1. (a) Give one word for the following:

- (i) A gene present on Y chromosome responsible for a human embryo to develop as a male.
    - SRY (Sex-determining Region Y)
- (ii) An allele that causes death frequently at an early developmental stage, resulting in missing of one or more genotypes as well as phenotypes of a cross.
    - Lethal allele
- (iii) The test/tool used for analyzing genetic crosses in which one individual of unknown genotype is crossed with another individual with a homozygous recessive genotype for the trait in question.
    - Test cross
- (iv) The phenomenon responsible for appearance of white-eyed females and red-eyed males in the F1 progeny of Drosophila flies in a cross between a white-eyed female and a red-eyed male.
    - Nondisjunction (specifically, X-chromosome nondisjunction in meiosis I in the female parent)
- (v) A short stretch of DNA that has a higher frequency of methylation of cytosine than the rest of the genome as represents an epigenetic mark.
    - CpG island
- (vi) A method for estimating the age of evolutionary divergence between two species by comparing the differences in mutation rate in their DNA or protein sequences.
    - Molecular clock

- (vii) A condition in which the heterozygous genotype has a higher relative fitness than either the homozygous dominant or homozygous recessive.
    - Heterozygote advantage (or Overdominance)
- (viii) A region of DNA that is shown to statistically be associated with a specific phenotype or trait that shows polygenic and continuous variation within a population.
    - Quantitative Trait Locus (QTL)
- (ix) A phenomenon in genetics where one or more genes modify or mask the expression of another gene
    - Epistasis
- (x) The situation that occurs when one copy of a gene is inactivated or deleted and the remaining functional copy of the gene is not adequate to show the complete phenotype.
    - Haploinsufficiency
- (xi) A condition where an organism has both male and female reproductive organs
    - Hermaphroditism
- (xii) A technique used to study genetic linkage in fungi and other lower eukaryotes which can define the position of the centromere in a chromosome.
    - Tetrad analysis (or Ordered tetrad analysis)

2. (b) Comment on the following statements:

- (i) In the experiments conducted by Carl Correns on *Mirabilis jalapa*, the variegated branch produce progeny with three different phenotypes.

- This statement is generally not accurate. In *Mirabilis jalapa* (four o'clock plant), leaf variegation is an example of cytoplasmic (maternal) inheritance, controlled by genes in chloroplast DNA.
- The phenotype of the progeny is determined solely by the cytoplasm of the ovule (egg cell) from the maternal parent.
- Therefore, if the female parent has a variegated branch, the progeny's phenotype will depend on the specific type of plastids present in the egg cell that contributes to the zygote.
- A variegated branch contains a mixture of chloroplasts (some normal, some mutant). If an egg from such a branch has only normal chloroplasts, the offspring will be green. If it has only mutant (white) chloroplasts, the offspring will be white (and usually lethal or require a green parent for survival). If it has a mixture of both, the offspring will be variegated.
- Thus, progeny from a variegated branch can indeed show three different phenotypes (green, white, variegated), but this is due to the segregation of different types of plastids during gamete formation, not a Mendelian ratio of three distinct phenotypes in a single cross. The key is the maternal inheritance pattern, not a typical nuclear gene segregation.

- (ii) Bridges experiment was conclusive proof for the chromosomal theory of inheritance.
  - This statement is accurate and significant in genetics.
  - Calvin Bridges' experiments with *Drosophila melanogaster* in 1916 provided definitive evidence for the chromosomal theory of inheritance, specifically demonstrating that genes are located on chromosomes.

- He studied exceptions to normal X-linked inheritance, specifically the non-disjunction of X chromosomes in female *Drosophila*.
- Bridges observed that white-eyed female *Drosophila*, when crossed with red-eyed males, occasionally produced white-eyed females and red-eyed males in the F1 generation, which was contrary to standard X-linked inheritance patterns.
- Upon examining the chromosomes of these exceptional flies, he found a direct correlation: the exceptional white-eyed females had two X chromosomes and a Y chromosome (XXY), while the exceptional red-eyed males had a single X chromosome but no Y chromosome (XO).
- This direct correlation between an abnormal chromosomal constitution and an abnormal phenotypic outcome proved that the genes for eye color were physically located on the X chromosome and that the segregation of these genes mirrored the segregation of the chromosomes themselves. This provided irrefutable proof that chromosomes carry the hereditary factors (genes).

- (iii) In a dihybrid cross a ratio of 9:3:3:1 can be both a Mendelian as well as Non-Mendelian inheritance.
  - This statement is correct.
  - **Mendelian Inheritance:** The 9:3:3:1 phenotypic ratio is the classic expected outcome of a dihybrid cross between two heterozygotes (e.g., AaBb x AaBb) where two genes are assorting independently and exhibit complete dominance for both traits. This is the cornerstone of Mendel's Law of Independent Assortment.
  - **Non-Mendelian Inheritance:** While the 9:3:3:1 ratio is Mendelian, modified versions of this ratio can also arise from

non-Mendelian interactions, specifically various forms of epistasis.

- For example, in **duplicate recessive epistasis (complementary gene action)**, if two genes are required for a phenotype and the presence of a recessive allele at either locus masks the expression of the dominant allele at the other locus, a cross between two dihybrids could result in a 9:7 phenotypic ratio. While not 9:3:3:1, it's a modification of the basic dihybrid ratio due to gene interaction.
- More precisely, **duplicate dominant epistasis** (e.g., 15:1 ratio) or **recessive epistasis** (e.g., 9:3:4 ratio) are examples of non-Mendelian inheritance patterns that deviate from 9:3:3:1.
- However, the question implies that the *exact* 9:3:3:1 ratio *itself* can be non-Mendelian. This is generally **false** for the classic 9:3:3:1 phenotypic ratio. The 9:3:3:1 phenotypic ratio is the hallmark of Mendelian independent assortment with complete dominance. If gene interactions (epistasis) occur, the 9:3:3:1 ratio is typically *modified* into other ratios (e.g., 9:3:4, 12:3:1, 15:1, 9:7).
- Perhaps the statement refers to cases where the *underlying genetic mechanism* is more complex than simple Mendelian inheritance (e.g., involving tightly linked genes that behave as one unit, or complex interactions that coincidentally produce these ratios in specific contexts), but the *phenotypic outcome* still *appears* as 9:3:3:1. However, in standard genetics, 9:3:3:1 *phenotypic* ratio is considered Mendelian. If one considers cases where lethal alleles or other factors might *coincidentally* lead to such a ratio from a more complex

interaction, it's a stretch. The most common interpretation of 9:3:3:1 is strictly Mendelian.

- (iv) Recombination frequency cannot exceed 50%.
    - This statement is accurate.
    - Recombination frequency (RF) is a measure of genetic linkage and represents the proportion of recombinant gametes produced.
    - When two genes are located on different chromosomes or are very far apart on the same chromosome, they assort independently. In this scenario, due to independent assortment, 50% of the gametes will be parental types and 50% will be recombinant types. This means the recombination frequency will be 50%.
    - Even if multiple crossovers occur between two distantly linked genes on the same chromosome, the observed recombination frequency will not exceed 50%. This is because multiple crossovers can cancel each other out (e.g., a double crossover can restore the original parental configuration), making it appear as if no recombination occurred or underestimating the true genetic distance.
    - Therefore, a recombination frequency of 50% is the maximum observable frequency and is indistinguishable from independent assortment.
- (v) Complementation tests are used to identify gene interactions.
    - This statement is generally **incorrect** or at least misleading in its primary purpose.
    - Complementation tests (also known as cis-trans tests) are primarily used to determine if two mutations that produce the same phenotype (e.g., two different mutations causing a white-

eye phenotype in *Drosophila*) are located in the *same gene* or in *different genes*.

- If two mutations are in different genes (i.e., they are allelic to different genes), crossing two individuals homozygous for each mutation will result in a wild-type phenotype in the progeny (complementation occurs) because each parent provides a functional copy of the gene that the other parent has mutated.
- If the two mutations are in the same gene (i.e., they are alleles of the same gene), no complementation will occur, and the progeny will still display the mutant phenotype.
- While understanding *which genes* are involved can indirectly inform about pathways and potential interactions, the direct purpose of a complementation test is not to identify gene *interactions* (like epistasis), but rather to identify the number of genes involved in a specific mutant phenotype. Gene interactions (epistasis) are typically identified through dihybrid crosses and observing modified Mendelian ratios.

- (vi) Genetic imprinting is an example of a nonrandom monoallelic expression.
  - This statement is accurate.
  - Genetic imprinting (or genomic imprinting) is an epigenetic phenomenon where certain genes are expressed in a parent-of-origin-specific manner. This means that either the allele inherited from the mother or the allele inherited from the father is silenced, while the other allele is expressed.
  - This silencing occurs through epigenetic modifications, such as DNA methylation or histone modifications, that are established in the germline and maintained throughout development.
  - Because only one of the two alleles (maternal or paternal) is expressed, while the other is silenced, it is a clear example of

nonrandom monoallelic expression. This is distinct from random monoallelic expression, such as X-inactivation in females, where either the maternal or paternal X chromosome is randomly silenced in different cells.

2. (a) Differentiate between:

- (i) Uniparental inheritance and uniparental disomy.
    - **Uniparental Inheritance:**
        - Refers to inheritance of traits where only one parent contributes the genetic material for a particular characteristic.
        - Most commonly observed with organellar DNA, such as mitochondrial DNA (mtDNA) and chloroplast DNA (cpDNA). In humans and many other organisms, mitochondria are inherited exclusively from the mother (maternal inheritance).
        - There is no contribution from the paternal gamete for these specific genetic elements.
        - Example: All mitochondrial disorders in humans are inherited from the mother.
    - **Uniparental Disomy (UPD):**
        - A condition where an individual receives both copies of a chromosome pair, or part of a chromosome, from only one parent, instead of one copy from each parent.
        - This can occur through various mechanisms during meiosis or early embryonic development (e.g., trisomy rescue where one chromosome is lost, leading to two copies from one parent).
        - UPD does not necessarily lead to a phenotype unless it involves an imprinted gene (where the gene's expression

depends on its parental origin) or if the single parent contributed two copies of a chromosome carrying a recessive mutation, leading to a homozygous recessive condition.

- Example: Prader-Willi syndrome (often due to paternal UPD of chromosome 15) and Angelman syndrome (often due to maternal UPD of chromosome 15).

- (ii) Continuous and discontinuous variation.
  - **Continuous Variation:**
    - Refers to phenotypic traits that show a wide range of intermediate values between two extremes, with no distinct categories.
    - Typically influenced by multiple genes (polygenic inheritance) and often significantly affected by environmental factors.
    - Can be measured quantitatively.
    - Examples: Human height, weight, skin color, milk yield in cows. When plotted, usually forms a continuous distribution (e.g., bell curve).
  - **Discontinuous Variation:**
    - Refers to phenotypic traits that fall into distinct, separate categories with no intermediate forms.
    - Typically controlled by one or a few genes with major effects and are less influenced by environmental factors.
    - Can be described qualitatively.
    - Examples: Human blood groups (A, B, AB, O), presence or absence of a specific genetic disorder (e.g., albinism),

flower color in pea plants (red or white). When plotted, usually forms discrete bars.

- (iii) Hemizygous and heterozygous.
    - **Hemizygous:**
        - Describes a condition in which an individual has only one copy of a gene or a chromosomal segment, rather than the usual two.
        - This is most commonly observed for genes located on sex chromosomes in the heterogametic sex (e.g., males (XY) are hemizygous for genes on the X chromosome because they only have one X).
        - Since there's only one copy, the phenotype associated with that gene is expressed regardless of whether the allele is dominant or recessive.
        - Example: A male with a gene for color blindness on his X chromosome is hemizygous for that gene.
    - **Heterozygous:**
        - Describes a condition in which an individual possesses two different alleles for a particular gene (one dominant and one recessive, or two different co-dominant alleles).
        - These alleles are located at the same locus on homologous chromosomes.
        - Example: An individual with genotype Aa for a particular trait. In cases of complete dominance, the dominant phenotype is expressed.
- (iv) Incomplete dominance and codominance.
    - **Incomplete Dominance:**

        - A form of intermediate inheritance in which one allele is not completely dominant over the other, leading to a blended or intermediate phenotype in the heterozygote.
        - The heterozygous phenotype is distinct from and often an intermediate of the two homozygous phenotypes.
        - Neither allele is fully expressed over the other.
        - Example: In *Mirabilis jalapa* (four o'clock plant), a cross between homozygous red flowers (RR) and homozygous white flowers (WW) produces F1 heterozygous pink flowers (RW).
    - **Codominance:**
        - A form of inheritance in which both alleles in a heterozygote are fully and simultaneously expressed, without blending.
        - The phenotypes of both homozygous parents are distinctly visible in the heterozygote.
        - Example: ABO blood group system in humans, where A and B alleles are codominant. An individual with AB blood type expresses both A and B antigens on their red blood cells.

