CSIR NET Life Science Questions with Solution

Q1. Which one of the following statements is **INCORRECT** regarding plant phytochrome (PHY), cyanobacterial phytochrome1 (Cph1), and bacterial phytochrome-like protein (BphP)?
(a) PHY has two PRD domains in the C-terminal moiety.
(b) Cph1 and BphP have histidine kinase domains at the N-terminal moiety.
(c) GAF domain is present in the N-terminal moiety of PHY, Cph1, and BphP.
(d) The cysteine residue that forms the linkage is located in the GAF domain in canonical phytochromes such as PHY and Cph1.

Q2. Which one of the following is referred to as **tuberonic acid**?
(a) Methyl jasmonate
(b) *cis*-jasmone
(c) Jasmonoyl-1-β-glucose
(d) 12-Hydroxy-(+)-7-isojasmonate

Q3. The defect in a major semi-dwarfing gene of rice, **sd-1**, leads to cultivars with short, thick culms and improved lodging resistance. The gene is related to which one of the following phytohormones?
(a) Gibberellins
(b) Abscisic acid
(c) Jasmonic acid
(d) Salicylic acid

Q4. In the model plant **Arabidopsis thaliana**, methionine is a precursor amino acid in the biosynthesis of:
(a) Alkaloids
(b) Glucosinolates
(c) Phenolics
(d) Terpenoids

Q5. How much hemoglobin is present approximately in each normal human red blood cell?
(a) 19 pg
(b) 29 pg
(c) 39 pg
(d) 49 pg

Q6. Which one of the following is involved in the pinching-off of the neck of the invaginating coated pit to form an endocytotic vesicle at the pre-synaptic terminal?
(a) Synaptojanin
(b) AP2
(c) Clathrin
(d) Dynamin

Q7. Aldosterone is synthesized exclusively in the zona glomerulosa due to the presence of _______ enzyme in addition to a dehydrogenase.
(a) 11 β-hydroxylase
(b) 17 α-hydroxylase
(c) 18-hydroxylase
(d) 21-hydroxylase

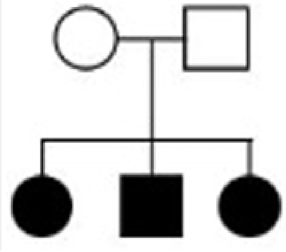
Q8. Which one of the following hormones has no supply store in the cells where it is synthesized?
(a) Catecholamines
(b) Insulin
(c) T_3 and T_4
(d) Steroids

Q9. Which one of the following is true for Genome-Wide Association Study (GWAS)?
(a) There is a need to make controlled crosses or work with human families with known parent-offspring relationships.
(b) All alleles in the population are assayed at the same time.
(c) Single nucleotide polymorphisms (SNPs) cannot be used for such studies.
(d) Knowledge about candidate genes is essential.

Q10. Which one of the following options contains only those types of mapping populations that are characterized by 'true-breeding' individuals?
(a) RILs and F_2 populations
(b) F_2 populations and BC_1F_2
(c) Doubled haploid populations and BC_1F_2
(d) Doubled haploid populations and RILs

Q11. In a family, the father has an X-linked mutation causing a late-onset lethal disorder, and the mother is **not a carrier**. Based on the above information, which one of the following statements about the children the couple may have is correct?
(a) There is a 50% chance that the son will show the disorder.
(b) No children will show the disorder.
(c) The probability that the parents have a daughter carrying a mutant allele is 25%.
(d) All daughters will carry the mutant allele.

Q12. In a mutagenesis experiment, the following pedigree was obtained. All progeny had the same phenotype. The mutation is most likely to have occurred:



(a) During maturation of the egg cell.
(b) In the maternal somatic cell.
(c) In the mother in the precursor to all germ cells.
(d) In the embryo during development.

Q13. Which one of the following statements is **NOT correct** about collenchyma?
(a) Collenchyma cell walls are thick, and they require more glucose for their production.
(b) Collenchyma cells are rigid.
(c) Collenchyma is usually produced in shoot tips and young petioles.
(d) Collenchyma is generally not present in subterranean shoots and roots.

Q14. Which one of the following terms describes the biological classification system based on common ancestry?
(a) Linnean taxonomy
(b) Binomial nomenclature
(c) Phylogenetic classification
(d) Rank-based classification

Q15. Select the species that was thought to be extinct because of climate change and habitat loss, but was recently rediscovered in the year 2022.
(a) Nicobar Wart Frog
(b) Harlequin Frog
(c) Nilgiri Cricket Frog
(d) Lemur Leaf Frog

Q16. Which one of the following four plant families has the largest number of species?
(a) Brassicaceae
(b) Cucurbitaceae
(c) Cactaceae
(d) Rosaceae

Q17. Which one of the following correctly shows the total estimated biomass of the lifeforms on Earth given here, in increasing order?
(a) Bacteria < Viruses < Fungi
(b) Bacteria < Fungi < Viruses
(c) Viruses < Fungi < Bacteria
(d) Fungi < Viruses < Bacteria

Q18. Which one of the following options lists landmasses that were all a part of the ancient Gondwana supercontinent?
(a) Australia, New Zealand, and North America
(b) Africa, Europe, India, New Zealand, and South America
(c) Africa, Europe, India, Madagascar, and North America
(d) Africa, Australia, Antarctica, India, Madagascar, and South America

Q19. Which one of the following anthropogenic activities contributes the most nitrogen to the global nitrogen cycle?
(a) Industrial production of fertilizers
(b) NO_x production due to combustion of fossil fuels
(c) Nitrogen fixation by soybean farming
(d) Nitrogen fixation by cultivation of legumes (excluding soybean)

