 1902, clearly showed that each chromosome is different, and meiosis reduces chromosome number in the gametes. Sutton's 1903 paper, *The Chromosomes in Heredity*, summarized and discussed the importance of his conclusions. The paper even more strongly drew the connection between Mendel's laws of heredity and chromosomes.

3. **Pedigree analysis:**
Pedigrees are used to analyze the pattern of inheritance of a particular trait throughout a family. Pedigrees show the presence or absence of a trait as it relates to the relationship among parents, offspring, and siblings.

Reading a pedigree



Common pedigree symbols and identifiers
Pedigrees represent family members and relationships using standardized symbols.
By analyzing a pedigree, we can determine **genotypes**, identify **phenotypes**, and predict how a trait will be passed on in the future. The information from a pedigree makes it possible to determine how certain alleles are inherited: whether they are **dominant**, **recessive**, **autosomal**, or **sex-linked**.
If the trait is dominant, one of the parents *must* have the trait. Dominant traits will not skip a generation. If the trait is recessive, neither parent is required to have the trait since they can be heterozygous.

For example, in X-linked recessive traits, males are much more commonly affected than females. In autosomal traits, both males and females are equally likely to be affected (usually in equal proportions).

4. Monohybrid Cross Definition

A monohybrid cross is a genetic mix between two individuals who have homozygous *genotypes*, or genotypes that have completely dominant or completely recessive alleles, which result in opposite *phenotypes* for a certain genetic trait.

Monohybrid crosses are used by geneticists to observe how the offspring of *homozygous*individuals express the *heterozygous* genotypes they inherit from their parents. Typically, this mix determines the dominant genotype.

A monohybrid cross can also signify a genetic mix between two individuals who have heterozygous genotypes. These crosses confirm the dominance of an allele

Examples of Monohybrid Cross

Gregor Mendel's Peas

Although he did not know it at the time, Gregor Mendel used monohybrid crosses to identify dominant and recessive traits in his landmark experiments with peas.

Gregor Mendel focused on several different genetic traits, but we will focus on one: stem length. Imagine that two types of pea plants grow in a garden. One type of pea plant has long stems, while the other has short stems. For the sake of this example, assume that both types of pea plant have a homozygous genotype (LL and ll), and that long stems (LL) are dominant over short stems (ll).

A monohybrid cross, or breeding a long-stemmed pea plant with a short-stemmed pea plant, allows scientists, like Gregor Mendel, to determine the dominance of long stems or short stems. A monohybrid cross also permits scientists to evaluate how heterozygous offspring express the genes they inherit.

As mentioned before, breeding a long-stemmed pea plant with a short-stemmed pea plant creates offspring that all have a heterozygous genotype (Ll). As long stems are dominant, all offspring will have the long-stemmed phenotype. In different terms, and as modeled by Gregor Mendel's classic pea example observing the offspring of a monohybrid cross allows for determination of dominant genotypes and, by extension, dominant phenotypes.

Huntington's Disease

Huntington's Disease is a progressive degenerative condition that occurs in 4 to 15 of every 100,000 people in the United States. Having no cure, it is a certain death sentence for those diagnosed. While little is known about this condition, geneticists are sure that it is inherited via a dominant gene.

At the simplest level, a monohybrid cross was used to determine the genetic nature of Huntington's disease. Everyone carries the aptly-named *Huntingtin* gene, the gene responsible for the complication. With this information, scientists paired the *Huntingtin*genes of an individual who is homozygous dominant for the condition (HH) with the *Huntingtin* genes of an individual who is homozygous recessive for the condition (hh).

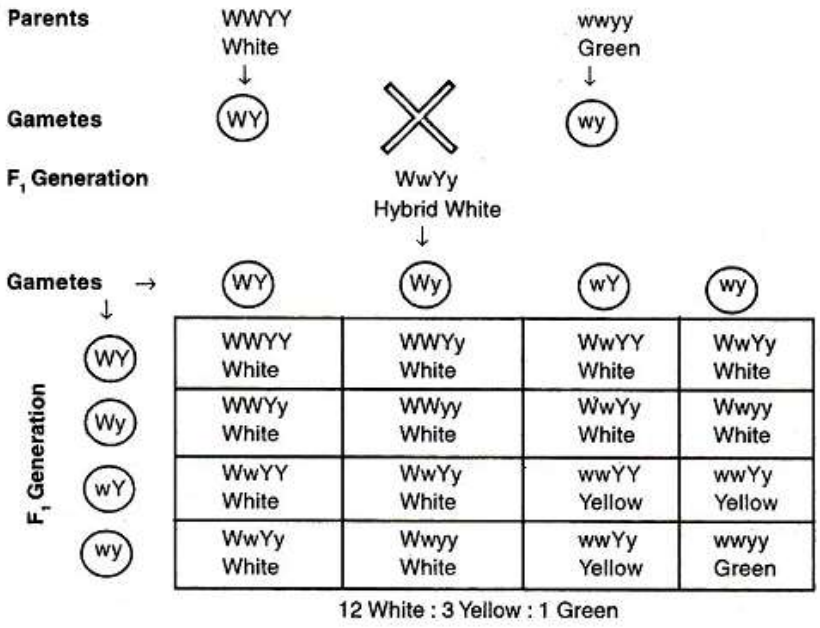
Although this example is highly abridged, the result remains that all offspring from the cross carried the dominant allele for Huntington's disease. While this experiment, if conducted on humans, would bring sad news to both parent and child, it would also highlight the dominant nature of the disease.

