BT301 – INTRODUCTION TO BIOTECHNOLOGY

FINAL TERM MOST IMPORTANT QUESTIONS

Prepared by: Sir Mughal, Admin BS ZOOLOGY ANNOUNCEMENT

Group link: https://chat.whatsapp.com/BjC6W0jZx8o9yaC2ISh1Gu

1. Explain Paulin and Corey structure of protein?

The Pauling-Corey structure refers to the alpha-helix, a common secondary structure in proteins. Proposed by Linus Pauling and Robert Corey, it is a right-handed coiled structure with hydrogen bonds stabilizing the helical shape. The backbone of the helix is formed by peptide bonds, and the side chains of amino acids extend outward. This structural model was crucial in advancing our understanding of protein architecture.

2. Why plasmid stability is important?

Plasmid stability is important because it ensures the maintenance of genetic information carried by the plasmid within a host cell during cell division. Stable plasmids are crucial for consistent expression of desired traits, such as antibiotic resistance or production of specific proteins, in biotechnological and research applications.

3. What is a chromosome jumping?

Chromosome jumping, also known as chromosome walking or jumping library, is a molecular biology technique used to sequence DNA by moving from one known region of a chromosome to an unknown neighboring region. It involves creating a series of clones that span a genomic region, with each clone overlapping the previous one. By "jumping" from one clone to another, researchers can gradually move along the chromosome, mapping and sequencing regions of interest. This technique is particularly useful for exploring unknown genomic regions or isolating specific genes.

4. Write short note on RFLP.

RFLP stands for Restriction Fragment Length Polymorphism. It is a molecular biology technique that exploits variations in DNA sequences to create a unique pattern of fragments after digestion with restriction enzymes. The resulting fragments, which vary in length due to polymorphisms in the DNA sequence, can be separated by gel electrophoresis.

RFLP analysis is commonly used for genetic fingerprinting, mapping genes, and studying genetic variations. The technique relies on the fact that individuals within a population may have different restriction sites in their DNA, leading to different fragment patterns. By comparing these patterns, researchers can identify genetic variations and study the inheritance of specific alleles. While RFLP was widely used in the past, newer techniques like PCR-based methods and DNA sequencing have largely replaced it for many applications due to their higher sensitivity and efficiency.

5. How microarray is important in biotechnology for health?

Microarrays are crucial in health biotechnology for high-throughput analysis of gene expression, genetic variations, and molecular interactions. They enable simultaneous examination of thousands of genes, aiding in disease diagnosis, classification, and identification of potential therapeutic targets.

6. Write disadvantages of RT-PCR.

Limited Quantitative Precision:

RT-PCR may not provide highly accurate quantitative results, especially in the case of low-abundance transcripts.

Susceptibility to Inhibitors:

PCR reactions can be affected by the presence of inhibitors, contaminants, or degraded RNA, leading to inaccurate or failed results.

Prone to Contamination:

RT-PCR is susceptible to contamination issues, such as carry-over contamination from previous reactions, which can compromise the reliability of results.

Requirement for High-Quality RNA:

The success of RT-PCR depends on the quality of RNA, and degraded or impure RNA samples can lead to unreliable results.

Limited Multiplexing Capability:

Multiplexing (simultaneous amplification of multiple targets) can be challenging in RT-PCR due to the potential for primer interactions and variations in primer efficiencies.

Labor-Intensive:

The process involves multiple steps, including RNA extraction, cDNA synthesis, and PCR amplification, making it labor-intensive and time-consuming.

Not Suitable for Genome-Wide Analysis:

RT-PCR is a targeted approach and is not suitable for genome-wide analysis, limiting its ability to discover novel transcripts or variations.

7. Write a short note on Shotgun sequence.

Shotgun sequencing is a DNA sequencing method used to determine the nucleotide sequence of an entire genome. The approach gets its name from the analogy of breaking a genome into small, random fragments (like shooting a shotgun) and then sequencing these fragments individually. The process involves the following steps:

1. Fragmentation: The genomic DNA is randomly sheared into smaller fragments. This can be done mechanically or enzymatically.

2. Cloning: The fragments are then cloned into vectors, such as bacterial artificial chromosomes (BACs) or plasmids, creating a library of DNA clones.

3. Sequencing: Each clone is sequenced individually using traditional Sanger sequencing or modern high-throughput sequencing technologies.

4. Assembly: Computational algorithms are then employed to align and assemble the sequenced fragments into the original genome sequence.

