

Chapter 13: Regulation of Gene Expression

1. Describe the structure of an operon and state the role of each component of the operon.
2. Explain how the *trp* and *lac* operons of prokaryotes are regulated. Describe the difference between positive and negative regulation of gene expression in prokaryotes.
3. Describe the five levels of genetic control in eukaryotes.
4. Explain how chromatin structure influences gene expression.
5. Identify the mechanisms of transcriptional, posttranscriptional, and translational control of gene expression.
6. List some common causes of spontaneous and induced mutations.
7. Explain how a frameshift and a point mutation may disrupt a gene's function.
8. Discuss how a mutation in a tumor suppressor gene and a proto-oncogene disrupts the cell cycle.
9. Identify which regulatory gene promotes apoptosis. Describe how that protein regulates the cell cycle.
10. Explain why the following genes are important for scientists to be familiar with and how they affect cells. p53, BRCA1 and BRCA2, bcl-2, RB tumor suppressor gene. [These should be mostly review, but if you need more information, do some research online!]

Chapter 14: Biotechnology and Genomics

1. Describe the steps involved in making a recombinant DNA molecule.
2. List the scientific benefits of using the polymerase chain reaction.
3. Describe one reason for reverse transcription and an organism that uses this process. Identify the enzyme involved in the process.
4. Explain how DNA profiling can be used to analyze DNA molecules.
5. Identify the benefits of genetically modified bacteria, plants, and animals to human society.
6. Describe the steps involved in the production of a transgenic animal.
7. Distinguish between a transgenic animal and a cloned animal.
8. Distinguish between *in vivo* and *ex vivo* gene therapy in humans. Identify an example of each type of gene therapy.
9. Distinguish between the genome and the proteome of a cell.
10. Identify the function of repetitive elements, transposons, and unique noncoding RNA sequences in the human genome.
11. Be familiar with the pGlo and DNA fingerprinting labs– the process used to obtain the data and how to interpret the data.

Past AP Exam Essay Questions**2000 Question 3**

Information transfer is fundamental to all living organisms. For two of the following examples, explain in detail how the transfer of information is accomplished.

- a) The genetic material in one eukaryotic cell is copied and distributed to two identical daughter cells.
- b) A gene in a eukaryotic cell is transcribed and translated to produce a protein
- c) The genetic material from one bacterial cell enters another via transformation, transduction, or conjugation

2002 Question 1

The human genome illustrates both continuity and change.

- a) Describe the essential features of two of the procedures/techniques below. For each of the procedures/techniques you describe, explain how its application contributes to understanding genetics.
 - The use of a bacterial plasmid to clone and sequence a human gene
 - Polymerase chain reaction (PCR)
 - Restriction fragment length polymorphism (RFLP) analysis
- b) All humans are nearly identical genetically in coding sequences and have many proteins that are identical in structure and function. Nevertheless, each human has a unique DNA fingerprint. Explain this apparent contradiction.

2009 Question 4

The flow of genetic information from DNA to protein in eukaryotic cells is called the central dogma of biology.

- a) Explain the role of each of the following in protein synthesis in eukaryotic cells.
 - RNA polymerase
 - Codons
 - tRNA
- b) Cells regulate both protein synthesis and protein activity. Discuss two specific mechanisms of protein regulation in eukaryotic cells.
- c) The central dogma does not apply to some viruses. Select a specific virus or type of virus and explain how it deviates from the central dogma.

2009 Form B Question 1

Describe how a plasmid can be genetically modified to include a piece of foreign DNA that alters the phenotype of bacterial cells transformed with the modified plasmid. Describe a procedure to determine which bacterial cells have been successfully transformed.

2010 Form B Question 2

Certain human conditions, such as sickle-cell anemia, result from single base-pair mutations in DNA.

- a) Explain how a single base-pair mutation in DNA can alter the structure and the function of a protein.
- b) Explain, using a specific example, the potential consequences of the production of a mutant protein to the structure and function of the cells of an organism.
- c) Describe how the frequency of an allele coding for a mutant protein may increase in a population over time.

2010 Form B Question 3

Bacteria play central biological roles.

- a) Bacteria may act as
 - Producers
 - Parasites
 - Mutualistic symbionts
 - Decomposers

Select three of the ecological roles above. For each one you choose, describe how bacteria carry out the role and discuss the ecological importance.

- b) Explain how bacteria can be altered to make genetically engineered products.

2012 Question 3

Information flow in cells can be regulated by various mechanisms.

- a. Describe the role of THREE of the following in the regulation of protein synthesis:
 - RNA splicing
 - repressor proteins
 - methylation
 - siRNA
- b. Information flow can be altered by mutation. Describe THREE different types of mutations and their effect on protein synthesis.
- c. Identify TWO environmental factors that increase the mutation rate in an organism, and discuss their effect on the genome of the organism.
- d. Epigenetics is the study of heritable changes in the phenotype caused by mechanisms other than changes in the DNA sequence. Describe ONE example of epigenetic inheritance.