Q. 3 A) Answer Any one of the following: (10)

1. What is Dominant Epistasis? Explain with a suitable example.

Epistasis is the phenomenon where the effect of one gene (locus) is dependent on the presence of one or more 'modifier genes', i.e. the **genetic background**. Thus, epistatic mutations have different effects in combination than individually. It arises due to interactions, either between genes, or within them, leading to non-linear effects. It is the interaction between two non allelic gene pairs. Dominant Epistasis is exhibited when one dominant gene masks the expression of the other dominant non allelic gene, where both gene control expression of the same trait. It can be explained by the following example.

- Example: In summer squash fruit colour may be white, yellow or green. White fruits are produced by a domain epistatic allele 'W'. At another locus 'Y' for yellow fruits is dominant to its allele 'y' for green fruits. Dominant white hides the effect of yellow or green. A consequence of this dominant epistasis is that the hybrid ratio is modified into **12 white: 3 yellow: 1 green**.

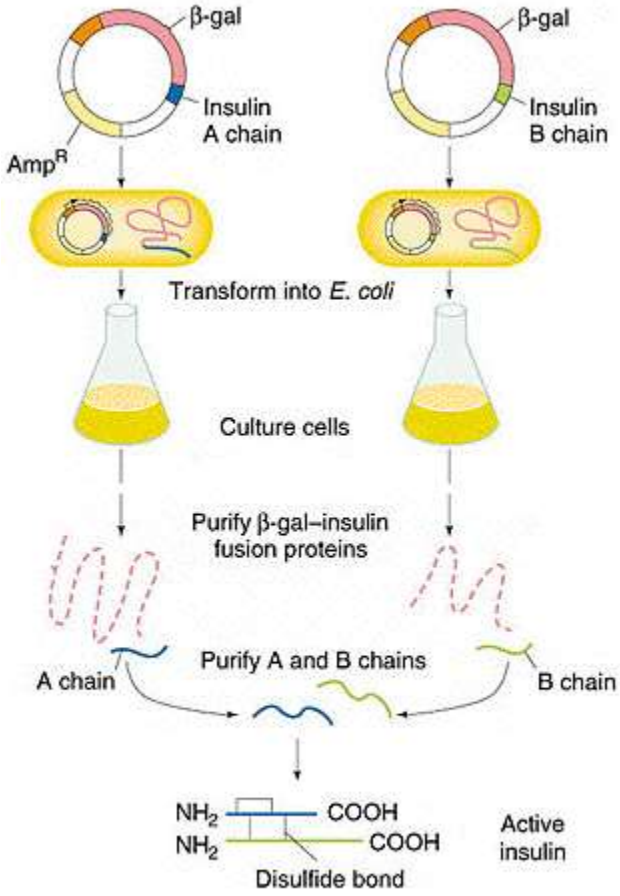


Inference:

In the above F2 ratio, it can be observed that dominant gene 'W' when present alone or as WW, masks the expression of any other gene or allele. It masks the expression of dominant gene 'Y' and the fruit colour is white instead of yellow, when gen 'W' is present. Here the gene 'W' is epistatic and gene 'Y' is hypostatic.

Thus due to the epistasic effect of gene 'W', the Mendelian dihybrid ratio of F2, changes from 9:3:3:1 to 12:3:1.