8. Write one way to increase expression in cloned genes.

One way to increase the expression of cloned genes is to optimize the promoter region. The promoter is a DNA sequence that initiates the transcription of a gene. By selecting a strong and well-matched promoter for the host organism, you can enhance the transcription rate and, consequently, increase the expression of the cloned gene. Additionally, adjusting other regulatory elements in the expression cassette, such as enhancers or ribosome binding sites, can also contribute to improved gene expression levels.

9. What are cosmids?

Cosmids are hybrid DNA molecules that combine features of plasmids and bacteriophages. They are used as vectors in molecular biology for cloning and manipulating large DNA fragments, making them useful for constructing genomic libraries and studying specific genes or genomic regions.

10. What is Fluorescent In Situ Hybridization (FISH)?

Fluorescent In Situ Hybridization (FISH) is a molecular biology technique that allows the visualization and mapping of specific DNA sequences within cells or tissues. The process involves using fluorescently labeled DNA probes that are complementary to the target DNA sequence of interest. Here's a brief overview:

1. Probe Design: Fluorescently labeled DNA probes are designed to be complementary to a specific target DNA sequence. These probes are usually labeled with fluorescent dyes of different colors.

2. Hybridization: The labeled probes are incubated with the biological sample (cells or tissue), allowing them to hybridize or bind specifically to the complementary target sequences within the sample.

3. Washing: Excess, unbound probes are washed away to remove nonspecific binding.

4. Detection: The sample is then examined under a fluorescence microscope to visualize the fluorescent signals emitted by the bound probes. Each color represents a specific DNA sequence.

11. What is primer and primer extension?

Primer:

A short single-stranded nucleic acid sequence that serves as a starting point for DNA synthesis in PCR (polymerase chain reaction) or DNA sequencing.

Primer Extension:

The process in which DNA polymerase synthesizes a complementary strand of DNA using a primer as a starting point, typically occurring during PCR or DNA replication.

12. What are main features of Real Time PCR and multiplex PCR?

Real-Time PCR:

Continuous Monitoring: Allows real-time monitoring of the amplification of DNA during the PCR reaction.

Quantification: Provides quantitative data on the amount of initial DNA present in the sample.

Fluorescent Probes: Uses fluorescent dyes or probes to detect accumulating PCR product in each cycle.

High Sensitivity: Enables the detection of PCR amplification as it occurs, facilitating precise quantification and analysis.

Multiplex PCR:

Multiple Targets: Amplifies multiple DNA targets in a single reaction tube.
Primers: Uses multiple sets of primers, each specific to a different target sequence.
Single Reaction: Reduces the time and resources needed for analyzing multiple targets.
Applications: Commonly used for genotyping, pathogen detection, and simultaneous amplification of related genes.

13. Write contributions of Franklin and Wilkins.

Rosalind Franklin and Maurice Wilkins made significant contributions to the understanding of the structure of DNA. Their work was crucial in providing essential data for James Watson and Francis Crick, who later proposed the double helix model of DNA. Here are their main contributions:

Rosalind Franklin:

1. X-ray Diffraction Studies: Franklin used X-ray crystallography to study the structure of DNA fibers and produced high-resolution images.
2. Photograph 51: Franklin's famous Photograph 51, taken in 1952, provided key insights into the helical structure of DNA.
3. Helical Parameters: Her analysis of X-ray diffraction data yielded important information about the helical nature of DNA, including the diameter and spacing of the helix.

Maurice Wilkins:

1. Collaboration with Franklin: Wilkins worked at King's College London alongside Franklin and used X-ray diffraction to study DNA.
2. Sharing Data with Watson and Crick: Wilkins shared Franklin's X-ray diffraction images, including Photograph 51, with James Watson and Francis Crick, providing crucial information for their model-building efforts.
3. Nobel Prize: Wilkins, along with Watson and Crick, was awarded the Nobel Prize in Physiology or Medicine in 1962 for their discoveries related to the structure of DNA.

14. Write a detailed note on RAPD.

RAPD (Random Amplified Polymorphic DNA):

Introduction:

Random Amplified Polymorphic DNA (RAPD) is a polymerase chain reaction (PCR)-based technique used for DNA fingerprinting and genetic marker analysis. It is a simple and rapid method that does not require prior knowledge of the DNA sequence.

Procedure:

1. Random Primers: RAPD utilizes short, arbitrary, single-stranded DNA primers (usually 10 nucleotides long) that bind to multiple sites in the genome.

2. DNA Amplification: The primers initiate the amplification of random genomic DNA segments through PCR. The reaction is performed with a mix of these primers, allowing the amplification of diverse, randomly distributed regions.