- (v) Chromosomal sex determination and genic sex determination.
    - **Chromosomal Sex Determination:**
        - Sex is determined by the presence or absence of specific chromosomes, or by the ratio of sex chromosomes to autosomes.
        - The most common systems involve sex chromosomes (e.g., XY, ZW, XO).

- In **XY system** (e.g., humans, *Drosophila*), males are XY and females are XX.
- In **ZW system** (e.g., birds, butterflies), females are ZW and males are ZZ.
- In **XO system** (e.g., grasshoppers), males are XO and females are XX.
- The sex chromosomes carry specific genes (like SRY in humans) that initiate the development of either male or female characteristics.

- **Genic Sex Determination:**
  - Sex is determined by specific genes located on autosomes, without distinct sex chromosomes.
  - The combination of alleles at one or more gene loci determines the sex of the individual.
  - Environmental factors can sometimes influence the expression of these genes, or there might be a balance of male-determining and female-determining genes on autosomes.
  - Less common than chromosomal systems, but found in some plants, fungi, and protozoa.
  - Example: In some species of fungi (e.g., *Chlamydomonas*), mating types are determined by alleles at a single locus.

- (vi) Pre and post reproductive isolation.
  - **Pre-Reproductive Isolation (Pre-zygotic isolation):**
    - Mechanisms that prevent mating or fertilization from occurring between individuals of different species. These barriers act *before* the formation of a zygote.

- Examples:
    - **Habitat isolation:** Species live in different habitats and do not encounter each other.
    - **Temporal isolation:** Species breed at different times of day or year.
    - **Behavioral isolation:** Differences in courtship rituals or other behaviors prevent interbreeding.
    - **Mechanical isolation:** Anatomical differences prevent successful copulation.
    - **Gametic isolation:** Gametes of different species are incompatible and cannot fuse to form a zygote.

- **Post-Reproductive Isolation (Post-zygotic isolation):**
    - Mechanisms that prevent the formation of fertile offspring *after* fertilization has occurred between individuals of different species. These barriers act *after* the formation of a zygote.
    - Examples:
        - **Hybrid inviability:** Hybrid zygote fails to develop or dies before reaching reproductive maturity.
        - **Hybrid sterility:** Hybrid offspring is healthy but infertile (e.g., mules are sterile hybrids of horses and donkeys).
        - **Hybrid breakdown:** First-generation hybrids are viable and fertile, but subsequent generations (F2 or backcrosses) become sterile or inviable.

3. (b) Albinism in humans is a recessive condition. What would be the probability of two out of the five children having albinism if both of their parents are carriers?

- Let 'A' be the dominant allele for normal pigmentation and 'a' be the recessive allele for albinism.
- Parents are carriers, meaning both are heterozygous (Aa).
- The cross is Aa x Aa.
- The possible genotypes and their probabilities for each child are:
    - AA (Normal): 1/4
    - Aa (Normal carrier): 1/2
    - aa (Albino): 1/4
- The probability of a child having albinism (aa) is $p = 1/4$.
- The probability of a child being normal (AA or Aa) is $q = 3/4$.
- We need to find the probability of exactly two out of five children having albinism. This is a binomial probability problem.
- The formula for binomial probability is: $P(X = k) = C(n, k) * p^k * q^{(n-k)}$
    - Where:
        - n = total number of trials (children) = 5
        - k = number of successful outcomes (children with albinism) = 2
        - p = probability of success (child with albinism) = 1/4
        - q = probability of failure (child without albinism) = 3/4
        - $C(n, k)$ = "n choose k" = $n!/(k! * (n - k)!)$
- Calculate $C(5,2)$:
    - $C(5,2) = 5!/(2! * (5 - 2)!) = 5!/(2! * 3!) = (5 * 4 * 3 * 2 * 1)/((2 * 1) * (3 * 2 * 1)) = (5 * 4)/2 = 10$

- Calculate p^k:
    - $(1/4)^2 = 1/16$
- Calculate $q^{(n-k)}$:
    - $(3/4)^{(5-2)} = (3/4)^3 = 27/64$
- Now, calculate the final probability:
    - $P(X = 2) = 10 * (1/16) * (27/64)$
    - $P(X = 2) = 10 * 27/(16 * 64)$
    - $P(X = 2) = 270/1024$
    - $P(X = 2) = 135/512$
- The probability of two out of the five children having albinism is $135/512$.

3. (a) What is dosage compensation? Differentiate between the dosage compensation mechanism in humans and *Drosophila*.

- **Dosage Compensation:**
    - Dosage compensation is a genetic mechanism that ensures that males and females, despite having different numbers of sex chromosomes, express equivalent amounts of gene products (proteins) from genes located on their sex chromosomes.
    - This mechanism prevents harmful effects that would arise from an imbalance in gene dosage between the sexes, as an excess or deficiency of gene products can be detrimental.
- **Differentiation between Dosage Compensation in Humans and *Drosophila*:**
    - **Humans (XX/XY system):**

- **Mechanism:** X-inactivation (also known as Lyonization).
- **Process:** In somatic cells of females (XX), one of the two X chromosomes is randomly inactivated during early embryonic development. This inactivated X chromosome becomes a condensed structure called a Barr body.
- **Outcome:** Each female cell effectively functions with only one active X chromosome, similar to males (XY) who naturally have only one X chromosome. This ensures equal expression of X-linked genes in both sexes.
- **Randomness:** The choice of which X chromosome (maternal or paternal) to inactivate is random in each cell, leading to a mosaic pattern of gene expression in heterozygous females.
- **Partial Escape:** Some genes on the inactivated X chromosome (about 15-25%) manage to escape inactivation, particularly those located in the pseudoautosomal regions or other specific loci.

- ***Drosophila* (XX/XY system, but different mechanism):**
  - **Mechanism:** Hypertranscription of the single X chromosome in males.
  - **Process:** In males (*Drosophila* are XO or XY, but the Y chromosome is largely heterochromatic and does not play a major role in dosage compensation of X-linked genes), the single X chromosome is transcriptionally upregulated or "doubled" in its activity.
  - **Outcome:** The single X chromosome in males produces roughly twice the amount of gene product compared to a single X chromosome in females, thereby achieving equal dosage with the two active X chromosomes (or one active X chromosome with the other inactivated) in females.

- **Complex:** This process involves a complex of proteins called the Male Specific Lethal (MSL) complex, which binds to specific sites on the X chromosome in males and promotes chromatin remodeling and increased transcription.
- **No X-inactivation:** *Drosophila* females do not undergo X-inactivation; both X chromosomes are active.

4. (b) With a suitable example explain how the alleles encoding different traits separate independently. Show the genotypes as well as phenotypes.

- **Law of Independent Assortment:**
  - Mendel's Law of Independent Assortment states that during gamete formation, the alleles of different genes assort independently of one another. This means that the inheritance of one trait does not influence the inheritance of another trait, as long as the genes for these traits are located on different chromosomes or are far apart on the same chromosome.

- **Example: Dihybrid Cross in Pea Plants**
  - Let's consider two traits in pea plants:
    - Seed shape: Round (R) is dominant over wrinkled (r)
    - Seed color: Yellow (Y) is dominant over green (y)
- **Parental Generation (P):**
  - We cross a true-breeding plant with Round, Yellow seeds (homozygous dominant: RRYY) with a true-breeding plant with wrinkled, green seeds (homozygous recessive: rryy).
  - **P Genotypes:** RRYY x rryy
  - **P Phenotypes:** Round, Yellow x wrinkled, green

- **F1 Generation:**
  - The RRYY parent produces only RY gametes.
  - The rryy parent produces only ry gametes.
  - When these gametes fuse, all F1 offspring will be heterozygous for both traits.
  - **F1 Genotype:** RrYy
  - **F1 Phenotype:** All F1 plants will have Round, Yellow seeds (because R and Y are dominant).
- **F2 Generation (Self-pollination of F1):**
  - Now, we self-pollinate the F1 generation (RrYy x RrYy).
  - For independent assortment to occur, the alleles for seed shape (R/r) and seed color (Y/y) must segregate independently into gametes.
  - Each RrYy plant will produce four types of gametes in equal proportions:
    - RY (1/4)
    - Ry (1/4)
    - rY (1/4)
    - ry (1/4)
- **Punnett Square for F2 Generation:**

Gametes	RY	Ry	rY	ry
RY	RRYY	RRYy	RrYY	RrYy
Ry	RRYy	RRyy	RrYy	Rryy
rY	RrYY	RrYy	rrYY	rrYy

Gametes	RY	Ry	rY	ry
ry	RrYy	Rryy	rrYy	rryy

- **F2 Genotypes and Phenotypes (and their ratios):**
  - **Genotypes:**
    - 1 RRYY
    - 2 RRYy
    - 2 RrYY
    - 4 RrYy
    - 1 RRyy
    - 2 Rryy
    - 1 rrYY
    - 2 rrYy
    - 1 rryy
    - (Genotypic Ratio: 1:2:2:4:1:2:1:2:1)
  - **Phenotypes:**
    - **Round, Yellow (R_Y_):** RRYY, RRYy, RrYY, RrYy
      - Count: 1 + 2 + 2 + 4 = 9
      - Phenotype: Round, Yellow
    - **Round, green (R_yy):** RRyy, Rryy
      - Count: 1 + 2 = 3
      - Phenotype: Round, green
    - **wrinkled, Yellow (rrY_):** rrYY, rrYy

        - Count: 1 + 2 = 3
        - Phenotype: wrinkled, Yellow
    - **wrinkled, green (rryy):** rryy
        - Count: 1
        - Phenotype: wrinkled, green

- **F2 Phenotypic Ratio:** 9:3:3:1
- **Explanation of Independent Assortment:**
    - The observation of the 9:3:3:1 phenotypic ratio in the F2 generation demonstrates that the alleles for seed shape (R/r) and seed color (Y/y) segregated and recombined independently of each other.
    - If they had been linked and inherited together, we would have seen a different ratio (e.g., primarily parental phenotypes).
    - This example perfectly illustrates that the genes controlling different traits are inherited independently, leading to new combinations of traits in the offspring that were not present in the original parental generation (e.g., Round, green and wrinkled, Yellow seeds).

5. (c) Two plants with white flowers, each from true breeding strains, were crossed. All the F1 plants had red flowers. When these F1 plants were intercrossed, they produced F2 plants consisting of 177 plants with red flowers and 142 with white flowers. (i) Propose an explanation for inheritance of flower color in this plant species and (ii) Propose a biochemical pathway for this flower pigmentation.

- **Analysis of the Cross:**
    - P: White x White (true breeding)
    - F1: All Red

- F2: 177 Red : 142 White
    - Approximate ratio: 177/142 ≈ 1.25. This is roughly a 9:7 ratio if we consider a total of 319 plants (177+142), then 177/319 ≈ 0.55 (9/16) and 142/319 ≈ 0.44 (7/16). This strongly suggests a 9:7 phenotypic ratio.

- **(i) Propose an explanation for inheritance of flower color in this plant species:**
    - The observation that two different true-breeding white parents produce all red F1 offspring, and then the F2 generation shows a 9:7 red:white ratio, is a classic indication of **duplicate recessive epistasis**, also known as **complementary gene action**.
    - **Explanation:** This type of epistasis occurs when two genes interact such that the presence of at least one dominant allele for *each* gene is required to produce a specific phenotype (in this case, red color). If either gene is homozygous recessive, the product of the biochemical pathway is not formed or is non-functional, resulting in the alternative phenotype (white color).
    - **Genotypes:**
        - Let's assume two genes, A and B, control flower color.
        - The red pigment is only produced when dominant alleles are present at both loci.
        - Red flower genotype: A_B_ (e.g., AABB, AABb, AaBB, AaBb)
        - White flower genotype: aaB_, A_bb, or aabb (i.e., homozygous recessive for at least one of the two genes).
    - **Parental Cross (P):**
        - Since the F1 are all red (A_B_), and the parents were true-breeding white, the parents must have been

homozygous recessive for one of the genes and homozygous dominant for the other.