2. Diagrammatically represent the technique of cloning of human gene in prokaryote.



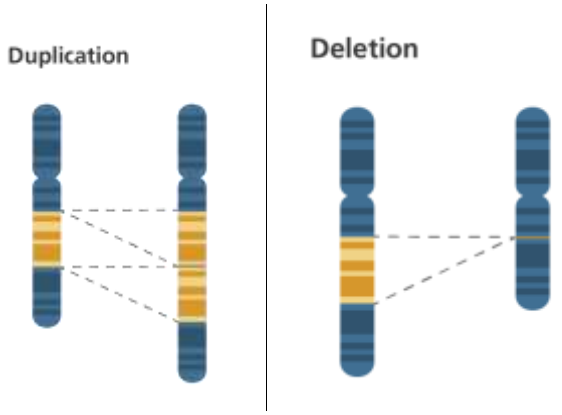
Q. 3 B) Explain Any two of the following: **(10)**

1. Any two types of Chromosomal Aberrations and their effect:

In genetics, a **Deletion** is a mutation (a genetic aberration) in which a part of a chromosome or a sequence of DNA is lost during DNA replication. Any number of nucleotides can be deleted, from a single base to an entire piece of chromosome. The smallest single base deletion mutations are believed to occur by a single base flipping in the template DNA, followed by template DNA strand slippage, within the DNA polymerase active site. Deletions can be caused by errors in chromosomal crossover during meiosis, which causes several serious genetic diseases. Deletions that do not occur in multiples of three bases can cause a frame shift by changing the 3-nucleotide protein reading frame of the genetic sequence. Deletion of a number of pairs that is not evenly divisible by three will lead to a frame shift mutation, causing all of the codons occurring after the deletion to be read incorrectly during translation, producing a severely altered and potentially non functional protein. In contrast, a deletion that is evenly

divisible by three is called an *in-frame* deletion. Deletions are responsible for an array of genetic disorders, including some cases of male infertility and two thirds of cases of Duchenne muscular dystrophy. Deletion of part of the short arm of chromosome 5 results in Cri du chat syndrome. Deletions in the SMN-encoding gene cause spinal muscular atrophy, the most common genetic cause of infant death.

Duplication: A portion of the chromosome is duplicated, resulting in extra genetic material. Known human disorders include Charcot-Marie-Tooth disease type 1A, which may be caused by duplication of the gene encoding peripheral myelin protein 22 (PMP22) on chromosome 17. (A structural change resulting in the doubling of genes in a section of the chromosome of prokaryotes and eukaryotes is referred to as duplication. If a segment of one chromosome is incorporated in another homologous chromosome, it is called intra-chromosomal duplication, but if the duplicated chromosome segment is either incorporated into a non-homologous chromosome or occurs as a fragment in the chromosomal set it is called inter-chromosomal duplication.



2. Multiple Allelism with a suitable example:

Alleles are alternative forms of a gene, and they are responsible for differences in phenotypic expression of a given trait (e.g., brown eyes versus green eyes). A gene for which at least two alleles exist is said to be polymorphic. Instances in which a particular gene may exist in three or more allelic forms are known as multiple allele conditions. It is important to note that while multiple alleles occur and are maintained within a population, any individual possesses only two such alleles (at equivalent **loci** on **homologous** chromosomes).

Examples of Multiple Alleles: ABO Blood group system, Caot colour in rabbit, Eye colour in Drosophila

Examples: Gene of the ABO blood group system, The ABO system in humans is controlled by three alleles, usually referred to as I^A, I^B, and I^O (the "I" stands for isohaemagglutinin). I^A and I^B are codominant and produce type A and type B antigens, respectively, which migrate to the surface of red blood cells, while I^O is the recessive allele and produces no antigen. The blood groups arising from the different possible genotypes are summarized in the following table.

Genotype	**Blood Group**
$I^A I^A$	**A**
$I^A I^O$	**A**
$I^B I^B$	**B**
$I^B I^O$	**B**
$I^A I^B$	**AB**
$I^O I^O$	**O**

Multiple Alleles: Rabbit Fur Colors

❖Fur colors (determined by 4 alleles): full, chinchilla, himalayan, albino

3. Use of Biotechnology in Agriculture with a suitable example.

The exploitation of biological processes for industrial and other purposes, especially the genetic manipulation of microorganisms for the production of antibiotics, hormones, etc.

Agricultural biotechnology, also known as **agritech**, is an area of agricultural science involving the use of scientific tools and techniques, including genetic engineering, molecular markers, molecular diagnostics, vaccines, and tissue culture, to modify living organisms: plants, animals, and microorganisms.[1] Crop biotechnology is one aspect of agricultural biotechnology which has been greatly developed upon in recent times. Desired trait are exported from a particular species of Crop to an entirely different species. These transgene crops possess desirable characteristics in terms of flavor, color of flowers, growth rate, size of harvested products and resistance to diseases and pests.