3. Amplification Products: The result is a set of DNA fragments of varying sizes, reflecting polymorphisms in the genomic regions covered by the primers. These fragments represent the unique fingerprint of the analyzed DNA.

4. Electrophoresis: The amplified DNA fragments are separated by gel electrophoresis, and the resulting banding pattern is visualized, often using ethidium bromide staining or other DNA-binding dyes.

Applications:

1. Genetic Diversity: RAPD is used to assess genetic diversity within and among populations. Variability in banding patterns indicates genetic differences.

2. DNA Fingerprinting: It is employed for individual identification, paternity testing, and forensic analysis due to the uniqueness of RAPD profiles.

3. Marker Analysis: RAPD markers can be used to construct genetic maps, identify linked genes, and study genetic traits in different organisms.

4. Taxonomy and Phylogenetics: RAPD is utilized to study evolutionary relationships and classify organisms based on genetic similarities and differences.

Advantages:
- Simplicity and rapidity in obtaining results.
- No prior sequence information is required.
- Applicability across various organisms.

Limitations:
- Lack of reproducibility in some cases.
- Sensitivity to reaction conditions.
- Difficulty in standardization and interpretation.

15. Write functions of mRNA.

Transcription Template: Serves as a template during transcription, carrying genetic information from the DNA to the ribosomes.

Messenger Molecule: Acts as a messenger between the nucleus and the ribosomes, conveying the genetic code for protein synthesis.

Codon Specification: Contains codons, three-nucleotide sequences that specify the amino acids to be incorporated into a growing polypeptide chain during translation.

Carries Genetic Information: Carries the genetic instructions from the DNA in the cell nucleus to the ribosomes in the cytoplasm where protein synthesis occurs.

Transcription and Translation Link: Bridges the processes of transcription and translation, ensuring the accurate synthesis of proteins based on the genetic code.

Alternative Splicing: Undergoes alternative splicing in eukaryotes, allowing different protein isoforms to be generated from a single gene.

Regulatory Roles: Some mRNAs play regulatory roles, influencing the expression of genes by interacting with other molecules involved in gene expression.

Degradation Control: The stability and degradation of mRNA molecules are regulated, influencing the duration of the genetic message and protein production.

16. What is SiRNA strategy?

The siRNA (Short Interfering RNA) strategy involves using short RNA molecules to specifically silence target gene expression by guiding the RNA-induced silencing complex (RISC) to degrade complementary mRNA, preventing protein synthesis. It is employed in gene knockdown studies and shows therapeutic potential for diseases with aberrant gene expression.

17. Write steps of cloning.

1. Selection of DNA: Choose the DNA fragment or gene of interest to be cloned.

2. Insertion into Vector: Introduce the DNA fragment into a cloning vector, often a plasmid or a viral vector.

3. Ligation: Use DNA ligase to covalently link the DNA fragment to the vector, forming a recombinant DNA molecule.

4. Transformation: Introduce the recombinant DNA into host cells, such as bacteria, using a method like heat shock or electroporation.

5. Selection: Identify transformed cells by selecting for a marker present on the vector, such as antibiotic resistance.

6. Culturing and Expression: Culture the selected cells to amplify the cloned DNA, and if applicable, induce expression of the inserted gene.

7. Harvesting: Collect the cells or the expressed protein or product.

8. Purification: Purify the cloned DNA or the expressed product for downstream applications or analysis.

18. What are types of chromosomes based on the location of centromere?

Based on the location of the centromere, chromosomes can be classified into four main types:

1. Metacentric Chromosomes:

Centromere is located near the middle, creating arms of approximately equal length resulting in a V-shaped or Y-shaped chromosome appearance.

2. Submetacentric Chromosomes:

Centromere is slightly off-center, resulting in one arm longer than the other and creates an L-shaped chromosome.

3. Acrocentric Chromosomes:

Centromere is near one end, leading to one very long arm and a much shorter arm. Often appears J-shaped or L-shaped.

4. Telocentric Chromosomes:

Centromere is located at the very end of the chromosome. Creates a rod-like structure with only one arm.

19. Differentiate between genetics and genomics.

Genetics:

1. Focus:

Genetics is the study of individual genes and their role in inheritance. It traditionally focuses on the study of single genes and their variations.

2. Scope:

It is concerned with the structure, function, and inheritance of genes at the molecular and organismal levels. It examines how traits pass from one generation to the next.

3. Methods:

Classical genetics involves Mendelian principles, studying traits governed by single genes. Molecular genetics explores the structure and function of genes at the DNA and molecular levels.

4. Applications:

Applied in understanding and treating genetic disorders, selective breeding, and traditional plant and animal breeding.