Q20. In which of the following ecosystems would the largest percentage of Net Primary Productivity (NPP) be taken up by the grazing food chain?
(a) Tropical rainforest
(b) Temperate deciduous forest
(c) Algal seabed
(d) Open ocean

Solutions

S1. Ans. (b)

Sol. The incorrect statement is **(b).** The histidine kinase domains in cyanobacterial phytochrome (Cph1) and bacterial phytochrome-like proteins (BphP) are not located in the N-terminal moiety; instead, they are found in the C-terminal region. The N-terminal region typically contains the chromophore-binding domains, such as PAS (Per/Arnt/Sim), GAF (cGMP phosphodiesterase/adenylyl cyclase/FhlA), and PHY (phytochrome-specific) domains. The histidine kinase domains are part of the signaling mechanism and are more commonly associated with the C-terminal portion of these proteins.

Information Booster:

1. **PRD domains** (PAS-related domains) in PHY are responsible for signal transduction. Plant phytochromes typically have two PRD domains in the C-terminal moiety.
2. **Histidine kinase domains** are usually located in the C-terminal part of bacterial and cyanobacterial phytochromes, which are involved in phosphorylation-mediated signaling.
3. The **GAF domain** in the N-terminal region binds the chromophore, facilitating light detection in all phytochromes.
4. The **cysteine residue** in the GAF domain forms a covalent linkage with the chromophore in canonical phytochromes.
5. Plant phytochromes like PHY diverge in their signaling mechanisms compared to bacterial phytochromes, emphasizing structural and functional diversity.

Additional Knowledge:

(a) PHY has two PRD domains in the C-terminal moiety

This statement is **correct**. PRD domains are responsible for interacting with other signaling partners, facilitating downstream responses in plant phytochromes.

(b) Cph1 and BphP have histidine kinase domains at the N-terminal moiety

This statement is **incorrect**. Histidine kinase domains are found in the C-terminal moiety. These domains are central to signal transduction via phosphorylation, a key feature of bacterial phytochromes.

(c) GAF domain is present in the N-terminal moiety of PHY, Cph1, and BphP

This statement is **correct.** The GAF domain is critical for chromophore attachment and light perception. It is universally present in the N-terminal region of phytochromes.

(d) The cysteine residue that forms the linkage is located in the GAF domain in canonical phytochromes such as PHY and Cph1

This statement is **correct**. The GAF domain houses the chromophore-binding cysteine residue, which covalently links to the chromophore, enabling light absorption.

S2. Ans. (d)

Sol. The correct answer is **(d) 12-Hydroxy-(+)-7-isojasmonate**. Tuberonic acid is a hydroxylated derivative of jasmonic acid, specifically **12-hydroxyjasmonic acid**. It plays a significant role in plant physiological processes such as tuber formation in potatoes and other plant developmental activities. Methyl jasmonate and *cis*-jasmone are related to the jasmonate family but do not represent tuberonic acid.

Information Booster:

1. Tuberonic acid (12-Hydroxyjasmonic acid) is a jasmonic acid derivative responsible for tuber induction in plants like potatoes.
2. Jasmonates, including tuberonic acid, are involved in plant responses to biotic and abiotic stresses.
3. Tuberonic acid regulates key processes such as senescence, secondary metabolism, and tuberization.
4. Methyl jasmonate acts as a signaling molecule but is chemically different from tuberonic acid.
5. Jasmonoyl-1-β-glucose is a conjugate that is primarily involved in jasmonate metabolism.

Additional Knowledge:

(a) Methyl jasmonate:

This is a volatile esterified form of jasmonic acid, involved in plant signaling. It is responsible for activating defense responses against pathogens and herbivores. It is not referred to as tuberonic acid but plays a role in stress responses.

(b) *cis*-Jasmone:

This is a structurally distinct jasmonate derivative that functions as a signaling molecule for plant-insect interactions. Unlike tuberonic acid, it lacks the hydroxylation at the 12th carbon.

(c) Jasmonoyl-1-β-glucose:

This is a conjugated form of jasmonic acid involved in its metabolism and storage. It is not associated with tuber induction but plays a role in maintaining jasmonate levels.

(d) 12-Hydroxy-(+)-7-isojasmonate:

This is the correct answer and corresponds to tuberonic acid. It is hydroxylated at the 12th carbon and actively involved in inducing tuber formation and other growth processes.

S3. Ans. (a)

Sol. The **sd-1** (semi-dwarfing 1) gene is linked to **gibberellins (GA)**, which are plant hormones that regulate growth and development. The mutation in the **sd-1 gene** leads to a reduction in gibberellin biosynthesis, causing the rice plant to have shorter stems (dwarf phenotype). This mutation has been widely used in breeding semi-dwarf rice varieties, significantly contributing to increased yield and lodging resistance during the Green Revolution. Lodging resistance is crucial because it prevents the plant from falling over under adverse conditions, thereby enhancing productivity.

Information Booster:

1. **Gibberellins (GA):** Plant hormones involved in stem elongation, seed germination, and flowering. Mutations in GA biosynthesis or signaling pathways often lead to dwarf phenotypes.
2. The **sd-1 gene** encodes an enzyme in the GA biosynthetic pathway. Mutations here reduce gibberellin levels.
3. **Semi-dwarf rice varieties** have short, sturdy stems that resist lodging, making them suitable for high-yield farming.
4. The Green Revolution relied heavily on such genetic modifications, improving crop yield worldwide.
5. Mutation in **sd-1** specifically affects internode elongation, reducing stem height while maintaining overall plant health.

