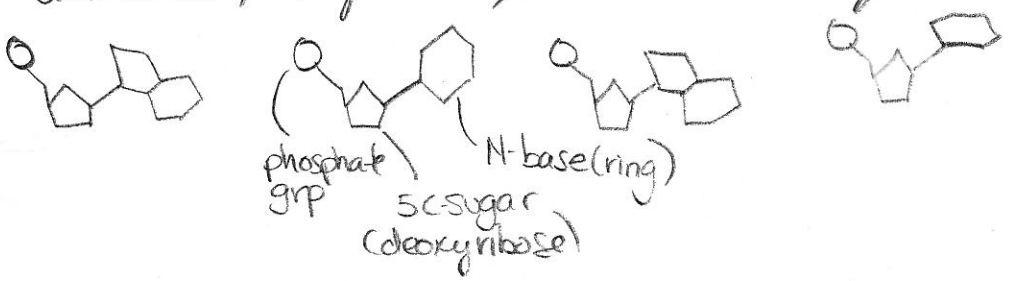
KEY Bio 12 DNA & Protein Synthesis: Study Guide

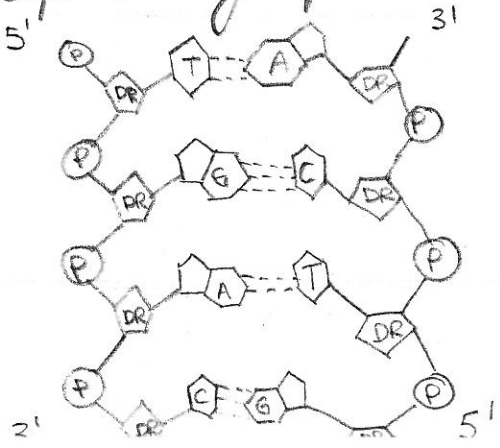
1. DNA and RNA → nucleus (made in nucleolus) and cytoplasm as mRNA, tRNA and rRNA (on ribosomes)
   → nucleus (coiled onto chromosomes or "strung out" as chromatin during protein synthesis)

2. 3 main DNA f(x)s:
   Store info: - controls cell activities via stored info.
   1/3 Replicate: - genetic instructions (code in genes) passed to offspring
   Undergo Mutations: - responsible for evolution because of mutations and recombination

3. Adenine, Thymine, Guanine, Cytosine




4. DNA is composed of complementary pairing of nucleotides to form a double helix. Ader always pairs w/ thymine of the other strand and Guanine pairs w/ cytosine via hydrogen bonding. The strands are antiparallel.
   1/3 with one strand running 5'-3' direction and the sister strand going 3'-5' end. The backbone of the double helix "ladder" is composed of sugar phosphate in repeating pattern covalently bonded.




1/2

5. a) C.B.P. means that A always pairs w/ T and G always pairs w/ C of sister strands of DNA: They pair up this way because A and T form 2 H-bonds and G and C form 3 hyd.-bonds. /1

b) H-bonding dictates A=T and G≡C. Also, the spacing between complementary bases on the 2 strands. Purines bond with pyrimidines. Both A and G (purines) are 2 rings in length whereas T and C (pyrimidines) are only 1 ring in length. There is only enough room for 3 rings between the 2 strands of DNA. /1

6. Chromosome, DNA, gene, nucleotide.

7. genes: segments of DNA that control a particular characteristic or function

chromosomes: contain many genes collected on rod-like structures that contain compact and highly coiled DNA (genetic info stored)

8. How does the Structure of DNA and c.b.p.ing promote the continuity of life? (4 marks)

- DNA carries the code of life!!
  - → the sequence of nucleotides along the DNA molecule carries a triplet code that directs the production of molecules for all life (mostly proteins)
- DNA (double helix w/ 2 complementary strands) provides a built-in mechanism for producing identical copies.
  - → replication is semi-conservative: ½ of new DNA is actually taken from the original molecule, further ensuring accuracy and integrity of replication.
  - → comp. base pairing (C≡G, A=T) allows replication to be semi-conservative, and ensures few mistakes are made in replication, transcription.
  - → repair mechanisms within nucleus can repair mistakes in replication and most damage to DNA.

#8 cont'd →

8. (cont'd)

- DNA is a very stable molecule
  → covalent bonds hold the backbone together.

DNA can be coiled tightly into chromosomes so huge amount of information can be packed into a tiny space.
→ can unzip, make an RNA copy of any necessary gene, and express it at the appropriate time.