Genomics:

1. Focus:

Genomics is the study of the entire genome, encompassing all genes and their interactions. It explores the organization and function of all the genetic material in an organism.

2. Scope:

It encompasses a broader and more holistic view, including the study of genes, non-coding DNA, and interactions among genes. It involves the analysis of entire genomes, such as the human genome.

3. Methods:

It involves high-throughput techniques to analyze complete DNA sequences and understand the structure and function of all genes in an organism. It includes bioinformatics for large-scale data analysis.

4. Applications:

Applied in personalized medicine, functional genomics, comparative genomics, and understanding the genetic basis of complex traits.

20. Define in short, primary, secondary and tertiary structure of proteins.

1. Primary Structure:

The primary structure of a protein refers to the linear sequence of amino acids in its polypeptide chain. The sequence is dictated by the genetic code encoded in DNA, and any alteration in this sequence can impact the protein's function. Amino acids are linked together by peptide bonds, forming the backbone of the polypeptide.

2. Secondary Structure:

Secondary structure involves the local folding of the polypeptide chain into specific patterns. Two common types of secondary structures are alpha helices and beta sheets. Alpha helices are formed by a helical coil of the polypeptide chain stabilized by hydrogen bonds while beta sheets involve a sheet-like structure where adjacent strands are connected by hydrogen bonds.

3. Tertiary Structure:

Tertiary structure refers to the three-dimensional arrangement of the entire polypeptide chain. This level of organization is influenced by interactions between amino acid side chains, including hydrogen bonds, disulfide bridges, hydrophobic interactions, and van der Waals forces. The folding results in a compact and functional protein structure.

21. Explain VNTR and its five applications.

VNTR, or Variable Number Tandem Repeat, refers to a type of genetic variation that involves the repetition of a short DNA sequence in tandem (in a consecutive manner) at a particular locus in the genome. These repetitive sequences vary in length among individuals, contributing to genetic diversity. VNTRs have several applications in various fields, including forensics, genetics, and anthropology. Here are five applications of VNTR:

1. DNA Fingerprinting:

VNTR analysis is commonly used in DNA fingerprinting for forensic purposes. The unique pattern of VNTR alleles in an individual's DNA can be used to identify and distinguish one person from another. By comparing the VNTR profiles of a crime scene sample with those of potential suspects, forensic investigators can establish or rule out connections between individuals and biological samples.

2. Population Genetics:

VNTR analysis is valuable in population genetics studies. The variation in the number of repeats at a specific VNTR locus can provide insights into the genetic diversity within and among populations. Researchers use VNTR data to study population structures, migrations, and evolutionary relationships among different groups.

3. Paternity Testing:

VNTR analysis can be employed in paternity testing to determine biological relationships between individuals. The comparison of VNTR profiles between a child and potential parents helps establish or exclude parentage. The unique pattern of VNTR alleles inherited from both parents can serve as a genetic marker for paternity testing.

4. Medical Genetics:

VNTRs are sometimes associated with certain genetic disorders. Studying the variations in the number of repeats can aid in identifying genetic markers linked to diseases. VNTR analysis can contribute to the understanding of the genetic basis of conditions and may have diagnostic implications in medical genetics.

5. Anthropology and Population History:

VNTR analysis plays a role in anthropological and population history research. By examining VNTR variation in different human populations, scientists can investigate historical migration patterns and demographic changes. These studies provide insights into human evolution, population movements, and the relatedness of different ethnic groups.

22. Write procedure of western blotting.

Western Blotting Procedure:

1. Protein Extraction:

- Lyse cells or tissues to release proteins.
- Use a lysis buffer to break down cell membranes and nuclei.

2. Protein Quantification:

- Measure protein concentration using methods like Bradford or BCA assay.

3. SDS-PAGE Electrophoresis:

- Separate proteins based on size using SDS-PAGE gel.
- Load samples into wells, apply electric current to migrate proteins.

4. Protein Transfer:

- Transfer separated proteins from gel to a membrane (usually nitrocellulose or PVDF).
- Employ wet or semi-dry transfer systems.

5. Blocking:

- Block non-specific binding sites on the membrane with a blocking agent

6. Primary Antibody Incubation:

- Incubate membrane with primary antibody specific to the target protein.
- Antibody binds to the protein of interest.

7. Washing:

- Remove excess unbound primary antibody by washing the membrane.

8. Secondary Antibody Incubation:

- Incubate membrane with a secondary antibody conjugated to a detection molecule (e.g., enzyme or fluorophore).

9. Washing:

- Remove excess unbound secondary antibody by washing the membrane.