Additional Knowledge:

(a) Gibberellins:

This option is **correct**. Gibberellins regulate plant height by promoting cell elongation. In the case of the **sd-1 gene**, a mutation leads to a reduction in gibberellin biosynthesis, resulting in the dwarf phenotype that prevents lodging and improves yield potential.

(b) Abscisic acid:

This option is **incorrect**. Abscisic acid (ABA) is primarily associated with stress responses, such as drought tolerance, by regulating stomatal closure and seed dormancy. It does not play a significant role in determining plant height or lodging resistance in rice.

(c) Jasmonic acid:

This option is **incorrect**. Jasmonic acid is involved in defense mechanisms against herbivores and pathogens, as well as wound responses. It is unrelated to the semi-dwarfing gene or plant height regulation.

(d) Salicylic acid:

This option is **incorrect.** Salicylic acid is primarily associated with systemic acquired resistance (SAR) in plants against pathogens. It has no direct role in controlling stem elongation or lodging resistance.

S4. Ans. (b)

Sol. The correct answer is **(b) Glucosinolates**. Methionine serves as a precursor for glucosinolates in **Arabidopsis thaliana**. Glucosinolates are sulfur-containing secondary metabolites derived from amino acids. They play an essential role in plant defense against herbivores and pathogens. In **Arabidopsis**, methionine-derived glucosinolates belong to the class of aliphatic glucosinolates, which are critical for chemical defense and stress tolerance.

Information Booster:

1. Glucosinolates are primarily found in the Brassicaceae family, including **Arabidopsis thaliana**, broccoli, and mustard.
2. Methionine-derived glucosinolates are aliphatic and contribute to the plant's resistance against herbivores.
3. The biosynthetic pathway includes the elongation of methionine followed by core structure formation and side-chain modifications.
4. Glucosinolates, when hydrolyzed, produce biologically active compounds such as isothiocyanates and nitriles.
5. Methionine-derived glucosinolates are essential for cross-species defense signaling.

Additional Knowledge:

(a) Alkaloids:

This option is **incorrect**. Alkaloids are nitrogen-containing compounds primarily derived from other amino acids like tryptophan, tyrosine, or ornithine. Methionine is not a direct precursor for alkaloid biosynthesis.

(b) Glucosinolates:

This option is **correct**. Methionine is a key precursor in the biosynthesis of aliphatic glucosinolates. These secondary metabolites contribute to plant defense by deterring herbivores and pathogens.

(c) Phenolics:

This option is **incorrect**. Phenolic compounds, such as flavonoids, lignins, and tannins, are typically derived from the shikimate pathway, involving phenylalanine as a precursor, not methionine.

(d) Terpenoids:

This option is **incorrect**. Terpenoids are derived from isoprenoid pathways, specifically involving precursors like isopentenyl pyrophosphate (IPP) and dimethylallyl pyrophosphate (DMAPP). Methionine is not involved in this biosynthesis pathway.

S5. Ans. (b)

Sol. The correct answer is **(b) 29 pg.** Each normal human red blood cell contains approximately **29 picograms (pg)** of hemoglobin. This quantity is crucial for the cell's oxygen-carrying capacity. Hemoglobin concentration in a red blood cell determines its ability to transport oxygen from the lungs to tissues and carbon dioxide back to the lungs for exhalation.

Information Booster:

1. **Hemoglobin content per RBC:** Typically around 29 pg in healthy individuals.
2. **Mean corpuscular hemoglobin (MCH):** A measure used in blood tests, calculated as the total hemoglobin divided by the red blood cell count. The normal range is 27–31 pg.
3. **Role of hemoglobin:** It binds oxygen via its iron-containing heme groups and facilitates oxygen delivery throughout the body.
4. **Variations in hemoglobin levels:** Low MCH indicates hypochromic anemia, while high MCH might suggest macrocytosis.
5. **Red blood cell count:** Normal RBCs contain a consistent hemoglobin amount, essential for maintaining efficient gas exchange.

Additional Knowledge:

(a) 19 pg:

This value is below normal and might indicate hypochromic anemia, where red blood cells lack sufficient hemoglobin. Conditions like iron deficiency can cause such low levels.

(b) 29 pg:

This is the **correct answer**. It represents the average hemoglobin content in a normal, healthy red blood cell. Hemoglobin concentration directly influences the oxygen-carrying capacity of blood.

(c) 39 pg:

This value is higher than normal and could indicate macrocytosis, a condition where red blood cells are larger than average, often seen in vitamin B12 or folate deficiency.

(d) 49 pg:

Such a high value is abnormal and might occur in extreme cases of macrocytosis or other pathological conditions involving abnormal red blood cell morphology.

S6. Ans. (d)

Sol. The correct answer is **(d) Dynamin**. Dynamin is a GTPase enzyme that plays a critical role in the scission of the neck of the invaginating coated pit to form a free endocytic vesicle during clathrin-mediated endocytosis. At the pre-synaptic terminal, this process ensures the recycling of synaptic vesicles, which is crucial for neurotransmission. Dynamin wraps around the neck of the coated pit and, through GTP hydrolysis, provides the mechanical force required to sever the membrane, allowing vesicle formation.

Information Booster:

1. **Dynamin** is a GTPase that catalyzes the final step in vesicle scission.
2. **Clathrin** forms a coat around vesicles but does not participate in membrane scission.
3. **AP2** is an adaptor protein complex that helps in cargo selection and clathrin recruitment.
4. **Synaptojanin** regulates vesicle uncoating by dephosphorylating phosphoinositides, aiding in vesicle recycling.
5. Dynamin dysfunction is linked to neurodegenerative diseases due to impaired synaptic vesicle recycling.