- Promoter and Regulator sequences on DNA code for molecules that control the expression of genes, such that sophisticated, multi-cellular organisms are possible (eg. your eye cells don't suddenly start producing digestive enzymes, even though they have the DNA for dig. enzymes).

9. a) DNA molecule forming 2 exact copies from 1.

b) (1) Unzip - double helix unwinds (DNA helicase) and unzips (H-bonds b/t comp. base pairs on 2 strands break).

(2) Comp.-base pairing - nucleotides (free in nucleoplasm) pair with each strand (now separated) - DNA ligase joining appropriate nucleotide

(3) adjacent nuc-bond - sugar phosphates of neighbouring nucleotides are covalently bonded (DNA polymerase) and the 2 DNA molecules rewind (DNA gyrase) into double helix. Process is semi-conservative

10. RNA - ribonucleic acid
- used for protein synthesis - 3 kinds: messenger, transfer, ribosomal
- made of nucleotides - phosphate - 5-carbon sugar - N-base

* except: 5-carbon sugar is ribose (not deoxy)

| | DNA | RNA |
|---|---|---|
| Sugar | deoxyribose | ribose |
| N-bases | A T G C | A U G C |
| # strands | double | single |

* backbone is covalently bonded phosphate + sugars of diff. nucleotides

11. Transcription: DNA → RNA

- a particular gene in a chromosome is transcribed into a ss. copy that can leave the nucleus
- when promoter sequence is free to bind to RNA polymerase

1. Unzip & unwind
   - DNA helicase causes a small portion of DNA to unwind and H bonds holding opposite strands to break. (strands can separate)

2. Adjacent Nucleotides in place
   - RNA polymerase reads DNA, DNA ligase brings appropriate nucleotide (RNA (U not T)) that is complementary to parent template strand (also called sense strand.) ← also have ribose NOT deoxyribo
   - RNA polymerase binds adjacent nucleotides together forming a long ss. mRNA molecule that can leave the nucleus
   - introns (non coding sections of the mRNA strand) are removed – only exons "exit" the nucleus to be read by ribosome

3. - Rewind: - helicase and gyrase recip/unwind H bonds on both strands of the DNA molecule (which remains unchanged.)

12. mRNA

C C G A U U G C

R-P-R-P-R-P-R-P-R-P-R-P-R-P-R-P-R-P-R-P-R-P-R-P-R-P-R

* R-sugar ribose
P-phosphate grp
CUGA - N-bases

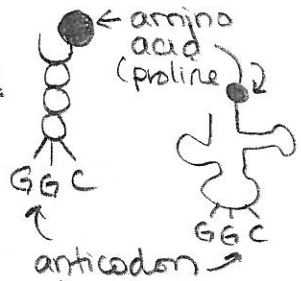
rRNA

structural part of ribosomes (so codons/anticodons can be read)

P-site } for tRNA binding place.
A-site

R-site – binding for mRNA codons

tRNA




* delivers aa's in the cytoplasm to the ribosome

(18) **Translation**: genetic code in mRNA 'language' is converted (translated) into amino acid / protein language

3 phases:

1. Initiation: - the mRNA's start codon (AUG) attaches to the 'R' site of ribosome.
   - tRNA carrying the amino acid methionine & with comp. anticodon UAC binds to the "P" site (left) of the ribosome, matching up w/ mRNAs start codon.

2. Elongation: more amino acids are added & connected together to form a polypeptide
   - incoming tRNA-aa complex ($tRNA_2$-$aa_2$) recognizes the codon at the "A" site (right) of the ribosome & binds there.
   - a peptide bond forms between $aa_1$ at the "P" site and $aa_2$ at the "A" site.
   - bond breaks b/t tRNA & aa → tRNA released from P site → Now, only $tRNA_2$-$aa_2$-$aa_1$ remain in "A" site.
   - ribosome moves over one codon to the right thus shifting the $tRNA_2$-$aa_2$-$aa_1$ complex to the "P" site.
   - $tRNA_3$-$aa_3$ can now move into "A" site binding with the next codon on mRNA.
   - process repeats → chain elongates.

3. Termination: - when a special codon called a STOP codon (UAA, UAG, UGA) is reached ("R"-site) elongation stops.
   - stop codons don't code for aa's., but signal translation to stop.
   - release factor binds to A site causing a water molecule to be added to the end of the polypeptide chain

& the chain to separates from the last tRNA
- mRNA broken down + ribosome broken down into large + small subunits
- new protein sent to ER + Golgi App for final processing

14. DNA TAC TTA GGG CAA ATT CGC TAT TTT TT
mRNA AUG AAU CCC GUU UAA GCG AUA AAA AA
aa methionine - Asparagine - Valine - Proline - stop

15. DNA - template for formation of mRNA / genetic instructions can ∴ leave nucleus and move to cytoplasm.
mRNA - contains codons (triplet code) that correlates to a specific amino acid in a polypeptide.
tRNA - brings specific amino acid to ribosome for attachment to growing polypeptide chain
contain anticodons that are complem to mRNA codons ∴ recognize the correct sequence of aa.
Ribosomes - site of protein synthesis - place for which mRNA and tRNA can come together (binding sites P-A+R.)