10. Detection:

- Visualize protein bands using a substrate that reacts with the enzyme on the secondary antibody (e.g., chemiluminescence for enzyme-linked antibodies).

11. Image Capture:

- Capture the chemiluminescent signal using an imaging system.

12. Analysis:

- Quantify protein bands using densitometry.
- Compare protein expression levels across samples.

23. What are effects of environment on allelic expression?

Effects of Environment on Allelic Expression:

Epigenetic Changes: Environmental factors can induce epigenetic modifications (e.g., DNA methylation) influencing the expression of specific alleles.

Temperature and Nutrients: External conditions like temperature and nutrient availability can impact gene expression, potentially affecting allelic expression patterns.

Exposure to Toxins: Environmental toxins can cause changes in gene expression, influencing allelic expression and potentially contributing to health-related outcomes.

Developmental Factors: Environmental cues during development can influence allelic expression patterns, shaping the phenotype of an organism.

Adaptation to Local Conditions: Populations may undergo allelic expression changes over generations in response to local environmental conditions, contributing to adaptation.

24. What is trisomy and its types?

Trisomy:

Trisomy is a genetic condition characterized by the presence of an additional chromosome in a cell, resulting in a total of three copies of that particular chromosome instead of the normal two. This numerical chromosomal abnormality can lead to various developmental and health issues.

Types of Trisomy:

1. Trisomy 21 (Down Syndrome):

It is caused by an extra copy of chromosome 21. Individuals with Down syndrome often exhibit intellectual disabilities, distinctive facial features, and may have associated health problems.

2. Trisomy 18 (Edwards Syndrome):

It is caused by an extra copy of chromosome 18. Individuals with Edwards syndrome typically experience severe intellectual disabilities and multiple physical abnormalities, often leading to a shortened lifespan.

3. Trisomy 13 (Patau Syndrome):

It is caused by an extra copy of chromosome 13. Patau syndrome results in severe intellectual disabilities and various congenital anomalies, affecting multiple organ systems.

4. Trisomy 8 (Warkany Syndrome 2):

It involves an extra copy of chromosome 8. Trisomy 8 is relatively rare and can result in a variety of developmental and physical abnormalities.

5. Trisomy 9:

It involves an extra copy of chromosome 9. Trisomy 9 is rare, and individuals with this condition may exhibit intellectual disabilities and multiple congenital anomalies.

6. Trisomy 16:

Full trisomy 16 is typically incompatible with life, leading to miscarriage early in pregnancy. Mosaicism involving trisomy 16 can result in surviving individuals with a range of developmental and health issues.

25. Differentiate between ring chromosome and Philadelphia chromosome.

1. Ring Chromosome:

Structure: A ring chromosome is a structural abnormality in which both ends of a broken chromosome fuse together to form a circular or ring-like structure.
Formation: It often occurs as a result of breakage in both arms of a chromosome, followed by the reunion of the broken ends in a circular configuration.
Effects: Ring chromosomes can lead to genetic imbalances and are associated with various developmental and health issues, depending on the specific chromosome involved and the extent of genetic material loss.

2. Philadelphia Chromosome:

Structure: The Philadelphia chromosome is a specific chromosomal abnormality involving a translocation between chromosomes 9 and 22.
Formation: It results from a reciprocal translocation between the long arms of chromosome 9 and 22, leading to the fusion of the ABL1 gene on chromosome 9 with the BCR gene on chromosome 22.
Association: The Philadelphia chromosome is strongly associated with chronic myeloid leukemia (CML) and a subset of acute lymphoblastic leukemia (ALL). The fusion gene created by the translocation, known as BCR-ABL1, produces a protein with abnormal tyrosine kinase activity, contributing to the development of these cancers.

26. What are effects of point mutation?

Silent Mutation:

- No change in amino acid sequence.
- Often occurs in non-coding regions.
- Typically has no discernible effect on the phenotype.

Missense Mutation:

- Single amino acid change in the protein.
- Impact depends on the nature of the amino acid substitution.
- Can be neutral, deleterious, or beneficial.

Nonsense Mutation:

- Introduces a premature stop codon.
- Leads to truncation of the protein.
- Often results in a nonfunctional or severely impaired protein.

Frameshift Mutation:

- Insertion or deletion of nucleotides.
- Causes a shift in the reading frame of mRNA.
- Results in altered amino acid sequence downstream of the mutation.

Splice Site Mutation:

- Affects proper splicing of pre-mRNA.
- Alters splicing patterns, leading to abnormal mRNA transcripts.
- Can result in dysfunctional or nonfunctional proteins.