An example use of Biotechnology in Agriculture is Bt cotton. It is a genetically modified organism (GMO) or genetically modified pest resistant plant cotton variety, which produces an insecticide to bollworm. Strains of the bacterium *Bacillus thuringiensis* produce over 200 different Bt toxins, each harmful to different insects. Most notably, Bt toxins are insecticidal to the larvae of moths and butterflies, beetles, cotton bollworms and ghtu flies but are harmless to other forms of life. The gene coding for Bt toxin has been inserted into cotton as a transgene, causing it to produce this natural insecticide in its tissues. In many regions, the main pests in commercial cotton are lepidopteran larvae, which are killed by the Bt protein in the genetically modified cotton they eat. This eliminates the need to use large amounts of broad-spectrum insecticides to kill lepidopteran pests (some of which have developed pyrethroid resistance). This spares natural insect predators in the farm ecology and further contributes to noninsecticide pest management.

Bt cotton is ineffective against many cotton pests such as plant bugs, stink bugs, and aphids; depending on circumstances it may be desirable to use insecticides in prevention. A 2006 study done by Cornell researchers, the Center for Chinese Agricultural Policy and the Chinese Academy of Science on Bt cotton farming in China found that after seven years these secondary pests that were normally controlled by pesticide had increased, necessitating the use of pesticides at similar levels to non-Bt cotton and causing less profit for farmers because of the extra expense of GM seeds

Bt cotton was created through the addition of genes encoding toxin crystals in the Cry group of endotoxin. When insects attack and eat the cotton plant the Cry toxins are dissolved due to the high pH level of the insect's stomach. The dissolved and activated Cry molecules bond to cadherin-like proteins on cells comprising the brush border molecules. The epithelium of the brush border membranes separates the body cavity from the gut while allowing access for nutrients. The Cry toxin molecules attach themselves to specific locations on the cadherin-like proteins present on the epithelial cells of the midge and ion channels are formed which allow the flow of potassium. Regulation of potassium concentration is essential and, if left unchecked, causes death of cells. Due to the formation of Cry ion channels sufficient regulation of potassium ions is lost and results in the death of epithelial cells. The death of such cells creates gaps in the brush border membrane.

4. Problem on Non Epistatic interaction:

Parents: RRPp X Rrpp

Phenotypes: Walnut comb Rose Comb

Gametes: RP RP Rp rp

Rp Rp Rp rp

Offsprings:

	RP	**RP**	**Rp**	**Rp**
Rp	**RRPp** **Walnut**	**RRPp** **Walnut**	**RRpp** **Walnut**	**RRpp** **Walnut**
Rp	**RRPp** **Walnut**	**RRPp** **Walnut**	**RRpp** **Rose**	**RRpp** **Rose**
rp	**RrPp** **Walnut**	**RrPp** **Walnut**	**Rrpp** **Rose**	**Rrpp** **Rose**
rp	**RrPp** **Walnut**	**RrPp** **Walnut**	**Rrpp** **Rose**	**Rrpp** **Rose**

Ratio: Genotypic: 4RRPp: 4RrPp: 4RRpp: 4Rrpp

Phenotypic: 8 Walnut: 8 Rose

Q.4. A) Answer <u>any one</u> of the following: (10)

1. Explain the process of Ecological Succession.

Ecological succession is the gradual process by which ecosystems change and develop over time. Nothing remains the same and habitats are constantly changing.
There are two main types of succession, primary and secondary.

Primary succession is the series of community changes which occur on an entirely new habitat which has never been colonized before. For example, a newly quarried rock face or sand dunes.

Secondary succession is the series of community changes which take place on a previously

colonized, but disturbed or damaged habitat. For example, after felling trees in a woodland, land clearance or a fire.

Steps in Ecological Succession:

- The species living in a particular place gradually change over time as does the physical and chemical environment within that area.

- Succession takes place because through the processes of living, growing and reproducing, organisms interact with and affect the environment within an area, gradually changing it.

- Each species is adapted to thrive and compete best against other species under a very specific set of environmental conditions. If these conditions change, then the existing species will be outcompeted by a different set of species which are better adapted to the new conditions.

- The most often quoted examples of succession deal with plant succession. It is worth remembering that as plant communities change, so will the associated micro-organism, fungus and animal species. Succession involves the **whole** community, not just the plants.

- Change in the plant species present in an area is one of the driving forces behind changes in animal species. This is because each plant species will have associated animal species which feed on it. The presence of these herbivore species will then dictate which particular carnivores are present.

- The structure or 'architecture' of the plant communities will also influence the animal species which can live in the microhabitats provided by the plants.

- Changes in plant species also alter the fungal species present because many fungi are associated with particular plants. more

- Succession is directional. Different stages in a particular habitat succession can usually be accurately predicted.

- These stages, characterised by the presence of different communities, are known as 'seres'.

- Communities change gradually from one sere to another. The seres are not totally distinct from each other and one will tend to merge gradually into another, finally ending up with a'climax' community.