16. Mutations - change in an organism resulting from a chemical change in the structure of a gene.

Gene
- alteration of a single nucleotide (addition, deletion or exchange)
- may or may not result in disease (affects only 1 gene)
- ex: cat, Albinism, Sickle Cell Anemia + many diseases (lacking enzymes is common)

Chromosome
- loss / addition of part or an entire chromosome.
- affects many genes -
- broad spectrum of changes to organism
- Trisomies, Turner's + Klinefelter's Syndromes.

(b)

| Gene Mutations | Chromosomal Mutati |
|---|---|
| Definition: An alteration in the code and structure of a single gene with a subsequent change in its expression. ✓ | Definition: A variation in re to the normal number of chromos inherited or in regard to the norm sequence of alleles on a chromosome. ✓ |

Differences

| | |
|---|---|
| (1) Affect only a single gene. | (1) Affect many genes because they affect entire chromosome or parts of chromosome. |
| (2) May be caused by a change in a single nucleotide (eg. substitutions, deletions, additions) | (2) Mistakes in meiosis's majo contributor. (Pieces of chromosomes can be lost, adde or whole chromosomes can be (lost or added.) |
| (3) The effect on invidual depends on the gene's role and the effects are sometimes unnoticeable or harmful on a smaller level. ✓ | (3) The effects or problems caused are drastic and doe more harm than gene mutations. ✓ |

17. **Mutagens:** Mutagens are any factors that can cause a mutation. Mutagens can be both internal or external. Four environmental mutagens that cause mutations in humans are UV rays from sunlight, DDT from pesticide radon and other radioactive decay products and presence of substances like benzene or asbestos in the environment.

18. (a)

| | | | | | |
|---|---|---|---|---|---|
| DNA sequence : | TAC | CAA | GGT | TCG | ACT |
| mRNA : | AUG | GUU | CCA | AGC | UGA |
| Amino acid : | Methionine | Valine | Proline | Serine | STOP |

This DNA sequence can be dramatically affected by adding or deleting a DNA nucleotide and this can greatly effect the structure and function of the resulting translated protein.

IF a Cytosine C nucleotide was added in the second amino acid of the above sequence the amino acids for that sequence will change and form a new protein which can cause mutations in organisms.

DNA : TAC GCA AGG TTC GAC T
mRNA : AUG CGU UCC AAG CUG A
A.A. : Methionine Arginine Serine Lysine Leucine -

The new sequence has totally different amino acids and does not have a stop codon and this completely alters the original protein.

If Guanine is removed from the second amino acid the following occurs:

mRNA : AUG UUC CAA GCU GA
A.A. : Methionine Phenyl. Glutamine Alanine -

The new sequence has a new set of amino acids and no stop codon which alters the original protein which would cause a genetic mutation and could lead to various disorders or no effect at all.

(b) Change in a DNA sequence that causes a change in the significant part of the mRNA codon (s) will cause a different amino acid to be translated and therefore a different protein will be made. These random changes and formation of different proteins leads to genetic disorders by drastically affecting metabolism and body structure / function.

(C) Two genetic disorders are PKU and Albinism

(i) PKU : PKU (phenylketonuria) is caused by defect in the enzyme that converts phenylalanine to tyrosine. The tyrosine then gets converted into phenyl pyruvic acid which can build up and cause severe nervous system damage or mental retardation

(ii) Albinism : This disorder occurs when the enzyme that converts tyrosine to melanin is defective and the subjects have no skin or hair pigment, and hence appear almost pure white.

19. Sometimes mutations are neutral and have no effect at all on an organism because the mutation will have no effect on the protein ide produced, or it will change an amino-acid on a non-vital part of the protein. Another reason for no effect mutations is the built in security system "**Wobble effect**" in the genetic code. With the wobble effect a change of a third nucleotide can still result in correct amino acid in place CGA → CGG and Arginine will still stay Arginine.

20. The importance of mutations to the history and future of life on this planet is the ability to evolve. Mutations can result in a certain adaptation that can protect humans from certain bacterial or viral agents.