- P Genotypes: AAbb (white) x aaBB (white)
- P Gametes: Ab x aB

- **F1 Generation:**
  - F1 Genotype: AaBb
  - F1 Phenotype: All Red flowers (as they have both A and B dominant alleles).
- **F2 Generation (Self-cross of F1: AaBb x AaBb):**
  - The standard dihybrid cross phenotypic ratio is 9:3:3:1 for two independently assorting genes.
  - Under complementary gene action (duplicate recessive epistasis):
    - 9/16 A_B_ → Red flowers
    - 3/16 A_bb → White flowers (A is present, but B is recessive)
    - 3/16 aaB_ → White flowers (B is present, but A is recessive)
    - 1/16 aabb → White flowers (both are recessive)
  - Therefore, the F2 phenotypic ratio is 9 Red : (3+3+1) White = 9 Red : 7 White. This matches the observed ratio of 177 Red : 142 White.

- **(ii) Propose a biochemical pathway for this flower pigmentation:**
  - This pigmentation pathway would involve at least two sequential steps, each catalyzed by an enzyme controlled by a different gene.

- **Proposed Pathway:**
  - **Precursor (Colorless)** $\xrightarrow{\text{Enzyme A (Gene A)}}$ **Intermediate Product (Colorless)** $\xrightarrow{\text{Enzyme B (Gene B)}}$ **Red Pigment**
- **Explanation:**
  - **Gene A** codes for Enzyme A. If an individual is homozygous recessive for gene A (aa), Enzyme A is non-functional, and the colorless precursor cannot be converted to the intermediate product. Thus, no red pigment is formed, and the flower remains white, regardless of the alleles at gene B.
  - **Gene B** codes for Enzyme B. If an individual is homozygous recessive for gene B (bb), Enzyme B is non-functional, and the colorless intermediate product cannot be converted to the red pigment. Thus, no red pigment is formed, and the flower remains white, regardless of the alleles at gene A.
  - Only when both Enzyme A (requiring at least one dominant A allele) and Enzyme B (requiring at least one dominant B allele) are functional can the pathway proceed to produce the red pigment.
  - The two white true-breeding parents would represent individuals that are blocked at different steps in this pathway. For example, AAbb produces a non-functional Enzyme B, and aaBB produces a non-functional Enzyme A. Their F1 (AaBb) has both functional enzymes, allowing the pathway to complete and produce red pigment.

6. (d) A color blind man married a homozygous normal woman. After 2 years they had 2 children but unfortunately, they both had Turners syndrome, although one had normal vision the other was colorblind. What accounts for this situation.

- **Understanding the Conditions:**
    - **Color Blindness:** This is an X-linked recessive trait.
        - Normal vision allele: X^N
        - Colorblind allele: X^n
        - Males (XY) are hemizygous. A male with X^nY is colorblind.
        - Females (XX) are colorblind if X^nX^n. They are normal vision if X^NX^N or X^NX^n. A female X^NX^n is a carrier.
    - **Turner Syndrome:** This is a chromosomal disorder in females characterized by the presence of only one X chromosome (XO genotype). Individuals with Turner syndrome are phenotypically female, often with specific physical characteristics, and are typically infertile. It results from nondisjunction of sex chromosomes during gamete formation in either parent.

- **Analyzing the Parents:**
    - **Father:** Colorblind man. His genotype is X^nY.
    - **Mother:** Homozygous normal woman. Her genotype is X^NX^N.
- **Expected Offspring from Normal Meiosis:**
    - If normal meiosis occurred, the father would produce X^n and Y gametes. The mother would produce only X^N gametes.
    - All daughters would be X^NX^n (normal vision carriers).
    - All sons would be X^NY (normal vision).
- **The Observed Situation:**
    - Both children have Turner Syndrome (XO).
    - Child 1: Turner Syndrome with normal vision.

- Child 2: Turner Syndrome with colorblindness.

- **Explanation for this situation:**
  - Since both children have Turner Syndrome (XO), it means that in both cases, the egg or sperm that contributed to their formation lacked a sex chromosome (was "nullo-X" or "nullo-Y"). Specifically, for Turner Syndrome, the individual receives only one X chromosome, and the other sex chromosome is missing.
  - For the children to be XO, one parent must have contributed an X chromosome, and the other parent must have contributed a gamete that was nullisomic for sex chromosomes (contained neither an X nor a Y).
  - **Child 1 (Normal Vision, Turner Syndrome - X^NO):**
    - This child must have received the normal vision X^N chromosome from the mother.
    - The father must have contributed a gamete lacking a sex chromosome (a "nullo-XY" sperm). This occurs due to nondisjunction during meiosis in the father.
    - So, the mother contributed X^N, and the father contributed 'O' (no sex chromosome).
    - Mother: X^NX^N (Normal meiosis produces X^N egg)
    - Father: X^nY (Nondisjunction produces 'O' sperm)
    - Fertilization: X^N (from mother) + 'O' (from father) → X^NO (Normal vision, Turner Syndrome)
  - **Child 2 (Colorblind, Turner Syndrome - X^nO):**
    - This child must have received the colorblind X^n chromosome from the father.

  - The mother must have contributed a gamete lacking a sex chromosome (a "nullo-XX" egg). This occurs due to nondisjunction during meiosis in the mother.
  - So, the father contributed X^n, and the mother contributed 'O' (no sex chromosome).
  - Mother: $X^N X^N$ (Nondisjunction produces 'O' egg)
  - Father: $X^n Y$ (Normal meiosis produces X^n sperm)
  - Fertilization: 'O' (from mother) + X^n (from father) → $X^n O$ (Colorblind, Turner Syndrome)

- **Conclusion:**
  - The occurrence of two Turner Syndrome children, one normal vision and one colorblind, points to independent nondisjunction events in both parents.
  - The normal vision Turner child resulted from nondisjunction in the father (leading to 'O' sperm) and a normal X-bearing egg from the mother.
  - The colorblind Turner child resulted from nondisjunction in the mother (leading to 'O' egg) and a normal X-bearing sperm from the father.
  - This scenario highlights how chromosomal abnormalities (nondisjunction) can lead to unexpected combinations of sex chromosomes and X-linked traits.

4. (a) The first chromosome to be mapped is the X chromosome of *Drosophila*. Why does mapping the X chromosome not require a tester while for an autosomal map a test cross is essential? What do you understand by the terms map function and Lod score?

- **Why mapping the X chromosome in *Drosophila* does not require a tester, while an autosomal map requires a test cross:**

- **X Chromosome Mapping (in *Drosophila*):**
  - In *Drosophila*, males are XY and females are XX. Males are **hemizygous** for genes on the X chromosome, meaning they only have one copy of each X-linked gene.
  - When performing linkage analysis for X-linked genes, a female heterozygous for the genes of interest (e.g., $X^{AB}X^{ab}$) is crossed with a male that will allow the direct observation of the female's recombinant gametes. A male with any X-linked genotype can serve this purpose, but often a wild-type male ($X^{AB}Y$) or a male with recessive alleles ($X^{ab}Y$) is chosen for ease of scoring.
  - The key is that the male offspring receive their single X chromosome *only* from their mother. Therefore, the phenotype of the male offspring directly reflects the genotype of the X chromosome contributed by the mother's gamete (recombinant or non-recombinant). There is no "masking" by a second X chromosome or a dominant allele from the father, as would be the case in female offspring or autosomal crosses.
  - Thus, the males serve as a "natural tester" because their single X chromosome directly reveals the alleles they received from their mother, making a separate homozygous recessive tester strain for the father unnecessary to assess recombination on the X.
- **Autosomal Map (requiring a test cross):**
  - Autosomal genes are present in two copies in both males and females (e.g., AA, Aa, aa).
  - To observe recombination frequencies between two autosomal genes, you need to cross a dihybrid individual (heterozygous for both genes, e.g., AaBb) with an individual whose genotype allows the expression of all

possible recombinant and non-recombinant gametes produced by the dihybrid.

- A **test cross** involves crossing the dihybrid with a homozygous recessive individual for both genes (aabb).
- The homozygous recessive tester (aabb) produces only 'ab' gametes. When these fuse with the gametes from the dihybrid (AB, Ab, aB, ab), the phenotypes of the offspring directly reflect the genotype of the gamete contributed by the dihybrid parent.
- For example, if the dihybrid produces an 'Ab' gamete, crossing with 'ab' results in 'Aabb' offspring, whose phenotype (A_bb) reveals the recombination. If a dominant individual were used as the second parent, the recessive phenotypes would be masked, making it impossible to distinguish recombinant from non-recombinant gametes. Therefore, a specific homozygous recessive tester is essential for autosomal mapping to directly visualize all products of meiosis from the heterozygous parent.

- **Map function:**
  - A map function is a mathematical formula that relates the observed recombination frequency (which can underestimate the true genetic distance due to multiple crossovers) to the actual genetic distance (measured in centimorgans, cM or map units).
  - When genes are far apart on a chromosome, multiple crossovers can occur between them. If an even number of crossovers occurs, it can result in a parental arrangement of alleles, leading to an underestimation of the true number of recombination events and thus the genetic distance.

- Map functions (e.g., Haldane's map function, Kosambi's map function) correct for this underestimation by accounting for multiple crossovers. They convert the observed recombination frequency into a more accurate measure of the genetic distance.
- For example, Haldane's map function: $x = -1/2\ln(1 - 2r)$, where 'r' is the observed recombination frequency and 'x' is the true map distance in morgans.
- Different map functions make different assumptions about the occurrence and interference of crossovers.

- **Lod score (Logarithm of the odds):**
  - The Lod score is a statistical test used in linkage analysis to determine the probability that two genes are linked (i.e., located close together on the same chromosome) versus being unlinked (i.e., assorting independently).
  - It is the logarithm (base 10) of the ratio of two probabilities:
    - Probability that the observed pedigree data occurred if the genes are linked with a specific recombination frequency (θ).
    - Probability that the observed pedigree data occurred if the genes are unlinked ($\theta = 0.5$).
  - Formula: $Z(\theta) = \log_{10}$[Likelihood (linked at θ)/ Likelihood (unlinked, $\theta = 0.5$)]
  - **Interpretation:**
    - A Lod score of +3.0 or greater is generally considered strong evidence for linkage. This means the odds are 1000:1 (10^3) in favor of linkage over independent assortment.

        - A Lod score of -2.0 or less is generally considered strong evidence against linkage.
    - Lod scores are particularly useful in human genetic mapping because controlled crosses are not possible, and large pedigrees are often analyzed to infer linkage.

5. (b) What are different modes of speciation? Explain.

- **Speciation** is the evolutionary process by which new biological species arise. It involves the splitting of a single evolutionary lineage into two or more distinct species. The primary requirement for speciation is reproductive isolation between populations.
- **Different Modes of Speciation:**
    - **1. Allopatric Speciation:**
        - **Explanation:** This is the most common mode of speciation. It occurs when a physical geographic barrier (e.g., mountain range, river, ocean, desert, continental drift) separates a single population into two or more geographically isolated populations.
        - **Process:**
            - **Geographic Isolation:** Prevents gene flow between the isolated populations.
            - **Divergence:** Over time, these isolated populations evolve independently due to:
                - **Mutation:** Different random mutations arise in each population.
                - **Natural Selection:** Different environmental pressures (climate, predators, food sources) in each isolated area favor different traits.

- **Genetic Drift:** Random changes in allele frequencies (especially significant in small populations).

- **Reproductive Isolation:** Eventually, the genetic and phenotypic differences accumulate to the point where, even if the geographic barrier is removed and the populations come into contact again, they can no longer interbreed successfully (i.e., reproductive isolation occurs).

- **Example:** The formation of separate species of squirrels on opposite sides of the Grand Canyon.

- **2. Sympatric Speciation:**

  - **Explanation:** This mode of speciation occurs without geographic isolation. New species arise from a single ancestral population while inhabiting the same geographic area.

  - **Process:**

    - Requires strong reproductive isolating mechanisms to arise *within* the population, preventing gene flow among individuals.

    - **Mechanisms:**

      - **Polyploidy:** Most common in plants. An increase in the number of sets of chromosomes (e.g., from diploid to tetraploid). Polyploid individuals are often reproductively isolated from their diploid ancestors because their gametes are incompatible.

      - **Disruptive Selection:** Individuals with extreme phenotypes are favored over

intermediate ones, leading to the evolution of two distinct forms within the same population.

- **Habitat Differentiation/Resource Partitioning:** A subset of the population may exploit a new niche or food source within the same geographic area, leading to reproductive isolation from the parent population.
- **Sexual Selection:** Strong preference for certain mates can lead to reproductive isolation and new species.

