

TOPIC : Molecular Basis of Inheritance

Pre-content/Content/ Post-Content	Learning Outcome/Objectives	
	General	Specific
Pre-Content Basic Knowledge of genetics, DNA. Content Structure of DNA and its packaging; RNA structure Which is the genetic material ? - experimental proof. Replication, transcription, translation Regulation of gene expression, Human Genome Project DNA fingerprinting. Post-Content Extraction of DNA, rDNA technology, project on DNA fingerprinting	Students will be able to: -Value the contribution of various geneticists who discovered various phenomena -Cite cases related to & solved through DNA finger-printing -Understand how society has benefitted from principles of genetics -Appreciate the advancements in biology like genome project, DNA fingerprinting, that can help find cure to a disease and solutions to other problems.	Students will be able to : - Draw the structure of DNA & RNA. - State the central dogma of molecular biology - Explain why DNA is the genetic material and how it can be synthesized & packaged - Draw structure of nucleosome - Describe the processes of replication, transcription and translation - List the salient features of HGP - Explain the methods used in genome sequencing - Comprehend the principle behind DNA finger-printing

Homework and Assignments:

To answer questions at the end of the chapter

To draw structure of DNA & RNA

Teacher's Activity	Student's Activity	Teacher's Observation And Remedial
Teacher will: -Ask students to draw structure of DNA; Model of DNA will be shown -Guide for Activity: A string & a ball will be given to students to wind twice around it -Activity based Learning: Blocks will be used to show base pairing & different kinds of mutations (Annexure 1) -Draw successive diagrams to explain Lytic cycle & Hershey & Chase experiment -Help answer open ended and other questions given in the text after discussing DNA replication and Meselson & Stahl's expt. -Transcription & translation will be explained through ppts and videos -Discuss how genetic code was deciphered through Activity based Learning (Annexure 2) -Conduct brain storming session to help arrive at the definitions of genes -Use smart board to draw and discuss gene expression as in 'lac operon' -Be Facilitator for Activity based Learning on HGP (Annexure 3) -Discuss DNA fingerprinting through ppt & practice questions -Explain the technique of DNA fingerprinting & ask its applications	Students will: -Try to draw the structure -Compare the structure with the diagram in the book & called it model of Nucleosome. -Give the base pairing rule; Note their observations, compare & discuss the result of the activity. -Familiarize themselves with the working of centrifuge and the lytic cycle of viruses -Draw diagram of replication fork & transcription unit; explain the steps of the two processes -State the role of tRNA, mRNA, rRNA -Explain the steps of translation -Mention salient features of genetic code after participating in the activity -State role of each segment of the lac operon -Try to understand the new concepts, by participating in the activity -Refer to some Journals & mention applications of DNA finger printing	Few students are able to draw Structure of DNA- in some cases, it was rectified & redrawn Students are able to draw diagram of nucleosome; Can apply Chargaff's rule. Students listed points regarding attributes of genetic material; on how frame-shift mutations can happen They can answer questions on replication, transcription & translation Students answer open-ended questions given in the text Enthusiastically participated in the activity Students describe 'lac operon' in E.coli Students are able to list salient features of Human Genome Project; Cite famous cases while stating applications of DNA fingerprinting

Teaching Aids : Model of DNA, low cost material-blocks, ball, string, markers, ppts, videos, computer, smart board

Methodology/Innovative Methods: Activity based Learning, Ques.-Ans. Method, Computer-Aided Instruction

Interdisciplinary Links: Forensic Science, Sociology, Law .

Vice-Principal

Principal

ANNEXURE 1

Activity – Gene Mutation

Subject	Biology
Class	XII
Chapter	Molecular Basis of Inheritance
Topic	Mutation
Duration	2 periods
Nature of the Activity	Individual

What will I learn? (Learning Outcome) –understand the mechanism of Gene Mutation, classify the kinds of gene mutations under- insertion, deletion, substitution, frame-shift mutation

Skills- Observing, Identifying, Classifying

What I have to do? –To perform an activity to demonstrate the kinds of point mutation

What do I require?