Additional Knowledge:

(a) Synaptojanin:

This is **incorrect**. Synaptojanin is a phosphoinositide phosphatase involved in uncoating clathrin-coated vesicles during vesicle recycling. It facilitates the dissociation of clathrin and other associated proteins after vesicle scission but does not directly mediate the pinching-off process.

(b) AP2:

This is **incorrect**. The adaptor protein complex AP2 is involved in cargo selection and recruitment of clathrin to the plasma membrane, enabling vesicle formation. It is essential for the initial stages of endocytosis but does not participate in the membrane scission.

(c) Clathrin:

This is **incorrect**. Clathrin forms a lattice-like coat around the invaginating pit, providing structural support. However, it does not mediate the actual pinching-off of the vesicle.

(d) Dynamin:

This is the **correct answer**. Dynamin assembles at the neck of the budding vesicle and, through GTP hydrolysis, drives the scission of the membrane to release the vesicle into the cytoplasm.

S7. Ans. (c)

Sol. The correct answer is **(c) 18-hydroxylase**. Aldosterone synthesis occurs in the zona glomerulosa of the adrenal cortex. This specificity is due to the unique presence of **18-hydroxylase**, which is essential for converting corticosterone to 18-hydroxycorticosterone and eventually to aldosterone. This enzyme, along with aldosterone synthase (CYP11B2), is critical for the final steps in aldosterone biosynthesis. Other zones of the adrenal cortex lack 18-hydroxylase, making aldosterone synthesis exclusive to the zona glomerulosa.

Information Booster:

1. **Zona glomerulosa:** The outermost layer of the adrenal cortex, responsible for aldosterone production.
2. **18-hydroxylase:** Also known as CYP11B2, it catalyzes the hydroxylation necessary for aldosterone synthesis.
3. **Aldosterone function:** Regulates sodium and potassium balance, critical for blood pressure homeostasis.
4. **Corticosterone:** A precursor converted to aldosterone in the presence of 18-hydroxylase.
5. Deficiency in **18-hydroxylase** can impair aldosterone synthesis, leading to electrolyte imbalances.

Additional Knowledge:

(a) 11 β-hydroxylase:

This enzyme (CYP11B1) is involved in cortisol and corticosterone synthesis in the zona fasciculata and zona glomerulosa. However, it is not exclusive to aldosterone synthesis and does not catalyze the hydroxylation at the 18th position.

(b) 17 α-hydroxylase:

This enzyme (CYP17A1) is present in the zona fasciculata and zona reticularis, involved in cortisol and androgen biosynthesis. It is absent in the zona glomerulosa, which explains why aldosterone synthesis occurs here and not in other zones.

(c) 18-hydroxylase:

This is the **correct answer**. It is a critical enzyme required for converting corticosterone to aldosterone. Its exclusive presence in the zona glomerulosa allows aldosterone synthesis to occur only in this layer.

(d) 21-hydroxylase:

This enzyme (CYP21A2) is involved in synthesizing precursors such as deoxycorticosterone and 11-deoxycortisol in the adrenal cortex. While necessary for mineralocorticoid and glucocorticoid production, it is not specific to aldosterone synthesis.

S8. Ans. (d)

Sol. The correct answer is **(d) Steroids**. Steroid hormones are not stored in the cells where they are synthesized. Instead, they are synthesized de novo from cholesterol upon stimulation and immediately released into the bloodstream. This is because steroids are lipid-soluble and can easily diffuse across cell membranes, making storage in vesicles or compartments impractical. In contrast, hormones like catecholamines, insulin, and thyroid hormones are stored in vesicles or specialized structures within their respective cells until they are needed

Information Booster:

1. **Steroid hormones** are synthesized in the adrenal cortex, gonads, and placenta.
2. They are derived from cholesterol and include hormones such as cortisol, aldosterone, estrogen, and testosterone.
3. The synthesis and release of steroid hormones are tightly regulated by feedback mechanisms involving the hypothalamus and pituitary gland.
4. Their lipid-solubility enables them to directly interact with intracellular receptors, influencing gene transcription.
5. The immediate release of steroids ensures rapid responses to physiological demands like stress or reproductive signaling.

Additional Knowledge:

(a) Catecholamines:

Catecholamines (e.g., adrenaline and noradrenaline) are stored in secretory granules within the chromaffin cells of the adrenal medulla. These granules ensure rapid release during stress or "fight-or-flight" responses.

(b) Insulin:

Insulin is stored in vesicles within pancreatic beta cells. It is secreted in response to elevated blood glucose levels. This storage allows for quick and efficient regulation of glucose homeostasis.

(c) T_3 and T_4:

Thyroid hormones are stored in the thyroid gland as part of the thyroglobulin matrix. When needed, they are cleaved from thyroglobulin and released into the bloodstream.

(d) Steroids:

This is the **correct answer**. Steroid hormones are synthesized on-demand and not stored, as their lipid-soluble nature allows them to diffuse freely across the cell membrane. This characteristic is a key distinction between steroid hormones and other hormone types.

S9. Ans. (b)

Sol. The correct answer is **(b) All alleles in the population are assayed at the same time**. Genome-Wide Association Studies (GWAS) analyze genetic variations across entire genomes in a large population to identify associations between specific genetic markers (such as SNPs) and traits or diseases. GWAS does not require controlled crosses or known family relationships, as it relies on naturally occurring genetic diversity in a population. Moreover, GWAS does not focus on candidate genes, as it surveys the whole genome to discover new associations.