2013 Question 5

The table below shows the amino acid sequence of the carboxyl-terminal segment of a conserved polypeptide from four different, but related, species. Each amino acid is represented by a three-letter abbreviation, and the amino acid residues in the polypeptide chains are numbered from the amino end to the carboxyl end. Empty cells indicate no amino acid is present.

| Species | Relative Amino Acid Positions | | | | | | | | | |
|---------|-------------------------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| | 1 | 2 | 3 | 4 | 5 | 6 | 7 | 8 | 9 | 10 |
| I | Val | His | Leu | Val | Glu | Glu | His | Val | Glu | His |
| II | Val | His | Leu | Lys | Glu | Glu | His | Val | Glu | His |
| III | Val | His | Leu | Val | Glu | Glu | His | Val | | |
| IV | Val | His | Leu | Val | Arg | Trp | Ala | Cys | Met | Asp |

- Assuming that species I is the ancestral species of the group, explain the most likely genetic change that produced the polypeptide in species II and the most likely genetic change that produced the polypeptide in species III.
- Predict the effects of the mutation on the structure and function of the resulting protein in species IV. Justify your prediction

2017 Question 3

Gibberellin is the primary plant hormone that promotes stem elongation. GA 3-beta-hydroxylase (GA3H) is the enzyme that catalyzes the reaction that converts a precursor of gibberellin to the active form of gibberellin. A mutation in the GA3H gene results in a short plant phenotype. When a pure-breeding tall plant is crossed with a pure-breeding short plant, all offspring in the F1 generation are tall. When the F1 plants are crossed with each other, 75% of the plants in the F2 generation are tall and 25% of the plants are short.

- The wild type allele encodes a GA3H enzyme with alanine (Ala), a nonpolar amino acid, at position 229. The mutant allele encodes a GA3H enzyme with threonine (Thr), a polar amino acid, at position 229. Describe the effect of the mutation on the enzyme and provide reasoning to support how this mutation results in a short plant phenotype in homozygous recessive plants.
- Using the codon chart provided, predict the change in the codon sequence that resulted in the substitution of alanine for threonine at amino acid position 229.
- Describe how individuals with one (heterozygous) or two (homozygous) copies of the wild type GA3H allele can have the same phenotype.

| | | Second Base in Codon | | | | |
|---------------------|----------------------------------|---|--------------------------------------|--|---|------------------|
| | | U | C | A | G | |
| First Base in Codon | U | UUU] Phe UUC] UUA] Leu UUG] | UCU] Ser UCC] UCA] UCG] | UAU] Tyr UAC] UAA] Stop UAG] Stop | UGU] Cys UGC] UGA] Stop UGG] Trp | U C A G |
| | C | CUU] Leu CUC] CUA] CUG] | CCU] Pro CCC] CCA] CCG] | CAU] His CAC] CAA] Glu CAG] | CGU] Arg CGC] CGA] CGG] | U C A G |
| | A | AUU] Ile AUC] AUA] AUG] Met or Start | ACU] Thr ACC] ACA] ACG] | AAU] Asn AAC] AAA] Lys AAG] | AGU] Ser AGC] AGA] Arg AGG] | U C A G |
| G | GUU] Val GUC] GUA] GUG] | GCU] Ala GCC] GCA] GCG] | GAU] Asp GAC] GAA] Glu GAG] | GGU] Gly GGC] GGA] GGG] | U C A G | |

Figure 1. The universal genetic code

2017 Question 6

A comet assay is a technique used to determine the amount of double-stranded breaks in DNA (DNA damage) in cells. The nucleus of an individual cell is placed on a microscope slide coated with an agarose gel. An electric current is applied to the gel that causes DNA to move (electrophoresis), and the DNA is stained with a fluorescent dye. When viewed using a microscope, undamaged DNA from the nucleus appears as a round shape (the head), and the fragments of damaged DNA extend out from the head (the tail). The length of the tail corresponds to the amount of the damage in the DNA (see Figure 1).

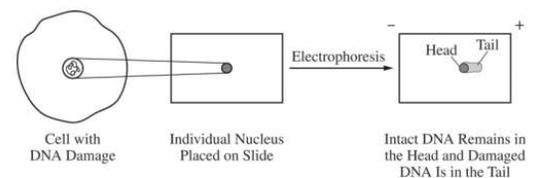


Figure 1. Comet assay to detect double-stranded breaks in DNA

- To explain the movement of DNA fragments in the comet assay, identify two properties of DNA and provide reasoning to support how the property contributes to the movement during the comet assay technique.
- In a different experiment, cells are treated with a chemical mutagen that causes only nucleotide substitutions in DNA. Predict the likely results of a comet assay for this treatment.