- building blocks on which different alphabets are written
- paper strips on which- A,T,G,C are written
- glue

What do I need to know?

DNA replication, Transcription, Translation, Universal Genetic code, Central dogma of Molecular Biology

- **Teacher's activity-** Teacher will give the instructions along with the protocol (Student's activity)
- Teacher will tell students to make a sentence having three alphabets in each word, like- Tim got red car. To proceed as per instructions, always keeping the reading frame such that only three letters were to be read together

How will I proceed?

- **Student's activity**
 1. To make a sentence like- TOM HAS ONE BAT, using the blocks
 2. Remove a block, say 'M' and read the sentence such that only three letters are read together
 3. Add a block, say 'C' after 'M' and read the sentence such that only three letters are read together
 4. Replace block 'M' with 'Y' and read the sentence
 5. See if the sentences framed in steps 2, 3, 4, make sense

6. Paste several strips of A,T,G,C on the blocks and make a model of a DNA fragment with sequence 5' AATCGGCATCGG 3'
7. Write the complimentary DNA strand, write the mRNA formed and the oligopeptide (using genetic code)
8. Similarly, remove the 3rd base from the model, write the complimentary DNA strand, write the mRNA formed and the oligopeptide (using genetic code)
9. Add 'T' after the 3rd base, write the complimentary DNA strand, write the mRNA formed and the oligopeptide (using genetic code)
10. Replace C on 4th place with T, write the complimentary DNA strand, write the mRNA formed and the oligopeptide (using genetic code)
11. Write the sequence of all the segments- DNA, mRNA, and the oligopeptide.
12. Compare your answers in step 7, with those in steps 8, 9,10

What have I observed?

Correct Sentence	TOM HAS ONE BAT
Sentence after removal of an alphabet (Step 2)	
Sentence after addition of an alphabet(Step 3)	
Sentence after replacement of an alphabet (Step 4)	
Correct Sequence	5' AATCGGCATCGG 3'
Complementary Sequence of the DNA after removal of a base (Step 8)	-----
Complementary Sequence of the DNA after addition of a base (Step 9)	-----
Complementary Sequence of the DNA after replacement of a base (Step 10)	-----
Sequence of the mRNA (in 5' to 3' direction) after removal of a base	----- Call it [I]
Sequence of the mRNA (in 5' to 3' direction) after addition of a base	----- Call it [II]
Sequence of the RNA (in 5' to 3' direction) after replacement of a base	----- Call it [III]
Oligopeptide formed from [I] { Refer to Genetic code given in Biology text book (Class XII) -Table 6.1 }	

Oligopeptide formed from [II] (Refer Genetic code given in text book -Table 6.1)	
Oligopeptide formed from [III] (Refer Genetic code given in text book -Table 6.1)	

Even a single gene mutation can lead to formation of an altered complimentary strand of DNA, an altered mRNA and addition of altered amino acids in the peptide chain, resulting in a truncated protein and thus abnormal phenotype/ functioning of the cell/ organism.

What have I learnt?

Addition/ deletion, can lead to frame shift mutation leading to formation of a different mRNA (after the point mutation), resulting in different amino acids hence leading to formation of a totally altered protein. Substitution could finally lead to replacement of correct amino acid with a different (altered) amino acid, hence forming an altered protein, leading to diseases like Sickle Cell Anaemia.

What would I like to know ?

What is Wobble hypothesis? What are silent mutations?

Let me Evaluate myself-

1. What is another term for point mutation?
2. List the points that you will include in the definition of 'Mutation.'
3. Explain how sickle cell anaemia is caused, from the point of central dogma of molecular biology.
4. If the sequence on mRNA strand is 5' AUGUCCUGAACUAA 3'

What will be the anticodons ? How many amino acids will be there in the oligopeptide formed from this RNA?

5. For the oligopeptide- Met – Arg – Ile – Gly

Write the codons. Compare your answers with your classmates. Some students may have different answers, still they are marked correct by the teacher. Why?