Information Booster:

1. **GWAS analyzes entire genomes** to detect genetic variants linked to traits or diseases.
2. **SNPs (Single Nucleotide Polymorphisms)** are the primary markers used in GWAS.
3. GWAS relies on statistical analysis to find significant associations between genetic markers and phenotypes.
4. Knowledge of candidate genes is **not essential**, as GWAS identifies previously unknown genetic contributors.
5. GWAS is widely used in studying complex traits, such as diabetes, cancer, and height.

Additional Knowledge:

(a) There is a need to make controlled crosses or work with human families with known parent-offspring relationships:

This is **incorrect**. GWAS does not require controlled crosses or familial data, as it works with a diverse population's naturally occurring genetic variation. This is in contrast to linkage studies, which often rely on family data.

(b) All alleles in the population are assayed at the same time:

This is the **correct answer**. GWAS simultaneously assays genetic variations across the entire genome, providing a comprehensive view of genetic diversity and its association with traits.

(c) Single nucleotide polymorphisms (SNPs) cannot be used for such studies:

This is **incorrect**. SNPs are the primary markers used in GWAS due to their high frequency in the genome and their role as indicators of genetic variation.

(d) Knowledge about candidate genes is essential:

This is **incorrect**. Unlike candidate gene studies, GWAS does not require prior knowledge of genes associated with the trait of interest. It is exploratory and scans the entire genome for potential associations.

S10. Ans. (d)

Sol. The correct answer is **(d) Doubled haploid populations and RILs (Recombinant Inbred Lines)**. Both these types of mapping populations consist of true-breeding individuals. True-breeding populations are homozygous for traits across generations, which makes them ideal for genetic studies and mapping.

1. **Doubled haploid populations** are created by inducing haploids to double their chromosome number, resulting in completely homozygous individuals.
2. **Recombinant Inbred Lines (RILs)** are generated through repeated selfing or sibling matings of the F_2 generation over several generations, leading to homozygosity.

Other options, like F_2 populations and BC_1F_2, are not true-breeding as they are heterozygous due to segregation during meiosis.

Information Booster:

1. **True-breeding populations** are essential for stable genetic mapping and trait inheritance studies.
2. **Doubled haploid populations** provide completely homozygous lines in a single generation, saving time.
3. **RILs** are commonly used in QTL mapping due to their homozygosity and recombination events.
4. F_2 populations are heterozygous and segregate, making them unsuitable for true-breeding classifications.
5. BC_1F_2 (backcross populations) are also heterozygous and not true-breeding.

Additional Knowledge:

(a) RILs and F_2 populations:

This is **incorrect**. While RILs are true-breeding, F_2 populations are not. F_2 populations are derived from the crossing of two F_1 individuals and are heterozygous for many loci.

(b) F_2 populations and BC_1F_2:

This is **incorrect**. Neither F_2 populations nor BC_1F_2 populations are true-breeding. Both consist of heterozygous individuals due to segregation during gamete formation.

(c) Doubled haploid populations and BC_1F_2:

This is **incorrect**. While doubled haploid populations are true-breeding, BC_1F_2 populations are heterozygous, making this combination invalid.

(d) Doubled haploid populations and RILs:

This is the **correct answer**. Both doubled haploids and RILs consist of true-breeding individuals. Doubled haploids are entirely homozygous, and RILs achieve homozygosity through multiple generations of selfing.

S11. Ans. (d)

Sol. The correct answer is **(d) All daughters will carry the mutant allele**.

In X-linked inheritance, fathers pass their X chromosome to all of their daughters and their Y chromosome to their sons. Since the father has an X-linked mutation, all daughters will inherit the mutant allele from him. Sons will inherit the Y chromosome from the father, and because the mother is not a carrier, they cannot inherit the mutation and will not show the disorder.

Information Booster:

1. **X-linked mutations:** Passed from father to daughters, not to sons.
2. **Daughters of an affected father:** Always inherit his mutant X chromosome.
3. **Sons of an affected father:** Only inherit the Y chromosome from their father, so they are unaffected.
4. **Mother is not a carrier:** Sons do not receive the mutant X chromosome, ensuring they are unaffected.
5. Late-onset lethal X-linked disorders typically do not affect females who are carriers, as the normal allele compensates.

Additional Knowledge:

(a) There is a 50% chance that the son will show the disorder:

This is **incorrect**. Sons inherit the Y chromosome from the father, so they cannot inherit an X-linked disorder from him. The mother does not carry the mutation, ensuring sons are unaffected.

(b) No children will show the disorder:

This is **incorrect**. While no sons will show the disorder, all daughters will carry the mutant allele, and they could potentially pass it on to their offspring.

(c) The probability that the parents have a daughter carrying a mutant allele is 25%:

This is **incorrect**. All daughters will inherit the mutant allele because the father passes on his X chromosome (with the mutation) to all daughters.

(d) All daughters will carry the mutant allele:

This is the **correct answer**. Since the father has an X-linked mutation, all his daughters will inherit the mutant X chromosome from him, making them carriers of the mutation.

S12. Ans. (c)

Sol. The correct answer is **(c) In the mother in the precursor to all germ cells.**

The fact that all progeny share the same phenotype suggests that the mutation is germline in origin. A mutation occurring in the precursor to germ cells in the mother would affect all germ cells she produces, thereby passing the mutation to all offspring. If the mutation occurred during egg maturation or in a somatic cell, it would not consistently affect all progeny. Mutations occurring in the embryo would not affect the germline of the mother and, hence, would not be transmitted.