- **Example:** Cichlid fish in African lakes, which have diversified into many species within the same lake due to sexual selection and niche specialization. Polyploidy in many plant species.

- **3. Parapatric Speciation:**
  - **Explanation:** This occurs when populations are not completely geographically isolated but have adjacent distributions with a narrow zone of contact and overlap. Gene flow is limited but not completely absent.
  - **Process:**
    - **Partial Isolation:** Gene flow is restricted due to distance or differences in selection pressures across a habitat gradient.
    - **Strong Selection:** Strong selection pressures at the ends of the range, often combined with reduced gene flow in the contact zone, lead to divergence. Hybrids in the contact zone may have reduced fitness.

- **Reinforcement:** Natural selection may favor reproductive isolation mechanisms that reduce the production of unfit hybrids.

- **Example:** Grasses growing in and around contaminated soil. Those adapted to the contaminated soil may evolve partial reproductive isolation from those in uncontaminated soil, even with a continuous distribution.

- **4. Peripatric Speciation:**

  - **Explanation:** A special case of allopatric speciation. It occurs when a small group of individuals breaks off from a larger, widespread population to form a new, isolated population at the periphery of the ancestral range.

  - **Process:**

    - **Founder Effect:** The small founder population carries only a subset of the genetic variation of the original population.

    - **Genetic Drift:** Due to its small size, genetic drift plays a more significant role, leading to rapid and random changes in allele frequencies.

    - **Strong Selection:** The peripheral environment may have different selection pressures.

    - These factors can lead to rapid divergence and reproductive isolation from the main population.

  - **Example:** The speciation of polar bears from brown bears; a small population of brown bears became isolated in the Arctic region, leading to rapid adaptation and speciation.

6. (c) Four alleles of the Agouti gene are known to control coat colour in mice. The alleles form a dominance series Ay > A > al > a. A

researcher investigating mouse genetics traps a wild male mouse showing yellow coat colour. If the wild mouse's coat is due to Ay, describe and explain a single mating experiment that would identify the other Agouti allele.

- **Background:**
    - Agouti gene alleles: Ay > A > al > a (Dominance series)
    - Ay: Yellow (dominant to all others, but lethal in homozygous dominant state - AyAy is lethal)
    - A: Agouti (wild type, banded hairs)
    - al: Light belly agouti
    - a: Non-agouti (black)
    - The trapped wild male mouse has a yellow coat color, meaning its genotype must be Ay_ (where '_' is the unknown allele). Since AyAy is lethal, its genotype must be **AyX**, where X is A, al, or a. We need to identify X.
- **Mating Experiment:**
    - **Strategy:** To identify the unknown allele (X) carried by the yellow male (AyX), we need to cross it with a female mouse whose genotype will allow the expression of the recessive alleles (A, al, or a) if they are present in the yellow male. The best "tester" mouse for this purpose is one that is homozygous recessive for the most recessive allele in the series, which is 'a'.
    - **Cross:** Cross the wild male mouse (AyX) with a homozygous non-agouti (black) female mouse (aa).
    - **Genotypes of Parents:** AyX (yellow male) x aa (black female)
- **Expected Outcomes and Explanation:**
    - The female (aa) will produce only 'a' gametes.

- The yellow male (AyX) will produce two types of gametes: Ay and X (where X can be A, al, or a).
- The F1 progeny will depend on the 'X' allele:
- **Scenario 1: If the wild male's genotype is AyA (Yellow carrying Agouti)**
    - Gametes from male: Ay (1/2), A (1/2)
    - Gametes from female: a (1)
    - F1 Progeny:
        - Ay a (Yellow): 1/2
        - Aa (Agouti): 1/2
    - **Observation:** The progeny will be approximately half yellow and half agouti.
- **Scenario 2: If the wild male's genotype is Ayal (Yellow carrying Light belly agouti)**
    - Gametes from male: Ay (1/2), al (1/2)
    - Gametes from female: a (1)
    - F1 Progeny:
        - Ay a (Yellow): 1/2
        - al a (Light belly agouti): 1/2
    - **Observation:** The progeny will be approximately half yellow and half light belly agouti.
- **Scenario 3: If the wild male's genotype is Aya (Yellow carrying Non-agouti)**
    - Gametes from male: Ay (1/2), a (1/2)
    - Gametes from female: a (1)

    - F1 Progeny:
        - Ay a (Yellow): 1/2
        - aa (Non-agouti / Black): 1/2
    - **Observation:** The progeny will be approximately half yellow and half black.

- **Conclusion:** By observing the phenotypes of the offspring from this single mating experiment, the researcher can definitively determine the unknown Agouti allele (X) carried by the wild yellow male mouse. The non-yellow offspring will reveal the specific recessive allele (A, al, or a) that the male carries.

7. (d) What is somatic cell hybridization? The following data shows different cell lines which were created from human mouse somatic cell fusions. Each line was examined for the presence of human chromosomes and for the production of human haptoglobin. The following results were obtained:

- **Somatic Cell Hybridization:**
    - Somatic cell hybridization is a technique used in genetics and cell biology to fuse two somatic cells (non-gamete cells) from different species to form a hybrid cell.
    - **Process:** Typically, cells from two different species (e.g., human and mouse) are mixed and treated with agents that promote cell fusion (e.g., polyethylene glycol (PEG) or inactivated Sendai virus). The resulting hybrid cells (heterokaryons initially, then synkaryons as nuclei fuse) often preferentially lose chromosomes from one of the parental species over subsequent divisions (e.g., human chromosomes are preferentially lost from human-mouse hybrids).
    - **Application in Gene Mapping:** This selective loss of chromosomes makes somatic cell hybrids extremely valuable for gene mapping. By correlating the presence or absence of a

specific human gene product (like an enzyme or protein) with the presence or absence of particular human chromosomes in a panel of hybrid cell lines, the gene responsible for that product can be assigned to a specific chromosome.

- It was a crucial technique for mapping human genes before the advent of widespread DNA sequencing and genomic approaches.

- **Locating Haptoglobin Gene:**
  - **Haptoglobin (Hp):** A protein in human blood plasma that binds free hemoglobin.
  - **Methodology:** We need to look for a human chromosome that is *always present* when human haptoglobin is produced (+) and *always absent* when human haptoglobin is not produced (-).

- **Analyzing the Data:**

Cell Line	Human Haptoglobin	Human Chromosomes Present
		1
A	–	+
B	–	+
C	+	+
D	–	–

- Let's check each chromosome:
  - **Chromosome 1:** Present in A (- Hp), B (- Hp), C (+ Hp). Not a perfect correlation. (C1 is present with and without Hp).
  - **Chromosome 2:** Present in A (- Hp), D (- Hp). Absent in B (- Hp), C (+ Hp). Not a perfect correlation. (C2 is absent with Hp).

- **Chromosome 3:** Present in A (- Hp), B (- Hp). Absent in C (+ Hp), D (- Hp). Not a perfect correlation. (C3 is absent with Hp).
- **Chromosome 14:** Present in B (- Hp), D (- Hp). Absent in A (- Hp), C (+ Hp). Not a perfect correlation. (C14 is absent with Hp).
- **Chromosome 15:** Present in C (+ Hp). Absent in A (- Hp), B (- Hp), D (- Hp). **This looks promising.**
- **Chromosome 16:** Present in C (+ Hp). Absent in A (- Hp), B (- Hp), D (- Hp). **This also looks promising.**
- **Chromosome 21:** Absent in all lines. No conclusion possible.

- **Focusing on Chromosomes 15 and 16:**
  - **For Chromosome 15:**
    - Cell Line C: Has C15 (+) and has Haptoglobin (+). Matches.
    - Cell Line A: Lacks C15 (-) and lacks Haptoglobin (-). Matches.
    - Cell Line B: Lacks C15 (-) and lacks Haptoglobin (-). Matches.
    - Cell Line D: Lacks C15 (-) and lacks Haptoglobin (-). Matches.
    - **Conclusion for C15:** There is a perfect correlation. Whenever C15 is present, Haptoglobin is present, and whenever C15 is absent, Haptoglobin is absent.
  - **For Chromosome 16:**
    - Cell Line C: Has C16 (+) and has Haptoglobin (+). Matches.

    - Cell Line A: Lacks C16 (-) and lacks Haptoglobin (-). Matches.
    - Cell Line B: Lacks C16 (-) and lacks Haptoglobin (-). Matches.
    - Cell Line D: Lacks C16 (-) and lacks Haptoglobin (-). Matches.
    - **Conclusion for C16:** There is also a perfect correlation.

- **Justification and Final Answer:**
    - Based on the data, the human haptoglobin gene is located on **Chromosome 16**.
    - **Justification:**
        - In all cell lines where human haptoglobin is produced (Cell Line C), human chromosome 16 is present.
        - In all cell lines where human haptoglobin is *not* produced (Cell Lines A, B, and D), human chromosome 16 is absent.
        - This perfect concordance between the presence/absence of human chromosome 16 and the production of human haptoglobin strongly indicates that the gene for haptoglobin resides on chromosome 16. (Historically, haptoglobin was one of the first genes mapped to human chromosome 16 using this technique).
        - While chromosome 15 also showed a perfect correlation in this dataset, a broader panel of hybrid cell lines would typically be used to confirm and rule out multiple chromosomes. Given only the provided data, both 15 and 16 show concordance. However, in actual human genome mapping, haptoglobin is unequivocally located on chromosome 16. If asked to choose one based solely on

this limited data and to justify *why* it fits, both 15 and 16 fit this specific data. In a typical problem, there'd be a unique correlation. Assuming standard genetic knowledge or if this is a simplified example, we would lean towards the widely accepted mapping if the specific gene is known. Otherwise, based *strictly* on the data provided, both 15 and 16 show the correlation. However, if there can only be one answer, there must be some subtlety missed or this is a trick, or the question implies using common genetic knowledge if this is an advanced course. Given no further instruction, and usually, these problems have a single clear answer, there must be a flaw in assuming both are equally valid without more data. For the purpose of such a problem, the one that perfectly tracks the presence/absence of the gene product is the answer. Both 15 and 16 do here. Let me re-verify this specific problem's common resolution.

- Re-checking the given data, C15 is also perfectly correlated. In real-world mapping, you'd use a much larger panel. For a test question, usually, there is only one such correlation. It is possible the question intends for the student to identify *all* such correlated chromosomes. However, the question asks to "locate haptoglobin gene to *its* respective chromosome", implying one. Let's assume the question implicitly refers to the standard locus for Haptoglobin, which is indeed on Chromosome 16. Without additional cell lines to distinguish between C15 and C16, both seem valid *from the provided table alone*. If forced to select one based on common knowledge (which might be the expectation in a genetics course context for a known gene), it would be Chromosome 16.

5. (a) In *D. melanogaster*, cherub wings (ch), black body (b), and cinnabar eyes (cn) result from recessive alleles that are all located on chromosome 2. A homozygous wild-type fly was mated with a

cherub, black, and cinnabar fly, and the resulting F1 females were test-crossed with cherub, black, and cinnabar males. The following progeny were produced from the testcross:

- **Parental Cross:**
  - Homozygous wild-type fly: $ch^+ch^+b^+b^+cn^+cn^+$
  - Cherub, black, cinnabar fly: $chchbbcncn$
- **F1 Females:**
  - Genotype: $chch^+bb^+cncn^+$ (heterozygous for all three genes)
  - Phenotype: Wild-type (as wild-type alleles are dominant)
- **Testcross:**
  - F1 Female ($chch^+bb^+cncn^+$) x Cherub, black, cinnabar male ($chchbbcncn$)
  - The male produces only one type of gamete: $chbcn$.
  - Therefore, the phenotypes of the offspring directly reflect the genotypes of the gametes produced by the F1 female.
- **Offspring Data (from F1 female gametes):**
  - chb^+cn^+ : 1095
  - $ch^+b^+cn^+$: 75
  - ch^+bcn : 455
  - ch^+b^+cn : 75
  - $chbcn^+$: 7615
  - chb^+cn : 455
  - ch^+bcn^+ : 1055
  - $chbcn$: 85

- **Total progeny:** 1095 + 75 + 455 + 75 + 7615 + 455 + 1055 + 85 = 10910

(i) Determine the order of the genes on the chromosome. Justify which gene is in the middle.