- Succession will not go any further than the climax community. This is the final stage.

  This does not however, imply that there will be no further change. When large organisms in the climax community, such as trees, die and fall down, then new openings are created in which secondary succession will occur.

- Many thousands of different species might be involved in the community changes taking place over the course of a succession. For example, in the succession from freshwater to climax woodland.

- The **actual species** involved in a succession in a particular area are controlled by such factors as the geology and history of the area, the climate, microclimate, weather, soil type and other environmental factors. For example, the species involved in a succession from open freshwater to climax woodland in Central Africa, would be quite different to those which have been quoted in these pages as occurring in Britain. However, the processes involved would be the same.

- Succession occurs on many different timescales, ranging from a few days to hundreds of years.

  It may take hundreds of years for a climax woodland to develop, while the succession of invertebrates and fungi within a single cow pat (cow dung), may be over within as little as 3months.

  By this time, the dung has been transformed into humus and nutrients and has been recycled back into the soil. The holes clearly visible in the cow pat (*right*) have been made by the animals which have colonized it.

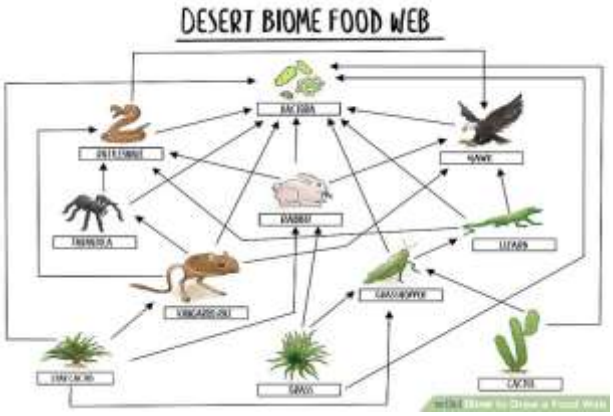
2. Calculate the mean, median and variance of the following data:

Height(in cm)	**95-105**	**105-115**	**115-125**	**125-135**	**135-145**
No. of Children	**19**	**23**	**36**	**70**	**25**

Mean: 34.6 Median:165.70 Variance:17,724

Q. 4. B) Answer any two of the following: (10)

1. Write a note on Desert Food Web. A desert ecosystem is defined by interactions between organism populations, the climate in which they live, and any other non-living influences on the habitat. Deserts are arid regions which are generally associated with warm temperatures, however cold deserts also exist. Deserts can be found on every continent. Several interacting food chains result in formation of food web as depicted below.



2. Explain any two forms of Taxis Movement with suitable example.

The movement of a cell (e.g. a gamete) or a microorganism in response to an external stimulus. Certain microorganisms have a light-sensitive region that enables them to move towards or away from high light intensities (positive and negative phototaxisrespectively). Many bacteria move in response to chemical stimuli (*chemotaxis*); a specific example is *aerotaxis*, in which atmospheric oxygen is the stimulus. Taxic responses are restricted to cells that possess cilia, flagella, or some other means of locomotion. The term is usually not applied to the movements of higher animals.

3. Describe pond as ecosystem.

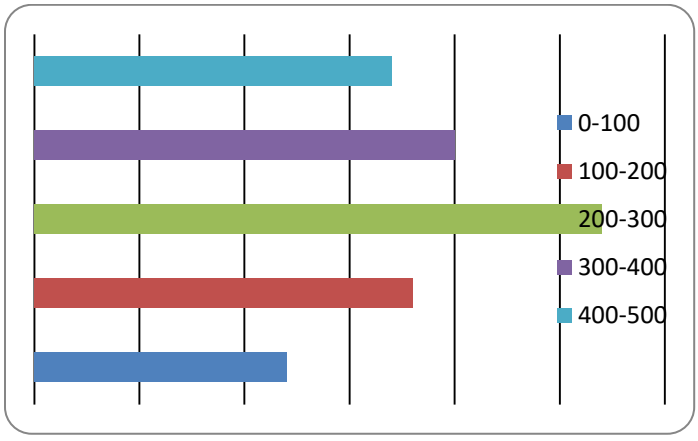
A pond is a quiet body of water that is too small for wave action and too shallow for major temperature differences from top to bottom. It usually has a muddy or silty bottom with aquatic plants around the edges and throughout. However, it is often difficult to classify the differences between a pond and a lake, since the two terms are artificial and the ecosystems really exist on a continuum. Generally, in a pond, the temperature changes with the air temperature and is relatively uniform. Lakes are similar to ponds, but because they are larger, temperature layering or stratification takes place in summer and winter, and these layers turnover in spring and fall. Ponds get their energy from the sun. As with other ecosystems, plants are the primary producers. The chlorophyll in aquatic plants captures energy from the sun to convert carbon dioxide and water to organic compounds and oxygen through the process of photosynthesis. Nitrogen and phosphorus are important nutrients for plants. The addition of these substances may increase primary productivity. However, too many nutrients can cause algal blooms, leading to eutrophication (Read Ponds & Eutrophication for more information). Producers • Phytoplankton, literally “wandering plants,” are microscopic algae that float in the open water and give it a green appearance. They carry out photosynthesis using carbon dioxide that is dissolved in the water and release oxygen that is used by the bacteria and animals in the pond. Phytoplankton are not actually plants-they are protists! • Periphytic algae are microscopic algae that attach themselves to substrates and give the rocks and sticks a greenish brown slimy appearance. They also carry out photosynthesis and produce oxygen, often near the bottom of the pond where it can be used by decomposers. • Submerged plants grow completely under water • Floating plants include