ANNEXURE 2

Activity – Deciphering Genetic Code

Subject	Biology
Class	XII
Chapter	Molecular Basis of Inheritance
Topic	Genetic Code
Duration	40 minutes
Nature of the Activity	Group Activity

What will I learn? (Learning Outcome) – understand how scientists work; learn the methodology of deciphering genetic code

Skills- Observing, Classifying, Critical Thinking, Conceptualising

What I have to do? – To act as Hargobind Khorana and Marshal Nirenberg who deciphered genetic code

What do I require?

- A chart of Genetic Code for reference, whiteboard, magnetic buttons, 20-22 square shaped cards each with the letters **U,C,A,G** written in bold on them (for ribonucleotide with Uracil, Cytosine, Adenine & Guanine, respectively), **20 amino acids** written in bold, on circular cards (a set of 6-7 for each amino acid)

What do I need to know?

Central Dogma of Molecular Biology, bases of DNA, RNA, names of all amino acids

What is a homopolymer and a copolymer; meaning of codon

- **Teacher's activity-** Teacher will give the instructions to students as to how to proceed
- Teacher will talk about the contribution of Hargobind Khorana and Marshal Nirenberg
- Class will be divided into two groups- 'Khoranas' (with U,C,A,G cards) and 'Nirenbergs' (with amino acids)
- The Hargobind Khoranas will keep cards with RNA bases and the Marshall Nirenbergs will keep the amino acid cards with them
- Teacher will call out for all the U's (for making a homopolymer)
- All the U's will get up and display the U cards on the white board
- For every 3 cards of the RNA bases, one amino acid will be placed (for 3 U's, one phenylalanine)
- Accordingly, all the Phenylalanine cards will be placed below the polynucleotide It will look like this-
UUUUUUUUUUUUUUUU
Phe-Phe-Phe-Phe-Phe

How will I proceed?

➤ Student's activity

1. To be ready with their respective cards and come and arrange these on the board in a straight line
2. First the bases will be arranged and below that the amino acids (3 RNA bases ~ 1 amino acid)
3. The teacher will call out for the C's
4. All the C's will be arranged in a line to form a ribonucleotide (by the students)
5. A homopolymer will be made
6. Accordingly, the Proline cards (for every 3 bases) will be placed below the polynucleotide, hence forming a polypeptide
7. The teacher will call out for the 'Khoranas' and bases GU (in this order)
8. A copolymer will be made
9. The teacher will call out for the 'Nirenbergs' and the amino acids will be arranged accordingly
10. The exercise will be repeated
11. Hence, other copolymers will be made, followed by the polypeptides
12. All the homopolymers and copolymers and subsequent polypeptides will be recorded

What have I observed?

Homopolymers and Copolymers	Subsequent Polypeptides
CCCCCCCCCCCCCCCC-----	Pro-Pro-Pro-Pro-Pro-Pro-----
GUGUGU-----	Val-Cys-Val-Cys-----
ACAC-----	-----
UA-----	-----
-----	-----

What have I learnt?

Deciphering the Genetic Code was a daunting task

The methodology used by scientists for finding genetic code

Fidelity in polypeptide synthesis, on the basis of codon on mRNA

What would I like to know ?

What were the specific contributions of scientists other than Hargobind Khorana & Marshall Nirenberg in accomplishing the task of deciphering genetic code?

Let me Evaluate myself-

1. Who all were awarded the Nobel prize for deciphering genetic code and in which year?
2. i) Name the amino acids that have only one codon ii) Name the stop codons and state their significance
3. Discuss the bold proposition given by George Gamow.
4. Which specific attribute of genetic code can be concluded from the following examples:
 - i) UAU & UAC both code for Tyrosine
 - ii) UAU codes for only Tyrosine and no other amino acid
 - iii) UAU codes for Tyrosine from bacteria to humans
5. For transcription, only one strand of DNA- the template strand, is used. Why?

ANNEXURE 3

Activity- An overview of the process of Whole Genome Sequencing

Subject	Biology
Class	XII
Chapter	Molecular Basis of Inheritance
Topic	Whole Genome Sequencing
Duration	1 ½ hours
Nature of the Activity	Group Activity

What will I learn? (Learning Outcome)

– understand the process and importance of genome sequencing, appreciate the advancements in the field of science

Skills- Analysing, critical thinking

What I have to do? Work in a group and carry out the steps of genome sequencing as per the steps given

What do I require?