Regulatory Region Mutations:

- Occur in non-coding regions like promoters or enhancers.
- Affect gene expression and transcription.
- Impact the amount of functional protein produced.

Gain-of-Function or Loss-of-Function:

- Gain-of-function mutations result in a protein with enhanced or new activities.
- Loss-of-function mutations lead to reduced or abolished protein function.
- Important in understanding the molecular basis of genetic disorders.

27. How large amount of DNA is packed in small volume?

DNA is tightly packed in a small volume through its double helix structure, wrapping around histone proteins to form nucleosomes. Further folding into chromatin, loop domains, and condensed chromosomes during cell division enables the compact packaging of a large amount of genetic information within the small volume of a cell nucleus.

28. What is cosmid vector?

A cosmid vector is a type of hybrid plasmid vector used in molecular biology to clone and manipulate DNA fragments. It combines features of plasmids and bacteriophages (cos sites) and can carry larger DNA inserts than typical plasmids, making it useful for genomic library construction and gene cloning.

29. What is genome mapping?

Genome mapping is the process of identifying and establishing the spatial relationships between genes and other features on a chromosome or an entire genome. It provides a structural overview of the genetic material, including the positions of genes, markers, and other genomic elements, aiding in understanding genetic organization and function.

30. Write primary structure of protein.

The primary structure of a protein is the linear sequence of amino acids that constitute its polypeptide chain. It is determined by the specific order of amino acids linked together by peptide bonds. The sequence is encoded by the genetic information in DNA, and it serves as the foundation for the higher levels of protein structure. The primary structure is crucial for the protein's overall function and biological activity.

31. What is importance of genetic research?

- Identifying genetic factors contributing to diseases helps in understanding their causes and developing targeted treatments.
- Genetic research aids in discovering and developing drugs based on the understanding of specific genetic mechanisms.
- Allows for personalized medical treatments based on an individual's genetic makeup, optimizing therapeutic interventions.
- Genetic information enables the prediction of susceptibility to certain diseases, facilitating preventive measures.
- Genetic research enhances crop yield, disease resistance, and nutritional content in agriculture.
- Helps in understanding and preserving genetic diversity in endangered species.
- Genetic markers aid in forensic investigations for accurate identification and solving crimes.
- Contributes to understanding the evolutionary relationships between species and the mechanisms driving evolution.

- Provides insights into reproductive issues, fertility treatments, and genetic disorders affecting pregnancy.

- Raises awareness about ethical implications, ensuring responsible use of genetic information and technologies.

- Facilitates advancements in biotechnology, such as gene therapy, genetically modified organisms, and synthetic biology.

- Genetic research contributes to addressing global health challenges by understanding infectious diseases and developing vaccines.

- Enables the development of genetic tests for early diagnosis and prognosis of various conditions.

- Genetic techniques serve as fundamental tools for studying biological processes and advancing scientific knowledge.

- Enhances education by providing insights into the genetic basis of life and promoting scientific literacy.

32. What is nutritional value of genetic engineering?

- Genetic engineering can enhance essential nutrient levels in crops.

- Genetically modified plants can better absorb and utilize nutrients from the soil.

- Genetic modifications can decrease naturally occurring anti-nutritional substances in crops.

- Genetic modifications for improved yield indirectly contribute to a more abundant food supply.

- Genetic engineering can confer disease resistance, preserving crop yield and nutritional quality.

- Sustainable agriculture practices facilitated by genetic engineering can positively impact the environment and indirectly support nutritional quality.

33. Write role of bio-fertilizers.

- Certain bio-fertilizers, like nitrogen-fixing bacteria (e.g., Rhizobium), convert atmospheric nitrogen into a form usable by plants, enhancing soil fertility.

- Phosphate-solubilizing bacteria release phosphorus from insoluble compounds, making it available to plants for better growth and development.

- Bio-fertilizers can facilitate the mobilization of potassium, promoting its availability to plants for essential physiological processes.

- Bio-fertilizers enhance nutrient uptake efficiency by promoting the development of a healthy and extensive root system.

- The activities of bio-fertilizers can enhance soil structure, promoting better water infiltration and root penetration.

- Bio-fertilizers often have lower environmental impacts compared to chemical fertilizers, reducing the risk of soil and water pollution.

- Bio-fertilizers support sustainable agricultural practices by promoting natural processes in the soil and reducing dependence on synthetic inputs.

- Bio-fertilizers contribute to the efficient cycling of nutrients in the ecosystem, maintaining soil fertility over the long term.

- Certain bio-fertilizers establish symbiotic relationships with leguminous plants, leading to nitrogen fixation and improved soil fertility.