plants that float on the surface and plants that are rooted on the bottom of the pond but have leaves and/or stems that float. • Emergent plants are rooted in shallow water but their stems and leaves are above water most of the time. • Shore plants grow in wet soil at the edge of the pond. Consumers • Zooplankton are microscopic animals that eat phytoplankton or smaller zooplankton. Some are single-celled animals, tiny crustaceans, or tiny immature stages of larger animals. Zooplankton float about in the open water portions of the pond and are important food for some animals. • Invertebrates include all animals without backbones. Macroinvertebrates are big enough to be seen with the naked eye. Some of them are only found in clean water. • Vertebrates are animals with backbones. In a pond these might include fish, frogs, salamanders, and turtles. Decomposers Animal waste and dead and decaying plants and animals form detritus on the bottom of the pond. Decomposers, also known as detritovores, are bacteria and other organisms that break down detritus into material that can be used by primary producers, thus returning the detritus to the ecosystem. As this material decomposes it can serve as a food resource for microbes and invertebrates. During decay microbes living on detritus can pull nutrients from the overlying water thus acting to improve water quality. In the process of breaking down detritus, decomposers produce water and carbon dioxide.

4. Construct a histogram for the following data:

The monthly profits in rupees of 100 shops distributed as follows:

Profit per shop	**0-100**	**100-200**	**200-300**	**300-400**	**400-500**	**500-600**
No.of Shops	**12**	**18**	**27**	**20**	**17**	**06**



Q.5. Answer any four of the following: (20)

1. Phenotypic ratio

Phenotypic ratio pertains to the relative number of offspring manifesting a particular trait or combination of traits. It can be determined by doing a test cross and identifying the frequency of a trait or trait combinations that will be expressed based on the genotypes of the offspring.

Example can be given to explain

2. Significance of Chi Square test:

The topic of gene interaction includes a sometimes bewildering array of different phenotypic ratios. Although these ratios are easily demonstrated in established systems such as the ones illustrated in this chapter, in an experimental setting a researcher may observe an array of different progeny phenotypes and not initially know the meaning of this ratio. At this stage, a hypothesis is devised to explain the observed ratio. The next step is to determine whether the observed data are compatible with the expectations of the hypothesis.

In research generally, it is often necessary to compare experimentally observed numbers of items in several different categories with numbers that are predicted on the basis of some hypothesis. For example, you might want to determine whether the sex ratio in some specific population of insects is 1:1 as expected. If there is a close match, then the hypothesis is upheld, whereas, if there is a poor match, then the hypothesis is rejected. As part of this process, a judgment has to be made about whether the observed numbers are a close enough match to those expected. Very close matches and blatant mismatches generally present no problem in judgment, but inevitably there are gray areas in which the match is not obvious. Genetic analysis often requires the interpretation of numbers in various phenotypic classes. In such cases, a statistical procedure called the χ^2 (chi-square) test is used to help in making the decision to hold onto or reject the hypothesis.

The χ^2 test is simply a way of quantifying the various deviations expected by chance if a hypothesis is true. For example, consider a simple hypothesis that a certain plant is a heterozygote (monohybrid) of genotype *A*/*a*. To test this hypothesis, we would make a testcross to *a*/*a* and predict a 1:1 ratio of *A*/*a* and *a*/*a* in the progeny. Even if the hypothesis is true, we do not always expect an exact 1:1 ratio. We can model this experiment with a barrel full of equal numbers of red and blue marbles. If we blindly removed samples of 100 marbles, on the basis of chance we would expect samples to show small deviations such as 52 red: 48 blue quite commonly and larger deviations such as 60 red:40 blue less commonly. The χ^2 test allows us to calculate the probability of such chance deviations from expectations if the hypothesis is true. But, if all levels of deviation are expected with different probabilities even if the hypothesis is true, how can we ever reject a hypothesis? It has become a general scientific convention that a probability value of less than 5 percent is to be taken as the criterion for rejecting the hypothesis. The hypothesis might still be true, but we have to make a decision somewhere, and the 5 percent level is the conventional decision line. The logic is that, although results this far from expectations are expected 5 percent of the time even when the hypothesis is true, we will mistakenly reject the hypothesis in only 5% of cases and we are willing to take this chance of error.