Information Booster:

1. **Germline mutations:** Mutations in germ cell precursors result in transmission to all offspring.
2. **Somatic mutations:** Affect only the individual where the mutation occurs and are not inherited.
3. **Egg cell maturation mutations:** May affect a single egg but will not consistently transmit the mutation to all progeny.
4. **Embryonic mutations:** Result in mosaicism and do not involve germline inheritance unless they occur early in development.
5. This pattern strongly indicates a mutation in the **germline precursor cells** of the mother.

Additional Knowledge:

(a) During maturation of the egg cell:

This is **incorrect**. A mutation during egg maturation would only affect that specific egg. It would not result in all progeny sharing the same phenotype, as observed in this case.

(b) In the maternal somatic cell:

This is **incorrect**. Somatic mutations are not transmitted to offspring as they do not affect germ cells. They are limited to the individual in whom they occur.

(c) In the mother in the precursor to all germ cells:

This is the **correct answer**. A mutation in the germ cell precursors would affect all gametes produced by the mother, explaining why all progeny inherit the mutation and display the same phenotype.

(d) In the embryo during development:

This is **incorrect**. A mutation in the embryo could lead to mosaicism but would not result in a germline mutation that is transmitted to all offspring.

S13. Ans. (b)

Sol. The correct answer is **(b) Collenchyma cells are rigid.**

Collenchyma cells are not rigid; they are flexible and provide structural support to growing parts of the plant such as young shoots and leaves. The flexibility of collenchyma is due to its unevenly thickened cell walls made of pectin and cellulose, which allow the cells to adapt to mechanical stress and provide tensile strength without rigidity.

In contrast, sclerenchyma cells are rigid and provide support to mature plant parts due to lignified walls.

Information Booster:

1. **Collenchyma structure:** Cells have thickened walls composed of pectin and cellulose, providing flexibility.
2. **Location:** Found in growing regions such as shoot tips, young stems, and petioles.
3. **Function:** Provides support and elasticity to plant parts, enabling them to withstand bending and stretching.
4. **Presence in roots:** Rarely found in subterranean parts due to limited mechanical stress in those areas.
5. **Differences from sclerenchyma:** Sclerenchyma is rigid and lignified, whereas collenchyma is flexible and non-lignified.

Additional Knowledge:

(a) Collenchyma cell walls are thick, and they require more glucose for their production:

This is **correct**. Collenchyma cells have thickened primary cell walls rich in cellulose and pectin, which require significant energy and glucose during production.

(b) Collenchyma cells are rigid:

This is **incorrect**. Collenchyma cells are characterized by their flexibility and ability to stretch, allowing young plant parts to grow while still providing structural support.

(c) Collenchyma is usually produced in shoot tips and young petioles:

This is **correct**. Collenchyma is commonly found in actively growing regions of the plant, where support and flexibility are needed.

(d) Collenchyma is generally not present in subterranean shoots and roots:

This is **correct**. Collenchyma is absent in underground parts like roots, as they do not require the same flexibility and mechanical support as above-ground parts.

S14. Ans. (c)

Sol. The correct answer is **(c) Phylogenetic classification**. Phylogenetic classification is a biological classification system that groups organisms based on their evolutionary history and common ancestry. It uses phylogenetic trees to depict relationships, showing how different species evolved from a common ancestor. This method emphasizes genetic, morphological, and molecular similarities and differences, providing a more accurate representation of evolutionary relationships than older systems like Linnean taxonomy.

Information Booster:

1. **Phylogenetic classification:** Groups organisms based on evolutionary lineage and genetic relationships.
2. **Phylogenetic tree:** A diagram that represents the evolutionary history of species.
3. **Modern techniques:** Molecular biology, DNA sequencing, and bioinformatics are crucial for constructing phylogenetic classifications.
4. **Advantages:** Reflects evolutionary history, eliminates artificial groupings, and provides insights into the origin of species.
5. **Comparison with Linnean taxonomy:** Linnean taxonomy focuses on hierarchical rank-based classification without emphasizing evolutionary history.

Additional Knowledge:

(a) Linnean taxonomy:

This is **incorrect**. Linnean taxonomy is a rank-based classification system developed by Carl Linnaeus. It organizes organisms into hierarchical categories such as kingdom, phylum, class, order, family, genus, and species. However, it does not necessarily consider evolutionary relationships.

(b) Binomial nomenclature:

This is **incorrect**. Binomial nomenclature is a system for naming species using two terms: genus and species (e.g., *Homo sapiens*). While it is used within classification systems, it does not describe a classification system based on common ancestry.

(c) Phylogenetic classification:

This is the **correct answer**. It is a modern system that uses common ancestry and evolutionary history to classify organisms. It reflects natural relationships among species, making it the most accurate classification method.

(d) Rank-based classification:

This is **incorrect**. Rank-based classification refers to systems like Linnean taxonomy that rely on hierarchical ranks (e.g., kingdom, phylum) rather than evolutionary relationships.

S15. Ans. (b)

Sol. The correct answer is **(b) Harlequin Frog**. Harlequin frogs (*Atelopus* species) were considered extinct in many regions due to habitat loss, climate change, and the devastating effects of chytridiomycosis (a fungal disease). However, some populations of Harlequin frogs were rediscovered in 2022, bringing hope for their conservation. These rediscoveries are a testament to the resilience of certain species and highlight the importance of preserving their habitats.