- Bio-fertilizers are adaptable to a wide range of crops, providing a versatile and eco-friendly option for different agricultural systems.

- In the long run, the use of bio-fertilizers can be cost-effective, as they contribute to sustainable soil health and reduce the need for synthetic fertilizers.

- Bio-fertilizers encourage the proliferation of beneficial microorganisms in the soil, contributing to a balanced and healthy microbial community.

Compiled by:
Sir Mughal
0313-2310940

34. Write steps of initiation and maintenance in callus medium?

Initiation of Callus Culture:

1. Selection of Explants:
Choose plant tissues (explants) for initiating callus culture. These can include segments from leaves, stems, roots, or other plant parts.

2. Surface Sterilization:
Clean and sterilize the selected explants to eliminate contaminants. Common methods include washing in detergent, followed by treatment with disinfectants like ethanol or sodium hypochlorite.

3. Explant Placement:
Place the sterilized explants onto a solid culture medium containing nutrients, plant growth regulators (PGRs), and a source of energy (usually sugars).

4. Incubation:
Incubate the culture in a controlled environment (temperature, light, and humidity) to promote the initiation of callus. Maintain aseptic conditions to prevent contamination.

5. Observation and Sub-culturing:
Monitor the explants for the development of callus tissue. Subculture the initiated callus onto fresh medium periodically to encourage its growth.

Maintenance of Callus Culture:

1. Sub-culturing:
Transfer a portion of the callus onto fresh medium periodically to provide essential nutrients and prevent depletion.

2. Medium Composition Adjustment:
Adjust the composition of the culture medium based on the requirements of the specific callus culture. This may include modifying the concentration of nutrients and growth regulators.

3. Monitoring Growth Conditions:
Regularly monitor and maintain optimal growth conditions, including temperature, light intensity, and humidity. Adjust environmental parameters as needed.

4. Controlled Environment:

Ensure a controlled environment to regulate factors like temperature and photoperiod, which can influence callus growth and development.

5. Sub-culture Interval:

Determine the optimal sub-culture interval based on the growth rate of the callus. Sub-culture too frequently to maintain actively growing callus and prevent overgrowth or senescence.

6. Observation and Documentation:

Continuously observe the characteristics of the callus, such as color, texture, and growth pattern. Document changes in morphology or any signs of contamination.

7. Scale-Up or Cryopreservation (Optional):

Depending on the goals of the callus culture, consider scaling up the culture for biomass production or cryopreserving valuable callus lines for long-term storage.

35. Write 6 symptoms of pesticides poisoning.

1. Nausea and vomiting
2. Headaches and dizziness
3. Difficulty breathing
4. Skin irritation
5. Eye irritation
6. Fatigue

36. Write advantages of genetically modified crops.

- Genetically modified crops often exhibit enhanced resistance to pests, diseases, and environmental stressors, leading to higher yields.

- Some genetically modified crops are designed to be resistant to pests, reducing the reliance on chemical pesticides and promoting environmentally friendly farming practices.

- Genetic modifications can enhance the nutritional profile of crops, providing essential vitamins and minerals, thus addressing nutritional deficiencies in certain foods.

- Some genetically modified crops are engineered to withstand water scarcity, allowing for better adaptation to arid or drought-prone regions.

- Genetic modifications can accelerate the growth and maturation of crops, potentially leading to quicker harvests and increased efficiency in agricultural production.

- Genetic modifications can improve the overall quality of crops by minimizing spoilage, reducing susceptibility to diseases, and ensuring better post-harvest storage.

37. Write method of regeneration.

In the context of biotechnology, regeneration often refers to the process of re-growing or redeveloping organisms or tissues from cells or genetic material. One common method involves using tissue culture techniques. Here's a general outline:

1. Selection of Source Material:
Choose the specific cells, tissues, or genetic material from the organism that will be used for regeneration. This could include stem cells, explants, or specific DNA sequences.

2. Initiation of Tissue Culture:
Place the selected material in a controlled environment conducive to cell growth. This is typically done through tissue culture, where cells are provided with the necessary nutrients and conditions for proliferation.

3. Cell Proliferation:
Allow the cells to multiply and proliferate in the culture medium. This phase may involve the use of growth hormones or other signaling molecules to encourage cell division.

4. Differentiation (if required):
Guide the cells to differentiate into specific cell types if the goal is to regenerate a particular tissue or organ. This may involve manipulating the culture conditions or adding differentiation-inducing factors.

5. Organism or Tissue Formation:
As the cells continue to divide and differentiate, they may eventually form tissues or even entire organisms in vitro.