2.

3. Schematically represent the grazing food chain.

4. Write a note on any two types of Mimicry.

Mimicry occurs when one animal displays physical or behavioral traits that copy those of a different species or their surroundings, and incur a survival advantage on account of it. Animals don't necessarily mimic other animals; often, they mimic plants or rocks. There are different types of mimicry; Batesian Mimicry. Batesian mimicryinvolves a palatable, unprotected species (the mimic) that closely resembles an unpalatable or protected species (the model). For example, lizards have learned to mimic tree trunk color which proves to be very successful as predators will simply move past them as they believe that they are simply looking at a tree. Another example of this type of mimicry can be seen with the Katydid who will mimic a leaf in both color and shape in an attempt to be hidden.

Some prey animals have evolved certain patterns on their bodies that mimic other animals in an attempt to startle their predators. The most common example of this type of mimicry can be found in some moths and butterflies who flash eye spots on their wings to predators. These eye spots startle the predator who believes that the eyes belong to a much larger animal that may be a threat to them.

In one form of mimicry known as aggressive mimicry, an organism will mimic a signal that is either deceptive or attractive to its prey. One example of this involves the praying mantis who will mimic flowers to attract insects that they can then capture and eat. Organisms can also imitate the behaviors of other organisms. Moth caterpillars, for example, will imitate the motion and body movements of a snake in order to scare off predators that are usually a prey item for snakes.

One of the most popular types of mimicry involves the warning coloration found on inedible or toxic organisms such as the monarch butterfly. Once these toxic organisms have adapted this warning coloration which warns predators to stay away, other organisms may start to mimic this warning coloration in an attempt to stay alive. Batesian mimics are those mimics that imitate unpalatable species even though they are palatable. Therefore, one species is harmful while the

other is harmless. The wasp is a great example of Batesian mimicry. The wasp is the model species in this example as it possesses a sting which enables it to escape from predators. The bright warning coloration of the wasp has been mimicked by many other insects. Even though the mimics are harmless, the predator will avoid them due to bad experiences with wasps with the same coloration. With Müllerian mimicry, many unpalatable species share a similar color pattern. Müllerian mimicry proves to be successful as the predator only has to be exposed to one of the species in order to learn to stay away from all the other species with the same warning color patterns. The black and yellow striped bodies of social wasps, solitary digger wasps, and caterpillars of the cinnabar moths warn predators that the organism is inedible.

5. Aneuploidy:

Aneuploidy is the presence of an abnormal number of chromosomes in a cell, for example a human cell having 45 or 47 chromosomes instead of the usual 46. It does not include a difference of one or more complete sets of chromosomes. A cell with any number of complete chromosome sets is called a *euploid* cell. An extra or missing chromosome is a common cause of genetic disorders, including some human birth defects. Some cancer cells also have abnormal numbers of chromosomes. Aneuploidy originates during cell division when the chromosomes do not separate properly between the two cells. Most cases of aneuploidy result in miscarriage and the most common extra autosomal chromosomes among live births are 21, 18, and 13.

Chromosome abnormalities are detected in 1 of 160 live human births.