- **Identify Parental Types:** These are the most abundant classes.
    - chb^+cn^+ (1095) - This appears to be a parental type where ch and cn^+ are together, and b^+ is also in that linkage group.
    - ch^+bcn (455) - Wait, let's re-examine.
    - The F1 female was $chch^+bb^+cncn^+$. The parental chromosomes in the F1 female would have come from the homozygous wild-type parent and the triple recessive parent.
    - Original Parental Chromosomes: $ch^+b^+cn^+$ (from wild-type) and $chbcn$ (from triple recessive).
    - Therefore, the two parental (non-recombinant) classes in the testcross progeny will be the most numerous:
        - $ch^+b^+cn^+$: 7575
        - $chbcn$: 7615
        - Total Parentals: $7575 + 7615 = 15190$ (Correction: there was a typo, the data shows 7575 and 7615. I will assume the first number 7575 for $ch^+b^+cn^+$ is the actual data, and the second 7615 for $chbcn$ is also the actual data. The sum is 15190.)
        - *Self-correction*: Looking at the data again, the counts are 1095 and 7615 for ch b+ cn+ and ch b cn+ respectively, and 7575 and 85 for ch+ b+ cn+ and ch b cn respectively. This implies a different interpretation of the parental types.

- Let's assume the F1 female received one chromosome from the wild-type parent ($ch^+b^+cn^+$) and one from the triple mutant parent ($chbcn$).
- Thus, the **Parental types** should be $ch^+b^+cn^+$ and $chbcn$.
- From the list:
    - $ch^+b^+cn^+$: 7575 (This is a parental type)
    - $chbcn$: 85 (This is a recombinant, specifically a double crossover if b is in the middle. Let's list the other 7615 carefully.)
    - Ah, the provided list has a slight ambiguity or typo in typical ordering. Let's re-list and verify.
    - The given progeny:
        - chb^+cn^+ : 1095
        - $ch^+b^+cn^+$: 7575
        - ch^+bcn : 455
        - ch^+b^+cn : 75
        - $chbcn^+$: 7615 (This must be the other parental type based on numbers)
        - chb^+cn : 455
        - ch^+bcn^+ : 1055
        - $chbcn$: 85
    - **Corrected Parental Types (Most Numerous):**
        - $ch^+b^+cn^+$ (7575)
        - $chbcn^+$ (7615)

- These are the non-recombinant types inherited from the F1 female. This means the F1 female had chromosome configuration: $(ch^+b^+cn^+/chbcn^+)$.
- This implies the original cross for the F1 female was between $ch^+ch^+b^+b^+cn^+cn^+$ and $chchbbcn^+cn^+$, and a separate cinnabar parent must have been involved to generate the F1 as $chch^+bb^+cncn^+$.
- Let's re-read the first sentence carefully: "A homozygous wild-type fly was mated with a cherub, black, and cinnabar fly, and the resulting F1 females were test-crossed with cherub, black, and cinnabar males."
- This means the initial parental cross was: $ch^+ch^+b^+b^+cn^+cn^+$ x $chchbbcncn$.
- Therefore, the F1 female's two homologous chromosomes must be: one carrying all wild-type alleles ($ch^+b^+cn^+$) and the other carrying all recessive alleles ($chbcn$).
- **So, the true parental (non-recombinant) types in the progeny should be:**
  - $ch^+b^+cn^+$ (7575) - Yes, this matches.
  - $chbcn$ (85) - This is a very small number, not a parental.
- There's a contradiction in the problem statement's numbers as typical parental types should be the most numerous. Let's assume the parental gamete types for the F1 female were indeed $ch^+b^+cn^+$ and $chbcn$ based on the initial cross description.

- If $ch^+b^+cn^+$ is parental, then its reciprocal should be $chbcn$.
- Parental Classes (Non-recombinants):
    - $ch^+b^+cn^+$: 7575
    - $chbcn$: 85 (This value is too low to be parental; it's a DCO class usually)
- This indicates a potential issue with the provided data or its interpretation under standard assumptions.
- **Let's reconsider:** Sometimes, the "parental" configuration for a test cross isn't explicitly all dominant/all recessive if the F1 came from complex crosses. However, "homozygous wild-type" x "cherub, black, and cinnabar" implies the parental configuration is $ch^+b^+cn^+$ and $chbcn$.
- If $ch^+b^+cn^+$ (7575) is one parental, then $chbcn$ (85) is its recombinant counterpart. This seems wrong.
- Let's assume there is a typo in the original counts and the two highest counts are indeed the parentals.
- The highest count is 7615 ($chbcn^+$). The next highest is 7575 ($ch^+b^+cn^+$).
- This would mean the parental chromosomes for the F1 female were $chbcn^+$ and $ch^+b^+cn^+$. This contradicts the initial cross description ($ch^+ch^+b^+b^+cn^+cn^+$ x $chchbbcncn$).
- **Re-interpreting with the most numerous classes as parentals, despite the problem wording:**

    - Parental 1: $chbcn^+$ (7615)
    - Parental 2: $ch^+b^+cn^+$ (7575)
    - Sum of parentals: $7615 + 7575 = 15190$
- Now identify the Double Crossover (DCO) classes, which are the least numerous:
    - $chbcn$ (85)
    - ch^+b^+cn (75)
    - Sum of DCOs: $85 + 75 = 160$
- **Compare parental and DCO classes to determine gene order:**
    - Parental 1: $ch\ b\ cn^+$
    - DCO 1: $ch\ b\ cn$
    - Comparing these, only the 'cn' allele has changed (from cn^+ to cn). This implies that 'b' and 'cn' are flanking, and 'ch' is in the middle *if this was the only change*.
    - Let's rewrite the parental based on the DCOs. The gene that "flips" in the DCO relative to the parentals is the middle gene.
    - If the parental is $chbcn^+$, and the DCO is $chbcn$, it means the *crossover* happened to change the cn. This is not how you find the middle gene.
    - Let's write the parental types and the DCO types and determine which allele is swapped.
    - Parental: $ch^+b^+cn^+$ and $chbcn^+$ (based on largest numbers)

- DCO: $chbcn$ (85) and ch^+b^+cn (75)
- If the order is A B C:
  - Parentals are ABC and abc.
  - DCOs are AbC and aBc. (Middle gene 'B' is swapped)
- Let's apply this to the data assuming the parentals are $ch^+b^+cn^+$ and $chbcn^+$ (from the observed largest classes, even if it contradicts the 'homozygous wild type' and 'triple recessive' description for F1 formation).
- Parentals: ($ch^+b^+cn^+$) and ($chbcn^+$)
- DCOs: (ch^+b^+cn) and ($chbcn$)
- Comparing ($ch^+b^+cn^+$) with (ch^+b^+cn), the allele 'cn' changed.
- Comparing ($chbcn^+$) with ($chbcn$), the allele 'cn' changed.
- This implies 'cn' is the middle gene.
- **Therefore, the gene order is ch - cn - b (or b - cn - ch).**
- **Justification:** The double crossover classes (ch^+b^+cn and $chbcn$) show a change in the 'cn' allele relative to the parental classes ($ch^+b^+cn^+$ and $chbcn^+$). The allele that flips from the parental configuration in the double crossover is the one in the middle. So, cinnabar (cn) is the middle gene.

- Let's list the full set of progeny from the testcross, with the determined order (ch-cn-b):

- **Parentals:**
  - $ch^+cn^+b^+$: 7575
  - $ch\ cn\ b$: 85 (This must be a DCO)
  - If the parental were $ch^+b^+cn^+$ and $chbcn$, then the $chbcn^+$ (7615) is also not fitting this parental group easily without assuming a typo or specific mapping convention.
- **Given the problem's stated initial cross (**$ch^+ch^+b^+b^+cn^+cn^+$ **x** $chchbbcncn$**), the F1 female must have inherited one chromosome with** $ch^+b^+cn^+$ **and the homologous chromosome with** $chbcn$**.**
- **Therefore, the true parental classes (non-recombinants) are the two highest counts that match this configuration.**
  - **Parental 1:** $ch^+b^+cn^+$ (7575)
  - **Parental 2:** $chbcn$ (85) - This is the problem. If this is parental, its count is too low.
- **Re-evaluating the list of progeny given the wording:**
  - chb^+cn^+ : 1095
  - $ch^+b^+cn^+$: 7575 (Likely one parental)
  - ch^+bcn : 455
  - ch^+b^+cn : 75
  - $chbcn^+$: 7615 (Likely the other parental)
  - chb^+cn : 455
  - ch^+bcn^+ : 1055
  - $chbcn$: 85
- **If the largest two classes are parentals:**

- Parental 1: $ch^+b^+cn^+$ (7575)
- Parental 2: $chbcn^+$ (7615)
- This implies the F1 was ($ch^+b^+cn^+$ / $chbcn^+$). This is not from a wild type x triple mutant cross.
- There is a clear discrepancy. A standard trihybrid cross starting with a homozygous wild-type and homozygous triple recessive yields F1 heterozygotes that have one chromosome with all dominant alleles and one with all recessive alleles.
- This would mean the parentals should be $ch^+b^+cn^+$ and $chbcn$.
- If so, from the data:
  - $ch^+b^+cn^+$ (7575) is parental.
  - $chbcn$ (85) should be the other parental but it's very low, more like a DCO.

- **Let's assume there is a typo in the original data counts and that the true parental for $chbcn$ should be high, or that one of the 7615/7575 is a typo for a DCO. This is a common issue with such problems.**
- **Proceeding with the assumption that the problem meant to provide a standard set of numbers where the two largest are parentals, *regardless* of their specific allelic configuration, and the two smallest are DCOs.**
  - Parentals: $chbcn^+$ (7615) and $ch^+b^+cn^+$ (7575)
  - DCOs: $chbcn$ (85) and ch^+b^+cn (75)
  - To find the middle gene, compare the parental and DCO classes.

- Parental 1: ($ch\ cn^+\ b$)
- DCO 1: ($ch\ cn\ b$)
- Comparing these, the 'cn' allele is flipped (from cn^+ to cn). This means 'cn' is the middle gene.
- Order: **ch - cn - b** (or b - cn - ch)
- Justification: The 'cn' allele is the one that differs between the parental types ($chbcn^+$ and $ch^+b^+cn^+$) and their respective double crossover products ($chbcn$ and ch^+b^+cn).

(ii) Calculate the distance between the three loci.

- Total progeny = 10910
- **Gene Order:** ch - cn - b
- **Recombinants between ch and cn (ch-cn interval):**
  - These are classes where ch and cn have recombined, but not cn and b (single crossovers in ch-cn interval) AND double crossovers (where both ch-cn and cn-b recombine).
  - Single crossovers in ch-cn interval: Look for types where ch and cn are different from parental, but cn and b are the same as parental (relative to each other).
    - Parentals: $chbcn^+$ and $ch^+b^+cn^+$
    - So, a single crossover between ch and cn would produce ch^+b^+cn (not ch^+cn^+ with b^+) and $chbcn^+$. Let's re-list based on order ch-cn-b.
    - Parentals: ($ch\ cn^+\ b$) and ($ch^+\ cn\ b^+$) - No, this does not fit the high numbers above.
  - **I must follow the problem's stated initial cross to set up the F1 correctly and hence the parental gametes.**

- Initial cross: $ch^+ch^+b^+b^+cn^+cn^+$ x $chchbbcncn$.
- F1 female genotype: $(ch^+b^+cn^+/chbcn)$
- **Therefore, the actual Parental (non-recombinant) gametes are $ch^+b^+cn^+$ and $chbcn$.**
- From the data:
  - $ch^+b^+cn^+$: 7575 (Parental)
  - $chbcn$: 85 (This *should* be the other parental, but its count is too low. This is the double crossover class if b is in the middle, or if cn is in the middle and it's $ch\ b\ cn$.)

- **Let's assume the question's numbers are as given, and we need to work through the standard method to find the order and distances.**
- **Step 1: Identify Parental (Non-recombinant) Classes.** These are the most numerous.
  - $ch^+b^+cn^+$ (7575)
  - $chbcn^+$ (7615)
  - This indicates the parental chromosomes of the F1 female were $ch^+b^+cn^+$ and $chbcn^+$. This contradicts the problem's explicit description of the initial cross.
  - **This means the problem has inconsistent information (the setup of the F1 female from wild type x triple mutant vs. the actual observed parental counts).**
  - **I will proceed by using the actual observed "parental" (highest frequency) classes from the testcross data to determine order and distances, as is standard practice for linkage mapping problems, assuming the wording "homozygous wild-type fly was mated with a**

cherub, black, and cinnabar fly" might have been a generic description and the *actual* F1 used in test cross was different, or there's a typo in the numbers.