Information Booster:

1. **Harlequin Frogs:** A group of brightly colored frogs from Central and South America. Many species in this genus are critically endangered or thought to be extinct.
2. **Rediscovery:** In 2022, researchers identified surviving populations in remote areas, emphasizing the need for conservation efforts.
3. **Threats:** The main threats include climate change, habitat destruction, and chytridiomycosis caused by the *Batrachochytrium dendrobatidis* fungus.

4. **Conservation Significance:** The rediscovery of presumed extinct species underlines the importance of habitat protection and disease mitigation.
5. **Global Efforts:** Conservationists are focusing on captive breeding and reintroduction programs to safeguard these species.

Additional Knowledge:

(a) Nicobar Wart Frog:

This is **incorrect**. The Nicobar Wart Frog (*Fejervarya nicobariensis*) is native to the Nicobar Islands and has not been reported extinct or rediscovered recently.

(b) Harlequin Frog:

This is the **correct answer**. Harlequin frogs, particularly species from the *Atelopus* genus, have been rediscovered in the wild after being presumed extinct. Their rediscovery highlights ongoing efforts to protect amphibian biodiversity.

(c) Nilgiri Cricket Frog:

This is **incorrect**. The Nilgiri Cricket Frog (*Minervarya nilagirica*) is found in the Western Ghats of India and is not considered extinct or rediscovered recently.

(d) Lemur Leaf Frog:

This is **incorrect**. The Lemur Leaf Frog (*Agalychnis lemur*) is critically endangered but has not been recently rediscovered. Conservation efforts for this species are ongoing in Central America.

S16. Ans. (d)

Sol. The correct answer is **(d) Rosaceae**. The Rosaceae family, commonly known as the rose family, contains the largest number of species among the options listed. It includes approximately 4828 species spread across around 90–100 genera. This family is highly diverse and includes economically and ecologically significant species like apples, cherries, roses, and strawberries.

In comparison, Brassicaceae (mustard family) and Cucurbitaceae (gourd family) have fewer species, while Cactaceae (cactus family) is primarily restricted to arid regions and has less diversity.

Information Booster:

1. **Rosaceae:**
   - Around 4828 species.
   - Includes genera like *Rosa* (roses), *Malus* (apples), and *Rubus* (blackberries).
   - Distributed in temperate regions.
2. **Brassicaceae:**
   - Approximately 4,000 species but fewer genera (~340).
   - Includes economically important crops like cabbage, mustard, and broccoli.
3. **Cucurbitaceae:**
   - Around 965 species in 98 genera.
   - Includes gourds, pumpkins, and cucumbers.
4. **Cactaceae:**
   - Contains about 1,500–2,000 species.
   - Mostly restricted to arid and semi-arid regions.

Additional Knowledge:

(a) Brassicaceae:

Also known as the mustard family, it includes herbaceous plants commonly found in temperate regions. While it has notable agricultural importance, such as cabbage (*Brassica oleracea*) and mustard (*Brassica nigra*), it has fewer species compared to Rosaceae.

(b) Cucurbitaceae:
Known as the gourd family, it is primarily tropical and includes plants like pumpkins (*Cucurbita*), watermelons (*Citrullus*), and cucumbers (*Cucumis*). The family is smaller in species count compared to Rosaceae.

(c) Cactaceae:
This family primarily consists of succulents adapted to arid climates. While iconic in deserts, the family is less diverse compared to Rosaceae, with fewer genera and species.

(d) Rosaceae:
This is the **correct answer**. It is a large and diverse family found globally, especially in temperate zones, with many species valued for their flowers, fruits, and ornamental uses.

S17. Ans. (c)

Sol. The correct answer is **(c) Viruses < Fungi < Bacteria**.

Viruses have the smallest estimated total biomass among the given lifeforms due to their small size and relatively lower abundance compared to bacteria and fungi. Fungi have a greater biomass than viruses, as they form large, multicellular structures like mycelia, which significantly contribute to global biomass. Bacteria, due to their massive abundance in almost all ecosystems, have the largest biomass among the three groups.

Information Booster:

1. **Viruses:**
   - Tiny biological entities with small genomes and minimal physical structure.
   - While they are abundant in numbers, their small size results in low total biomass.
2. **Fungi:**
   - Includes multicellular organisms such as mushrooms and molds.
   - Their biomass is significantly larger due to extensive mycelial networks.
3. **Bacteria:**
   - Found in nearly all environments, from soil to oceans.
   - Their massive abundance and cellular size contribute to the largest biomass among these groups.
4. **Global Distribution:** Bacteria dominate biomass in many ecosystems, while fungi are significant in terrestrial ecosystems. Viruses play a critical role in microbial ecosystems but have the smallest biomass.

Additional Knowledge:

(a) Bacteria < Viruses < Fungi:
This is **incorrect**. Bacteria have a much larger biomass than viruses or fungi.

(b) Bacteria < Fungi < Viruses:
This is **incorrect**. Viruses have the smallest biomass, not the largest.

(c) Viruses < Fungi < Bacteria:
This is the **correct answer**. Viruses have the lowest biomass, fungi have a moderate biomass, and bacteria have the largest.

(d) Fungi < Viruses < Bacteria:
This is **incorrect**. Fungi have a larger biomass than viruses.

S18. Ans. (d)

Sol. The correct answer is **(d) Africa, Australia, Antarctica, India, Madagascar, and South America**.

The ancient Gondwana supercontinent existed during the Paleozoic and Mesozoic eras. It comprised the landmasses of present-day **Africa, South America, Australia, Antarctica, India, and Madagascar**. These continents were connected and later drifted apart due to plate tectonics. North America and Europe were part of a different supercontinent, **Laurasia**, and were not part of Gondwana.