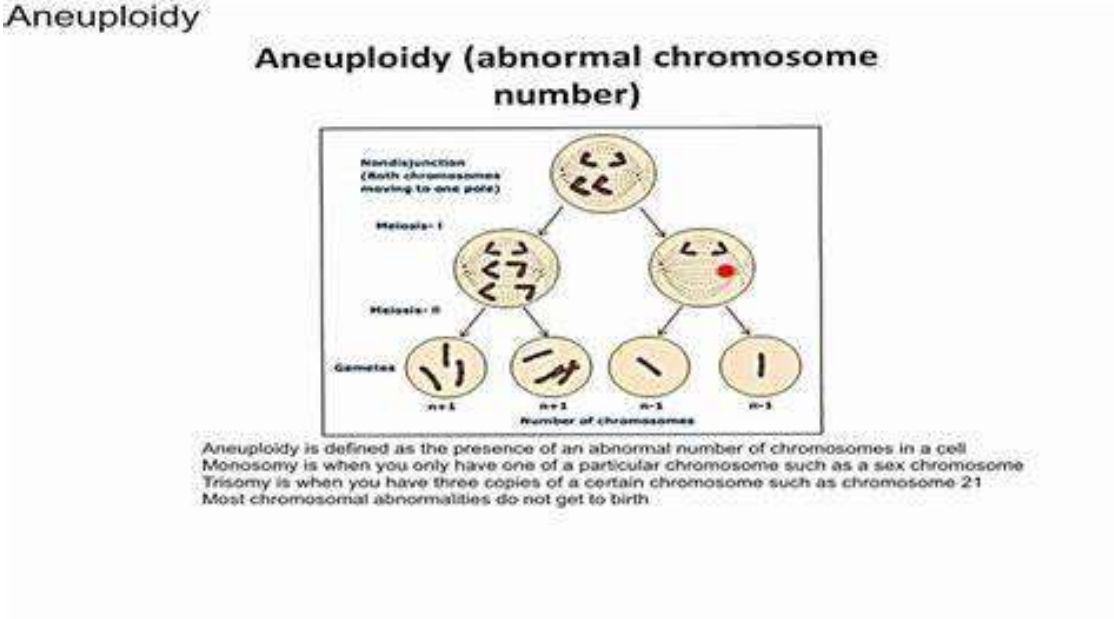
Mechanisms

Nondisjunction usually occurs as the result of a weakened mitotic checkpoint, as these checkpoints tend to arrest or delay cell division until all components of the cell are ready to enter the next phase. If a checkpoint is weakened, the cell may fail to 'notice' that a chromosome pair is not lined up on the mitotic plate, for example. In such a case, most chromosomes would separate normally (with one chromatid ending up in each cell), while others could fail to separate at all. This would generate a daughter cell lacking a copy and a daughter cell with an extra copy.

Completely inactive mitotic checkpoints may cause nondisjunction at multiple chromosomes, possibly all. Such a scenario could result in each daughter cell possessing a disjoint set of genetic material. *Merotelic attachment* occurs when one kinetochore is attached to both mitotic spindle poles. One daughter cell would have a normal complement of chromosomes; the second would lack one. A third daughter cell may end up with the 'missing' chromosome. Multipolar spindles: more than two spindle poles form. Such a mitotic division would result in one daughter cell for each spindle pole; each cell may possess an unpredictable complement of chromosomes.

Monopolar spindle: only a single spindle pole forms. This produces a single daughter cell with its copy number doubled. A *tetraploid intermediate* may be produced as the end-result of the monopolar spindle mechanism. In such a case, the cell has double the copy number of a normal cell, and produces double the number of spindle poles as well. This results in four daughter cells with an unpredictable complement of chromosomes, but in the normal copy number.

Aneuploidy



6. Sex Limited traits:

Sex-limited genes are genes that are present in both sexes of sexually reproducing species but are expressed in only one sex and remain 'turned off' in the other. In other words, sex-limited genes cause the two sexes to show different traits or phenotypes, despite having the same genotype. This term is restricted to autosomal traits, and should not be confused with sex-linked characteristics, which have to do with genetic differences on the sex chromosomes (see sex-determination system). Sex-limited genes are also distinguished from sex-influenced genes, where the same gene will show differential expression in each sex. Sex-influenced genes commonly show a dominant/recessive relationship, where the same gene will have a dominant effect in one sex and a recessive effect in the other (for example, male pattern baldness).

Genotype	Phenotype in Males	Phenotype in Females
BB	bald	bald
Bb	bald	nonbald
bb	nonbald	nonbald

Sex-limited genes are responsible for sexual dimorphism, which is a phenotypic (directly observable) difference between males and females of the same species. These differences can be reflected in size, color, behavior (ex: levels of aggression), and morphology. An example of sex-limited genes are genes which instruct the male elephant seals to grow big and fight, at the same time instructing female seals to grow small and avoid fights. These genes are also responsible for some female beetles' inability to grow exaggerated mandibles.

The overall point of sex-limited genes is to resolve intralocus sexual conflict. In other words, these genes try to resolve the "push-pull" between males and females over trait values for optimal phenotype. Without these genes, organisms would be forced to settle on an *average* trait value, incurring costs on both sexes. With these genes, it is possible to 'turn off' the genes in one sex, allowing both sexes to attain (or at least, approach very closely) their optimal phenotypes.

Expression of Lactation in Cattle

Female Genotypes	Female Phenotypes
XXLL	Female Lactating
XXLl	Female Lactating
XXll	Female not lactating
Male Genotypes	Male Phenotypes
XYLL	Male not lactating
XYLl	Male not lactating
Xyll	Male not lactating