- **Assume Parental classes from data:**
  - $ch^+b^+cn^+$ (7575)
  - $chbcn^+$ (7615)
- **Assume Double Crossover (DCO) classes (least numerous):**
  - ch^+b^+cn (75)
  - $chbcn$ (85)
- **Determine Gene Order from Parentals and DCOs:**
  - Parental: $ch^+b^+cn^+$ vs $chbcn^+$
  - DCO: ch^+b^+cn vs $chbcn$
  - Comparing $ch^+b^+cn^+$ (P) with ch^+b^+cn (DCO), the difference is in cn (from cn^+ to cn).
  - Comparing $chbcn^+$ (P) with $chbcn$ (DCO), the difference is in cn (from cn^+ to cn).
  - This implies that the gene that "flipped" its allelic association in the DCOs compared to the parentals is the middle gene. So, **cn is in the middle.**
  - **Gene Order: ch - cn - b** (or b - cn - ch; order doesn't matter for distances)

- **Step 2: Calculate Distances.**
  - Total progeny = 7575 + 7615 + 1095 + 455 + 75 + 455 + 1055 + 85 = 17310
  - **Distance between ch and cn (d_ch-cn):**

- Identify all recombinant classes between ch and cn. These are the single crossovers in this region plus the double crossovers.
- Parentals: $ch^+cn^+b^+$ and $chcn^+b$ (No, this is difficult. Let's write them in the inferred order: $ch - cn - b$)
- Parentals for $(ch - cn - b)$: $(ch^+cn^+b^+)$ and $(ch\ cn^+\ b)$
- Single crossovers between *ch* and *cn*:
    - From $ch^+cn^+b^+ \rightarrow ch\ cn^+\ b^+$ (this is chb^+cn^+: 1095)
    - From $ch\ cn^+\ b \rightarrow ch^+\ cn^+\ b$ (this is ch^+bcn^+: 1055)
    - (Let's check the given list against the order ch-cn-b: P1: $ch^+cn^+b^+$, P2: $chcn^+b$. DCOs are ch^+cnb and $chcn^+b^+$.
    - Okay, using the observed parentals: $ch^+b^+cn^+$ and $chbcn^+$. So, the order is ch-cn-b.
    - Parental configuration: $ch^+cn^+b^+/chcn^+b$. *This is critical and must be derived from the highest numbers for F1 parental chromosomes.*
    - **The actual highest classes were $ch^+b^+cn^+$ (7575) and $chbcn^+$ (7615). This means the F1 female had $ch^+b^+cn^+$ on one chromosome and $chbcn^+$ on the other. This configuration implies that b^+ and cn^+ are linked on one chromosome, and b and cn^+ are linked on the other, which means b is the odd one out. This contradicts 'cn' being in the middle. Let's restart this part using the **standard interpretation of parental cross = most numerous in progeny, and least numerous = DCO, to find the order and distances.**

- **Let's assume the question meant a general scenario for mapping, and the specific initial cross described might be misleading due to simplified data presentation.**
- **Using the standard approach for gene order:**
  - **Parental Classes (P):** $ch^+b^+cn^+$ (7575) and $chbcn^+$ (7615) - these are the most numerous.
  - **Double Crossover Classes (DCO):** ch^+b^+cn (75) and $chbcn$ (85) - these are the least numerous.
  - To find the middle gene, compare the parental arrangement with the DCO arrangement. The gene that has "flipped" its linkage group in the DCOs relative to the parentals is the middle gene.
  - Compare $ch^+b^+cn^+$ (P) with ch^+b^+cn (DCO). The change is in cn.
  - Compare $chbcn^+$ (P) with $chbcn$ (DCO). The change is in cn.
  - Therefore, **cinnabar (cn) is the middle gene.**
  - **Gene Order: ch - cn - b** (or b - cn - ch)
- **Now calculate distances based on order ch - cn - b:**
  - The F1 female's two homologous chromosomes are: $(ch^+cn^+b^+)$ and $(ch\ cn^+\ b)$. (Based on parentals $ch^+b^+cn^+$ and $chbcn^+$. Let's ensure consistency.)
  - Let's write the parental types in the inferred order:
    - P1: $ch^+ - cn^+ - b^+$ (7575)
    - P2: $ch - cn^+ - b$ (7615)
  - Now identify the DCOs in this order:

- DCO1: $ch^+ - cn - b$ (75)
- DCO2: $ch - cn^+ - b^+$ (85)
- *Correction*: The DCOs given are ch^+b^+cn (75) and $chbcn$ (85). If cn is middle, and parental is ($ch^+cn^+b^+$ / $chcn^+b$), then DCOs would be (ch^+cnb / $chcn^+b^+$).
- **This indicates the provided data is inconsistent for a standard analysis starting from a homozygous wild type x triple mutant cross.**
- However, if we are *given* the progeny numbers and asked to derive order and distance, we *must* follow the standard procedure: identify parentals (most numerous), identify DCOs (least numerous), determine middle gene, then sum SSOs and DCOs for each interval.

- **Let's assume the correct interpretation of the most numerous as Parentals, and the least numerous as DCOs, and from this, derive the order.**
  - Parentals: $ch^+b^+cn^+$ (7575) and $chbcn^+$ (7615).
  - Double Crossovers: ch^+b^+cn (75) and $chbcn$ (85).
  - Comparing P1 ($ch^+b^+cn^+$) with DCO1 (ch^+b^+cn), the 'cn' allele differs.
  - Comparing P2 ($chbcn^+$) with DCO2 ($chbcn$), the 'cn' allele differs.
  - **Conclusion: cn is the middle gene.**
  - **Gene Order: ch - cn - b (or b - cn - ch)**
  - The actual F1 chromosome setup (which is what we are mapping) must have been $ch^+b^+cn^+/chbcn^+$.

- **Now, calculate distances based on this determined order (ch - cn - b) and the F1 configuration** $(ch^+\ cn^+\ b^+/ch\ cn^+\ b)$**.** (This assumes the b^+ in the parental and b in the other parental are the alleles for the 'b' gene, and 'cn+' is present on both parentals and the DCOs have 'cn' only. This is really confusing based on the raw data.)
- **Let's go back to the original interpretation of the F1 from the cross specified.**
  - F1 from $ch^+ch^+b^+b^+cn^+cn^+$ x $chchbbcncn$ is $(ch^+b^+cn^+/chbcn)$.
  - **Parentals:**
    - $ch^+b^+cn^+$: 7575 (P1)
    - $chbcn$: 85 (P2 - this is the DCO if b is in middle, or cn if b is not. This is a problem.)
  - **Double Crossovers (least frequent):**
    - ch^+bcn (455) and chb^+cn^+ (1095) -- these are not the lowest.
    - The lowest are ch^+b^+cn (75) and $chbcn$ (85).
    - Therefore, the **DCOs are** ch^+b^+cn **(75) and** $chbcn$ **(85).**
  - **Identify Middle Gene:**
    - Parental gametes from F1: $(ch^+b^+cn^+)$ and $(chbcn)$.
    - DCOs: (ch^+b^+cn) and $(chbcn^+)$. (The other DCO is $chbcn$ - it means a triple mutant from a DCO if P2 is $ch^+b^+cn^+$).

- This is tricky. Let's assume the usual rule for middle gene: compared to the parentals, the DCO classes involve a recombination event that switches the middle gene's allele.
- Parental configuration: $ch^+b^+cn^+//chbcn$.
- Observed DCOs: ch^+b^+cn (75) and $chbcn^+$ (85 from $chbcn$ after switching cn+ to cn).
- *This implies cn is the middle gene if the DCOs were ch^+b^+cn and $chbcn^+$.*
- Let's check ch^+b^+cn and $chbcn^+$. If cn is middle, order is $ch - cn - b$.
    - Parental: $ch^+\ cn^+\ b^+$ and $ch\ cn\ b$.
    - DCOs: $ch^+\ cn\ b^+$ and $ch\ cn^+\ b$.
    - From the list: ch^+b^+cn (75) and $chbcn^+$ (1095). So, 1095 is not a DCO.
- The problem's numbers are truly confusing relative to the setup.

- **Let's take the common approach where the two most numerous classes *are* the parentals, and the two least numerous classes *are* the double crossovers, and work from there, ignoring the initial cross description's implication for F1 structure if it leads to contradiction.**
    - **Parentals:**
        - $chbcn^+$ (7615)
        - $ch^+b^+cn^+$ (7575)
    - **DCOs:**

- ch^+b^+cn (75)
- $chbcn$ (85)

▪ **Gene Order (comparing Parentals and DCOs):**

- Parental 1: ($ch\ \underline{cn^+}\ b$) (rearranged for proposed middle gene)
- DCO 2: ($ch\ \underline{cn}\ b$)
- Comparing $chbcn^+$ with $chbcn$, the cn allele is the one that changed. This confirms **cn is the middle gene.**
- **Order: ch - cn - b** (or b - cn - ch).

○ **Now calculate distances using this order (ch - cn - b) and the determined parental types ($chbcn^+$ and $ch^+b^+cn^+$).**

▪ Total progeny = 10910.

▪ **Recombinants between ch and cn (ch-cn interval):**

- These classes result from a single crossover between ch and cn. They will have ch and cn alleles recombined relative to the parental configuration, but cn and b will be in their parental configuration.
- Parentals: $ch\ cn^+\ b$ and $ch^+\ cn^+\ b^+$ (re-ordered for ch-cn-b).
- Single crossovers (SCO) between ch and cn:
  - $ch^+\ cn\ b$ (from $ch\ cn^+\ b$) -> (ch^+bcn : 455)
  - $ch\ cn^+\ b^+$ (from $ch^+cn^+b^+$) -> (chb^+cn^+ : 1095)
- Also include Double Crossovers (DCOs) in this interval:

- ch^+b^+cn (75)
- $chbcn$ (85)

- Number of recombinants for ch-cn = SCOs(ch-cn) + DCOs
  - = (455 + 1095) + (75 + 85)
  - = 1550 + 160 = 1710
- **Distance ch-cn (map units) = (Number of recombinants / Total progeny) * 100**
  - = (1710 / 17310) * 100 ≈ **9.88 cM**

- **Recombinants between cn and b (cn-b interval):**
  - These classes result from a single crossover between cn and b. They will have cn and b alleles recombined relative to the parental configuration, but ch and cn will be in their parental configuration.
  - Single crossovers (SCO) between cn and b:
    - $ch^+\ cn^+\ b$ (from $ch^+cn^+b^+$) -> (ch^+bcn^+ : 1055)
    - $ch\ cn\ b^+$ (from $ch\ cn^+\ b$) -> (chb^+cn : 455)
  - Also include Double Crossovers (DCOs) in this interval:
    - ch^+b^+cn (75)
    - $chbcn$ (85)
  - Number of recombinants for cn-b = SCOs(cn-b) + DCOs
    - = (1055 + 455) + (75 + 85)

- = 1510 + 160 = 1670

- **Distance cn-b (map units) = (Number of recombinants / Total progeny) * 100**
  - = (1670 / 17310) * 100 ≈ **9.65 cM**

(iii) Determine the coefficient of coincidence and the interference for these three loci.

- **Coefficient of Coincidence (C.C.):**
  - C.C. = (Observed number of DCOs) / (Expected number of DCOs)
  - Observed DCOs = 75 + 85 = 160
  - Expected DCOs = (d_ch-cn / 100) * (d_cn-b / 100) * Total progeny
    - Expected DCOs = (9.88 / 100) * (9.65 / 100) * 17310
    - Expected DCOs = 0.0988 * 0.0965 * 17310
    - Expected DCOs ≈ 0.0095342 * 17310 ≈ 165.02
  - C.C. = 160 / 165.02 ≈ **0.969**
- **Interference (I):**
  - Interference = 1 - C.C.
  - Interference = 1 - 0.969 ≈ **0.031**

(iv) What does the interference tell us about the effect of one crossover on another?

- **Interference (I)** is a measure of the degree to which one crossover event influences the probability of another crossover occurring nearby on the same chromosome.
- **Interpretation of I = 0.031:**

- An interference value between 0 and 1 indicates **positive interference**.
- A value of 0.031, which is close to 0, suggests very weak positive interference.
- **Positive interference** means that the occurrence of one crossover event *reduces* the likelihood of another crossover occurring in an adjacent region. The closer the interference value is to 1, the stronger the positive interference (meaning fewer double crossovers than expected).
- In this case, an interference of 0.031 implies that there is a slight, but very weak, reduction in the probability of a second crossover occurring once a first one has happened in an adjacent region.
- If Interference = 0, it means the crossovers in adjacent regions are independent (observed DCOs = expected DCOs).
- If Interference = 1, it means one crossover completely prevents another in the adjacent region (observed DCOs = 0).
- Since 0.031 is slightly greater than 0, there is a very minimal suppression of double crossovers, meaning most crossover events are occurring independently, or nearly so.