Props/ Materials required- 2 sets of alphabets (A-Z), scissors (2), labels of EcoRI and BamHI, long string/
cut outs of YAC/ BAC (2 each), brown tape

What do I need to know?

rDNA Technology; Aim and need for finding genome sequence; the methods of genome sequencing; the steps of genome sequencing; meaning of analogy

- **Teacher's activity-** Teacher will give the instructions along with the protocol (Student's activity)
- **Teacher will explain that the English alphabet(A-Z) is taken to be analogous to a given DNA sequence, say-**
5' AATTCCAATCCGGATCCGGTTACCTTACCGAATTCAATTCC 3'
3' TTAAGGTTAGGCCTAGGCCAATGGAATGGCTTAAGTTAAGG 5'

EcoRI recognises and cuts between G & A in

5'GAATTC 3'

3'CTTAAG 5'

And BamHI recognises and cuts between the 2 G's in 5'GGATCC 3'
3'CCTAGG 5'

Teacher will facilitate the whole activity

How will I proceed?

- **Student's activity**

Assign the roles as-

1. All the labels will be worn as crowns
2. Two volunteers as restriction endonucleases(molecular scissors)- EcoRI, BamHI
3. One volunteer as DNA ligase (molecular glue)
4. Four volunteers as YAC/ BAC
5. One student to read and note the sequence
6. Rest of the group (with more student volunteers) - Two DNA sequences (Each one A-Z)
7. Cutting of the two sequences by two different restriction endonucleases (EcoRI between F & G, BamHI between K & L)

Steps-

To be followed, supported with a slide showing the process

1. Students to stand in 2 lines from A-Z (DNA sequence)
2. EcoRI to cut at the assigned point in one of the lines (A-Z) and generate 2 fragments

BamHI to cut at the assigned point in the 2nd line (A-Z) and generate 2

fragments

3. The broken sequences of line 1 and 2 to be joined to the 4 different YAC, using tape (Volunteer acting as DNA ligase)

(Teacher will explain the next few steps (Cloning these in different vectors -amplification upon insertion in host cell, Arranging sequences based on overlapping regions, Sequences annotated and assigned to different chromosomes))

4. Reading the sequence (equivalent to Automated DNA Sequencing (by Sanger's method))

What have I observed?

The English Alphabet	ABCDEFGHIJKLMNOPQRSTUVWXYZ
Fragments generated by cutting with EcoR1 between F & G	-----, -----
Fragments generated by cutting with BamH1 between K & L	-----, -----
Overlapping Sequence	-----
The given sequence	5' AATTCCAATCCGGATCCGGTTACCTTACCGAATTCAATTCC 3' 3' TTAAGGTTAGGCCTAGGCCAATGGAATGGCTTAAGTTAAGG 5'
Fragments generated by cutting with EcoR1	-----, -----
Fragments generated by cutting with BamH1	-----, -----
Overlapping Sequence	-----

What have I learnt?

Correct sequence of the genome can be generated by comparing the overlapping fragments (like we did for the English Alphabet)

What would I like to know ?

Can genome sequencing of pathogens help find cures to the diseases caused by them?

Let me Evaluate myself-

1. What are the steps of whole genome sequencing?
2. Differentiate between the two methods of genome sequencing- by identifying ESTs and whole genome sequencing
3. Why was sequencing of human genome, a challenging process? Why 24 chromosomes were sequenced under Human Genome Project?
4. Generate a fragment 28bp long, that can be cut by restriction enzymes Sal I and Pvu I. In the given sequence, ensure that only one recognition site of each enzyme is there, with a gap of at least 5bp. How many fragments will be generated if it is cut by –
 - i) Only Sal I
 - ii) Only Pvu I
 - iii) Both Sal I and Pvu I
5. What is the relative time required for genome sequencing of prokaryotes and eukaryotes? How can the technique be useful in finding correct sequence of viral genome, as they keep mutating?