6. Acclimatization and Transplantation:
Gradually acclimatize the regenerated tissues or organisms to environmental conditions outside the controlled culture. If necessary, transplant the regenerated material into the target environment.

7. Monitoring and Optimization:

Monitor the regenerated organisms or tissues for health and functionality. Adjust the culture conditions or other parameters as needed to optimize the regeneration process.

38. Define autoradiography.

Autoradiography is a technique used in molecular biology and histology to visualize the distribution of radioactive substances in a sample. It involves exposing a photographic or emulsion film to a specimen containing radioactive isotopes, producing an image that corresponds to the location and intensity of radioactively labeled molecules in the sample.

39. What is pseudo gene?

A pseudogene is a DNA sequence that resembles a functional gene but has become inactivated or nonfunctional over the course of evolution. Pseudogenes can result from mutations, duplications, or rearrangements in the DNA that render them unable to produce a functional protein or RNA molecule. While they may have similarities to actual genes, pseudogenes typically do not contribute to the organism's physiology or development. They are considered as remnants of once-functional genes and are often used in evolutionary studies to trace genetic changes over time.

40. What are expression libraries?

Expression libraries are collections of DNA sequences that represent the expressed genes of an organism. These libraries are created by isolating and cloning the messenger RNA (mRNA) molecules present in a particular tissue or cell type. The process involves converting mRNA into complementary DNA (cDNA) and then inserting this cDNA into a vector, such as a plasmid or a viral vector. The resulting collection of clones represents the genes that are actively transcribed and expressed in the chosen tissue at a specific point in time.

41. What is pilandromic sequence?

A palindromic sequence refers to a nucleotide or amino acid sequence that reads the same backward as forward. In the context of DNA sequences, this means that the sequence on one strand is identical to its complementary sequence on the opposing strand when read in the opposite direction. Palindromic sequences are often relevant in molecular biology and genetics due to their association with certain features, such as recognition sites for restriction enzymes.

42. Write uses of hybrid sequence.

- Hybrid sequences result from the combination of genetic material from two different parent organisms, promoting genetic diversity.

- Hybridization in plants and crops can lead to improved characteristics such as higher yield, disease resistance, and environmental adaptability.

- Hybrid vigor, also known as heterosis, often results in hybrids exhibiting superior traits compared to their parent organisms, including better growth, fertility, and overall performance.

- Hybridization in animals, especially livestock, can lead to improved traits such as increased growth rate, disease resistance, and overall productivity.

- Hybrid sequences allow for selective breeding to emphasize specific traits, helping to develop organisms with desired characteristics.

- Hybridization can contribute to the conservation and preservation of endangered species by increasing genetic variability and improving reproductive success.

- Hybrid sequences are often used in the creation of transgenic organisms, where genes from one species are introduced into the genome of another to confer specific traits or functions.

- Genetic engineering techniques use hybrid sequences to introduce specific genes into crops, leading to improvements in traits such as pest resistance, herbicide tolerance, and nutritional content.

43. What is inverse PCR?

Inverse PCR (iPCR) is a molecular biology technique used to amplify DNA fragments adjacent to a known sequence. It involves the amplification of DNA sequences by using primers that are oriented in the opposite direction to the traditional PCR method. This technique is particularly useful for identifying and studying regions flanking known DNA sequences, such as insertion sites in transgenic organisms or regions adjacent to a known DNA modification.

44. What is pregnancy test?

A papyrus described a test in which a woman who might be pregnant could urinate on wheat and barley seeds over the course of several days: “If the barley grows, it means a male child. If the wheat grows, it means a female child. If both do not grow, she will not bear at all.” Testing of this theory in 1963 found that 70 percent of the time, the urine of pregnant women did promote growth, while the urine of non-pregnant women and men did not. Scholars have identified this as perhaps the first test to detect a unique substance in the urine of pregnant women, and have speculated that elevated levels of estrogens in pregnant women’s urine may have been the key to its success

45. Write chemical composition of DNA.

The chemical composition of DNA includes:

Nucleotides:

Adenine (A), Thymine (T), Cytosine (C), and Guanine (G).

Deoxyribose Sugar:

The sugar component in the DNA backbone is deoxyribose.

Phosphate Groups:

Phosphate groups link the nucleotides together, forming the backbone of the DNA molecule.

46. What is chain termination?

Chain termination refers to the process by which the synthesis of a DNA or RNA strand is abruptly halted during enzymatic replication or sequencing. This interruption prevents the addition of further nucleotides to the growing chain. Chain termination is a crucial concept in DNA sequencing techniques, particularly in the Sanger sequencing method.

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