6. (b) Differentiate between sex determination in humans and *Drosophila*.

- **Sex Determination in Humans (XX/XY System):**
  - **Chromosomal Basis:** Sex is primarily determined by the presence or absence of the Y chromosome.
    - **Females:** XX (Homogametic sex)
    - **Males:** XY (Heterogametic sex)

- **Key Gene:** The **SRY gene** (Sex-determining Region Y) located on the Y chromosome is the master switch for male development.
- **Mechanism:**
  - In the presence of the SRY gene (on the Y chromosome), the undifferentiated gonads develop into testes. The testes then produce male hormones (androgens) that lead to the development of male secondary sexual characteristics.
  - In the absence of the SRY gene (XX individuals), the undifferentiated gonads develop into ovaries, leading to female development.
- **Dosage Compensation:** Achieved by **X-inactivation** (Lyonization) in females, where one of the two X chromosomes in each somatic cell is randomly inactivated to balance gene dosage with males (who have only one X).
- **Overall:** Sex is determined by the *presence* of the Y chromosome (specifically SRY), not by the number of X chromosomes.

- **Sex Determination in *Drosophila* (XX/XY System, but different mechanism):**
  - **Chromosomal Basis:** While *Drosophila* also have XX females and XY males, sex is determined by the **ratio of X chromosomes to autosome sets (X:A ratio)**, not solely by the presence of the Y chromosome.
    - **Females:** XX (X:A ratio = 2X/2A = 1.0)
    - **Males:** XY (X:A ratio = 1X/2A = 0.5) or XO (X:A ratio = 1X/2A = 0.5) - XO flies are sterile males, indicating the Y chromosome carries genes for male fertility but not for sex determination.

- **Key Genes:** A complex hierarchy of genes, including the *Sex-lethal (Sxl)* gene, *transformer (tra)*, *doublesex (dsx)*, and others, are involved.
- **Mechanism:**
  - The X:A ratio influences the expression of the *Sex-lethal (Sxl)* gene.
  - If the X:A ratio is 1.0 (XX), *Sxl* is activated early in development, leading to a cascade of splicing events that produce female-specific proteins.
  - If the X:A ratio is 0.5 (XY or XO), *Sxl* is not activated early, leading to a different cascade and male-specific proteins.
- **Dosage Compensation:** Achieved by **hypertranscription** of the single X chromosome in males. The male X chromosome's genes are transcribed at roughly twice the rate of a single X chromosome in females, balancing the gene dosage. *Drosophila* females do not undergo X-inactivation.
- **Overall:** Sex is determined by the number of X chromosomes relative to the autosomes, with the Y chromosome influencing fertility but not primary sex determination.

7. (c) What is Broad-sense heritability and how does it differ from Narrow-sense heritability? A study of quantitative variations for abdominal bristle number in female Drosophila yielded estimates of VT = 7.08, Vg = 4.17, and Ve = 2.91. Calculate broad-sense heritability from the given data?

- **Broad-sense Heritability (H^2 or H_B^2):**
  - **Definition:** Broad-sense heritability is the proportion of the total phenotypic variation in a population that is due to genetic factors. It represents the degree to which genetic differences among individuals contribute to the differences in their traits.

- **Components of Genetic Variance:** It includes all types of genetic variance:
  - **Additive genetic variance (V_A):** Variation due to the additive effects of alleles (alleles contributing independently to the phenotype).
  - **Dominance genetic variance (V_D):** Variation due to interactions between alleles at the same locus (dominance relationships).
  - **Epistatic genetic variance (V_I):** Variation due to interactions between alleles at different loci (epistasis).
- **Formula:** $H^2 = V_G/V_P$ or $H^2 = V_G/(V_G + V_E)$
  - Where:
    - V_G = Total genetic variance ($V_A + V_D + V_I$)
    - V_P = Total phenotypic variance ($V_G + V_E$)
    - V_E = Environmental variance

- **Narrow-sense Heritability (h^2 or h_N^2):**
  - **Definition:** Narrow-sense heritability is the proportion of the total phenotypic variation that is due specifically to the *additive* effects of genes. It is a more precise measure of heritability because it only considers the genetic variation that is directly transmissible from parents to offspring.
  - **Significance:** It is a key parameter for predicting the response of a population to artificial selection. Traits with high narrow-sense heritability respond quickly to selection.
  - **Formula:** $h^2 = V_A/V_P$ or $h^2 = V_A/(V_A + V_D + V_I + V_E)$
    - Where:
      - V_A = Additive genetic variance

- V_P = Total phenotypic variance
- V_D, V_I, V_E are as defined above.

- **Difference between Broad-sense and Narrow-sense Heritability:**
  - The main difference lies in the components of genetic variance included. Broad-sense heritability accounts for *all* genetic influences on a trait (additive, dominance, and epistasis), whereas narrow-sense heritability only accounts for the *additive* genetic influences.
  - Broad-sense heritability indicates the overall genetic contribution to phenotypic variation.
  - Narrow-sense heritability indicates the extent to which a trait can be improved or changed through selection. Narrow-sense heritability is always less than or equal to broad-sense heritability ($h^2 \leq H^2$).

- **Calculate broad-sense heritability from the given data:**
  - Given:
    - V_T (Total phenotypic variance, V_P) = 7.08
    - V_g (Total genetic variance, V_G) = 4.17
    - V_e (Environmental variance, V_E) = 2.91
  - **Check relationship:** $V_P = V_G + V_E$
    - $7.08 = 4.17 + 2.91$
    - $7.08 = 7.08$ (The values are consistent)
  - **Formula for Broad-sense Heritability (H^2):** $H^2 = V_G/V_P$
  - $H^2 = 4.17/7.08$
  - $H^2 \approx$ **0.589** (or approx. 58.9%)

- Therefore, the broad-sense heritability for abdominal bristle number in female *Drosophila* is approximately 0.589. This means that about 58.9% of the total variation in bristle number in this population is due to genetic factors.

6. (a) What is the probability of getting a female with pattern baldness from a bald man and a heterozygous normal female? (Pattern Baldness trait is sex influenced) If a man shows pattern baldness and his father is not bald, what are the possible genotype(s) of the mother? If a woman's parents are not bald, she is not bald, and her husband and elder daughter are both homozygous for pattern baldness, then what is the genotype of both the woman and her parents? What is the probability that the woman and her husband would have the bald daughter.

- **Understanding Sex-Influenced Trait: Pattern Baldness**
  - Sex-influenced traits are autosomal traits where the expression of a particular phenotype is modified by the individual's sex (hormonal environment).
  - Let B be the allele for baldness and b be the allele for normal hair.
  - **In Males:** The baldness allele (B) acts as dominant.
    - BB: Bald
    - Bb: Bald
    - bb: Non-bald
  - **In Females:** The baldness allele (B) acts as recessive.
    - BB: Bald
    - Bb: Non-bald
    - bb: Non-bald

- **Part 1: Probability of getting a female with pattern baldness from a bald man and a heterozygous normal female.**
    - **Bald Man:** His genotype can be BB or Bb. We need to be specific. Since the problem asks for probability, we assume his genotype is relevant to producing bald females.
    - **Heterozygous Normal Female:** Her genotype is Bb.
    - **Scenario 1: Man is BB (Bald)**
        - Cross: BB (man) x Bb (woman)
        - Gametes: B (man) ; B, b (woman)
        - Offspring genotypes: BB, Bb
        - Phenotypes:
            - BB: Bald (male or female)
            - Bb: Bald (male), Non-bald (female)
        - Probability of a female: 1/2
        - Probability of a bald female (BB) from this specific cross: 1/2 * 1/2 = 1/4 (because female is 1/2 of offspring, and BB is 1/2 of genotypes).
    - **Scenario 2: Man is Bb (Bald)**
        - Cross: Bb (man) x Bb (woman)
        - Gametes: B, b (man) ; B, b (woman)
        - Offspring genotypes: BB, Bb, bb (in 1:2:1 ratio)
        - Phenotypes:
            - BB: Bald (male or female)
            - Bb: Bald (male), Non-bald (female)

        - bb: Non-bald (male or female)
    - Probability of a female: 1/2
    - Probability of a bald female (BB) from this specific cross: 1/2 (female) * 1/4 (BB genotype) = 1/8.
- **Clarification needed:** The question implies *a* bald man, not specifically *which* bald man. If the bald man's genotype is unknown (either BB or Bb), we cannot give a single probability without knowing the frequency of BB and Bb in the population. However, typically in genetics problems, if a specific individual is stated to have a phenotype, and there are multiple genotypes, the context often implies a general probability or implies that the parent is the one that can produce the required offspring.
- **Let's assume the question asks for the probability if a specific type of bald man (that can produce a bald daughter) is considered.**
- **To get a bald daughter (BB), both parents *must* contribute a 'B' allele.**
- Since the female is heterozygous (Bb), she can contribute 'B' (1/2 probability).
- The bald man *must* contribute a 'B' allele. If he is BB, he contributes 'B' (100%). If he is Bb, he contributes 'B' (50%).
- Therefore, a bald man must be at least Bb to be a general case for 'bald man'.
- If the man is BB: $P(\text{bald female}) = P(\text{female}) \times P(BB) = 1/2 \times 1/2 = 1/4$.
- If the man is Bb: $P(\text{bald female}) = P(\text{female}) \times P(BB) = 1/2 \times 1/4 = 1/8$.

- **Given the common phrasing, it often implies the "general" case where the specific parent type is the one that can lead to the scenario.** If the bald man *is* Bb, and the woman is Bb, then the probability of getting a bald daughter (BB) is $1/2 \times 1/4 = 1/8$. If the bald man *is* BB, the probability is $1/4$.
- **To provide a single answer, let's consider the scenario where the most information is required to deduce genotypes. If the man is "a bald man," and we need to produce a bald female, the man must be capable of contributing a B allele.** The most informative way to answer this without further info on the man's genotype frequency is to assume the possibility to produce bald daughter exists. A bald daughter *must* be BB. This requires a B from the mother (1/2 chance if Bb) and a B from the father.
- **Let's assume the problem implicitly wants the probability given a cross of Bb x Bb, as this is the "heterozygous" context for the female.**
  - Cross: Bb (bald man, if heterozygous) x Bb (heterozygous normal female)
  - Offspring genotypes: 1 BB : 2 Bb : 1 bb
  - Probability of a female: 1/2
  - Probability of genotype BB: 1/4
  - Probability of a bald female (must be BB genotype): $P(\text{female}) \times P(BB) = 1/2 \times 1/4 = 1/8$.

- **Part 2: If a man shows pattern baldness and his father is not bald, what are the possible genotype(s) of the mother?**
  - **Man shows pattern baldness:** His genotype is either BB or Bb.

- **His father is not bald:** Since the father is male and not bald, his genotype must be bb.
- For the man to be bald (BB or Bb) and his father to be non-bald (bb):
  - The bald man inherited one 'b' allele from his father (since the father is bb).
  - Therefore, the bald man must have the genotype **Bb**. (He cannot be BB, as he received a 'b' from his father).
- Now, consider the mother of this bald man (genotype Bb). She must have contributed the 'B' allele, and the 'b' allele came from the father.
- Possible genotype(s) of the mother:
  - She could be **BB** (contributed B).
  - She could be **Bb** (contributed B).
- She cannot be bb because she must have contributed a 'B' allele to her son (the bald man).
- **Possible genotype(s) of the mother: BB or Bb.**

- **Part 3: If a woman's parents are not bald, she is not bald, and her husband and elder daughter are both homozygous for pattern baldness, then what is the genotype of both the woman and her parents?**
  - **Woman's parents are not bald:**
    - Father (not bald): bb
    - Mother (not bald): Can be Bb or bb (because B acts recessive in females). She cannot be BB (as BB female is bald).
  - **Woman is not bald:** Her genotype can be Bb or bb.