Information Booster:

1. **Gondwana Formation:**
   - Existed approximately 500–180 million years ago.
   - Formed from the breakup of the supercontinent Pangaea.
2. **Gondwana Landmasses:**
   - Included Africa, South America, India, Australia, Antarctica, and Madagascar.
3. **Breakup of Gondwana:**
   - Started around 180 million years ago during the Jurassic period.
   - Led to the drifting of continents to their current positions.
4. **Role in Biogeography:**
   - Explains the distribution of certain species and fossils across continents (e.g., Glossopteris fossils found in South America, Africa, and Antarctica).

Additional Knowledge:

(a) Australia, New Zealand, and North America:
This is **incorrect**. While Australia and New Zealand were part of Gondwana, North America was part of Laurasia.

(b) Africa, Europe, India, New Zealand, and South America:
This is **incorrect**. Europe was part of Laurasia, not Gondwana.

(c) Africa, Europe, India, Madagascar, and North America:
This is **incorrect**. Neither Europe nor North America were part of Gondwana.

(d) Africa, Australia, Antarctica, India, Madagascar, and South America:
This is the **correct answer**. These landmasses were all part of Gondwana before the continents drifted apart.

S19. Ans. (a)

Sol. The correct answer is **(a) Industrial production of fertilizers.**

The industrial production of fertilizers, primarily through the Haber-Bosch process, is the largest contributor of nitrogen to the global nitrogen cycle. This process fixes atmospheric nitrogen (N_2) into ammonia (NH_3), which is used in synthetic fertilizers. These fertilizers significantly enhance agricultural productivity but also contribute to nitrogen imbalances in ecosystems, leading to eutrophication, groundwater contamination, and greenhouse gas emissions.

While other sources like fossil fuel combustion and biological nitrogen fixation also contribute nitrogen, their impact is smaller compared to industrial fertilizer production.

Information Booster:

1. **Haber-Bosch Process:** Converts atmospheric nitrogen into ammonia, enabling large-scale fertilizer production.
2. **Global Impact:** Industrial fertilizers have increased global nitrogen inputs by more than 50%, primarily in agriculture.
3. **Environmental Consequences:** Excess nitrogen runoff causes eutrophication in water bodies, leading to dead zones and biodiversity loss.
4. **Other Sources:** Biological nitrogen fixation by legumes and fossil fuel combustion also contribute but on a smaller scale.
5. **Mitigation Efforts:** Strategies like precision farming, crop rotation, and reduced fertilizer use aim to address nitrogen pollution.

Additional Knowledge:

(a) Industrial production of fertilizers:

This is the **correct answer**. The Haber-Bosch process fixes over 120 million metric tons of nitrogen annually. This nitrogen is added to agricultural systems, significantly increasing crop yields but causing ecological challenges due to overuse and runoff.

(b) NO_x production due to combustion of fossil fuels:

This is **incorrect**. While fossil fuel combustion contributes nitrogen oxides (NO_x) to the atmosphere, its contribution is smaller compared to industrial fertilizer production. NO_x also contributes to air pollution and acid rain but is less impactful in the global nitrogen cycle.

(c) Nitrogen fixation by soybean farming:

This is **incorrect**. Soybeans are a significant source of biologically fixed nitrogen due to their symbiotic relationship with nitrogen-fixing bacteria, but their contribution is less than industrial fertilizers.

(d) Nitrogen fixation by cultivation of legumes (excluding soybean):

This is **incorrect**. While other legumes like alfalfa and clover also fix nitrogen biologically, their global contribution is smaller than that of industrial nitrogen fixation.

S20. Ans. (d)

Sol. The correct answer is **(d) Open ocean**.

In open ocean ecosystems, the largest percentage of Net Primary Productivity (NPP) is consumed directly by the grazing food chain. This is because phytoplankton, which form the base of the food web in aquatic ecosystems, are consumed almost immediately by zooplankton and other primary consumers. Unlike terrestrial ecosystems where much of the NPP enters the detrital food chain as dead plant material, the grazing food chain dominates in the open ocean due to the direct consumption of primary producers.

Information Booster:

1. **Open Ocean:**
    - Primary producers: Phytoplankton.
    - Most NPP is consumed directly by herbivores like zooplankton.
    - Little organic matter contributes to detrital pathways due to rapid consumption.
2. **Tropical Rainforest:**
    - High NPP, but most of it enters the detrital food chain as leaf litter and organic debris.
3. **Temperate Deciduous Forest:**
    - Moderate NPP, with a significant portion entering the detrital food chain due to leaf shedding and decomposition.
4. **Algal Seabed:**
    - Significant NPP but a smaller percentage is directly consumed compared to open ocean ecosystems.
5. **Key Factor in Open Oceans:**
    - Rapid turnover and efficient energy transfer between trophic levels contribute to the grazing food chain's dominance.

Additional Knowledge:

(a) Tropical rainforest:

This is **incorrect**. Although tropical rainforests have very high NPP, most of it enters the detrital food chain through decomposing leaves, fruits, and other organic matter rather than being consumed directly by herbivores.

(b) Temperate deciduous forest:

This is **incorrect**. Like tropical rainforests, a significant portion of NPP enters the detrital pathway rather than the grazing food chain.

(c) Algal seabed:

This is **incorrect**. While algal beds have high NPP, a larger proportion is retained in the system for structural growth, and less is consumed directly compared to open ocean ecosystems.

(d) Open ocean:

This is the **correct answer**. The grazing food chain dominates in open oceans due to the immediate consumption of phytoplankton by zooplankton and other grazers.