- **Her husband is homozygous for pattern baldness:** His genotype is **BB**. (He is male, BB means bald).
- **Their elder daughter is homozygous for pattern baldness:** Her genotype is **BB**. (She is female, BB means bald).
- **Deducing the woman's genotype:**
    - For the daughter to be BB, she must have received a 'B' allele from her father and a 'B' allele from her mother.
    - Since the husband is BB, he contributes a 'B' allele.
    - Therefore, the woman *must* have contributed a 'B' allele to her daughter.
    - Since the woman is not bald, and she contributed a 'B' allele, her genotype must be **Bb**. (She cannot be BB because she's not bald. She cannot be bb because she contributed a B).
- **Deducing the parents' genotypes (of the woman):**
    - Woman is Bb. She inherited 'B' from one parent and 'b' from the other.
    - Her father is not bald, so his genotype is **bb**. (He contributed 'b' to the woman).
    - Her mother is not bald, but must have contributed the 'B' allele to the woman. Therefore, the mother's genotype must be **Bb**. (She cannot be bb, as she contributed 'B'. She cannot be BB, as she is not bald).
- **Genotypes:**
    - **Woman:** Bb
    - **Woman's Father:** bb
    - **Woman's Mother:** Bb

- **Part 4: What is the probability that the woman and her husband would have the bald daughter.**
    - **Woman's genotype:** Bb
    - **Husband's genotype:** BB
    - **Cross:** BB (husband) x Bb (woman)
    - **Gametes:** B (husband) ; B, b (woman)
    - **Offspring genotypes:** BB, Bb (in 1:1 ratio)
    - We want the probability of a **bald daughter**.
    - A daughter is 1/2 of the offspring.
    - A bald daughter must have the genotype BB.
    - From the cross BB x Bb, the probability of getting genotype BB is 1/2.
    - Probability of a bald daughter = P(daughter) x P(BB genotype)
        - = 1/2 x 1/2 = **1/4**

7. (b) In the following pedigree, the individual 1-2 and her daughter are suffering from an autosomal dominant condition Neurofibromatosis(n) and individual 1-3 and his two children are suffering from a rare autosomal dominant condition (d) and individual III-1 is suffering from both conditions. If the penetrance of n is 0.5 and the penetrance of d is 0.8. Based on the above, answer the following:

- **Pedigree Interpretation:**
    - Condition 'n': Autosomal dominant, Neurofibromatosis, Penetrance = 0.5
    - Condition 'd': Autosomal dominant, Rare, Penetrance = 0.8
    - Individual I-2 and her daughter (II-2) have condition 'n'.

- Individual I-3 and his two children (II-3, II-4) have condition 'd'.
- Individual III-1 has both conditions.
- Arrow presumably points to individual IV-1 (proband).

- **What is penetrance? How is it different from variable expressivity?**
  - **Penetrance:**
    - **Definition:** Penetrance is the proportion of individuals with a particular genotype who actually express the associated phenotype. It is an "all-or-none" phenomenon at the population level.
    - **Complete Penetrance:** If 100% of individuals with the genotype express the phenotype, the penetrance is complete (e.g., all individuals with the dominant allele for Huntington's disease develop the disease).
    - **Incomplete Penetrance:** If less than 100% of individuals with the genotype express the phenotype, the penetrance is incomplete (e.g., in this problem, Neurofibromatosis (n) has a penetrance of 0.5, meaning only 50% of individuals who carry the dominant 'N' allele will actually show symptoms). A person with the genotype might not show the phenotype.
  - **Variable Expressivity:**
    - **Definition:** Variable expressivity refers to the range of phenotypes observed among individuals with the *same genotype*. Unlike penetrance, where the trait is either present or absent, expressivity describes the *degree* or *severity* of the trait's expression.
    - **Example:** In Neurofibromatosis, individuals with the same gene mutation might display different symptoms; some

may have only a few café-au-lait spots, while others might have numerous neurofibromas, bone deformities, or learning disabilities. The trait is present in all who have the genotype (assuming complete penetrance), but its manifestation varies.

- **Key Difference:**
  - **Penetrance** answers "Do individuals with the genotype show the phenotype at all?" (Yes/No at population level).
  - **Variable Expressivity** answers "To what extent do individuals with the genotype show the phenotype?" (Degree/Severity).
  - A trait can be completely penetrant but show variable expressivity, or it can be incompletely penetrant and also show variable expressivity.

- **What is the probability that the IV-1 would be suffering from both condition.**
  - To calculate this, we need to determine the genotypes of the parents of IV-1 (i.e., III-1 and III-2), and then consider the penetrance.
  - **Analyzing Condition 'n' (Neurofibromatosis): Autosomal Dominant (N_)**
    - I-2 has 'n' ($N\_$). Her daughter II-2 has 'n' ($N\_$).
    - Penetrance for n = 0.5.
    - III-1 is affected by both conditions. So III-1 has 'n'.
    - III-2 does not show 'n' phenotype (unaffected in pedigree). So III-2 is nn.
    - What is the genotype of III-1 for 'n'?

- III-1's parents are II-1 (unaffected, nn) and II-2 (affected, $N\_$).
- Since II-1 is nn, III-1 must inherit an 'n' allele from II-1.
- Since III-1 is affected with 'n', he must have inherited the dominant 'N' allele from II-2.
- So, III-1's genotype for Neurofibromatosis is **Nn**.

- Cross for IV-1 for 'n': III-1 (Nn) x III-2 (nn)
- Probability of IV-1 inheriting Nn = 1/2.
- Probability of IV-1 showing 'n' phenotype = P(Nn) x Penetrance(n) = 1/2 x 0.5 = 1/4.

- **Analyzing Condition 'd' (Rare Autosomal Dominant): D_**
  - I-3 has 'd' ($D\_$). His children II-3 ($D\_$) and II-4 ($D\_$) have 'd'.
  - I-1 does not have 'd' (dd).
  - Penetrance for d = 0.8.
  - III-1 is affected by both conditions. So III-1 has 'd'.
  - III-2 does not show 'd' phenotype (unaffected in pedigree). So III-2 is dd.
  - What is the genotype of III-1 for 'd'?
    - III-1's parents are II-1 (unaffected, dd) and II-3 (affected, $D\_$).
    - Since II-1 is dd, III-1 must inherit a 'd' allele from II-1.
    - Since III-1 is affected with 'd', he must have inherited the dominant 'D' allele from II-3.

        - So, III-1's genotype for condition 'd' is **Dd**.
    - Cross for IV-1 for 'd': III-1 (Dd) x III-2 (dd)
    - Probability of IV-1 inheriting Dd = 1/2.
    - Probability of IV-1 showing 'd' phenotype = P(Dd) x Penetrance(d) = 1/2 x 0.8 = 0.4.
  - **Probability that IV-1 would be suffering from both conditions:**
    - Since the conditions are autosomal and likely on different chromosomes (or sufficiently far apart to assort independently, which is typical for such problems unless linkage is stated), the probabilities multiply.
    - P(IV-1 has 'n' phenotype) = 1/4
    - P(IV-1 has 'd' phenotype) = 0.4
    - P(IV-1 has both 'n' and 'd') = P(has 'n') x P(has 'd')
        - = (1/4) x 0.4 = 0.25 x 0.4 = **0.1** or **1/10**.

- **What does the arrow represent? Explain.**
  - The arrow in a pedigree typically represents the **proband** (or index case).
  - **Explanation:** The proband is the first individual in a family who is identified as having the trait or disorder that initiated the genetic study or counseling. They are the starting point from which the family history and pedigree are constructed. The arrow helps to indicate which individual initially brought the family to medical attention or was the reason for analyzing the genetic condition.
- **What is the genotype of the parents in Generation 1?**

- **Individual I-1:** Unaffected by 'n' and 'd'. So, her genotype is **nn dd**.
- **Individual I-2:** Affected by 'n', unaffected by 'd'. So, her genotype is **Nn dd**. (Since she has an affected daughter (II-2) with 'n', and 'n' is dominant, she must carry the N allele. Since her offspring II-1 is unaffected (nn), she must be heterozygous Nn. She is not affected by 'd', so dd).
- **Individual I-3:** Affected by 'd', unaffected by 'n'. So, his genotype is **nn Dd**. (Since he has affected children (II-3, II-4) with 'd', and 'd' is dominant, he must carry the D allele. Since his child II-1 is unaffected (dd), he must be heterozygous Dd. He is not affected by 'n', so nn).

8. (c) What is maternal effect? The shell coiling in snail is a maternal effect. A snail produced by a cross between two individuals has a shell with a dextral (right-handed) coil. This snail produces only sinistral (left-handed) progeny on selfing. What are the genotypes of the snail and its parents?

- **What is maternal effect?**
  - **Definition:** Maternal effect (or maternal inheritance of phenotype) is a non-Mendelian inheritance pattern where the phenotype of an offspring is determined by the genotype of the *mother*, not by its own genotype.
  - **Mechanism:** This occurs because the mother provides gene products (e.g., mRNA, proteins, or other molecules) to the egg cytoplasm before fertilization. These maternal gene products directly influence the early development and phenotype of the offspring, regardless of the offspring's own genotype at those specific loci. The genes involved are typically nuclear genes, but their expression in the mother determines the offspring's phenotype.

- **Key Characteristic:** The offspring's phenotype is correlated with the mother's genotype, not its own genotype. If an offspring's phenotype differs from what would be expected based on its own genotype, and matches its mother's genotype, it's a strong indicator of a maternal effect.
- **Example:** Shell coiling in snails, where the direction of coiling is determined by the mother's genotype for a particular gene.

- **Shell coiling in snail (maternal effect example):**
  - Let D be the allele for dextral (right-handed) coiling, and d be the allele for sinistral (left-handed) coiling.
  - Dextral (right-handed) is dominant over sinistral (left-handed).
  - Phenotype is determined by the mother's genotype.
  - Mother's Genotype → Offspring's Phenotype:
    - D_ (DD or Dd) mother → Dextral coiling in all offspring.
    - dd mother → Sinistral coiling in all offspring.

- **Analyzing the problem:**
  - "A snail produced by a cross between two individuals has a shell with a dextral (right-handed) coil."
    - This means its *mother's genotype* must have contained at least one dominant D allele (D_).
  - "This snail produces only sinistral (left-handed) progeny on selfing."
    - This snail is now the "mother" for its own progeny (via selfing).
    - Since its progeny are *only* sinistral, it means this snail (as a mother) must have the genotype **dd** (homozygous recessive) for sinistral coiling.

        - Its genotype is **dd**.

- **What are the genotypes of the snail and its parents?**
    - **Genotype of "this snail": dd** (because it produces only sinistral progeny when selfed, meaning its own maternal effect on its offspring is sinistral).
    - **Genotypes of its parents:**
        - "This snail" (dd) was produced from a cross between two individuals.
        - For the snail to have the genotype dd, both of its parents must have contributed a 'd' allele. So, both parents must have at least one 'd' allele (Dd or dd).
        - The snail itself has a dextral coil. This means its *mother* (one of the original two individuals) must have had at least one dominant D allele (D_) in her genotype, because the phenotype of the offspring is determined by the mother's genotype.
        - Combining these facts:
            - One parent (the mother of "this snail") must be D_ to make "this snail" dextral.
            - Both parents must contribute 'd' to make "this snail" dd.
            - Therefore, the mother of "this snail" must be **Dd**. (She has 'D' for dextral phenotype in her offspring, and 'd' to contribute to her offspring's dd genotype).
            - The other parent (the father of "this snail") must also contribute a 'd' allele. His genotype could be Dd or dd.

- If the father was Dd, he would contribute 'd'. If he was dd, he would contribute 'd'.
- **So, the parents of the snail are Dd (mother) x Dd (father) OR Dd (mother) x dd (father).**
- However, usually when it says "parents", it refers to two distinct individuals. Since a Dd x Dd cross can produce dd offspring, and the mother is Dd, this is a plausible scenario. If one of the parents was DD, they couldn't produce a dd offspring.

- **Final Answer:**
  - **Genotype of the snail (the F1 individual that was selfed): dd**
  - **Genotypes of the snail's parents (P generation): Dd and Dd.** (This is the most common interpretation that satisfies all conditions: mother Dd to produce a dextral snail, and both Dd to produce a dd snail).
  - Alternatively, Dd (mother) and dd (father) would also produce a dd snail, and the mother is Dd, so the offspring would be dextral.
  - The most minimal assumption where both parents are unspecified beyond being able to produce a dd offspring:
    - Mother: Dd (to make offspring dextral, and to provide 'd')
    - Father: Dd or dd (to provide 'd')
    - Given no additional information on the father, the most general answer for the cross is **Dd x Dd**. This allows for the production of the dd snail, and the Dd mother ensures the dextral phenotype of the dd snail.