**Summary of Genetics & Protein Synthesis (Quick Guide)**

We will use the following images to review. We will also be adding a new piece of information now and again in order to tie things together.

<table>
<thead>
<tr>
<th>Some terms/concepts to remember before we begin:</th>
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<tbody>
<tr>
<td>1. The sequence of nucleotide bases in the DNA molecule determines the sequence of AAs in the final resulting polypeptide.</td>
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<td>2. The central dogma states, during gene expression (turning a gene into a protein), information flows:</td>
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<td>DNA   ➔   RNA (mRNA) ➔   Protein (polypeptide)</td>
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<td>3. We will transcribe an mRNA in the nucleus using the DNA molecule.</td>
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<tr>
<td>* Gene = stretch of DNA used to code for 1 polypeptide. Of course, it is what is use to make 1 mRNA.</td>
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<td>* Codon = 3 bases (triplet) that signals 1 AA in the final product.</td>
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<td>* Therefore, a “gene” is a sequence of bases found on the DNA molecule. They have a “start” and a “stop” sequence.</td>
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<tr>
<td>4. We will then translate in the cytoplasm using a ribosome, which will “string together” the AAs following the instructions on the mRNA</td>
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Concept 1 – Nucleotides polymerize into Nucleic Acids, of which there is more than one type.

The sequence of nucleotide bases will form the instructions for protein synthesis.

The abbreviations below are simply for convenience, as there are so many similar terms.

Follow the numbers in blue circles:

(1) Nucleotides (NTs) are the building blocks of larger nucleic acids (NAs). They consist of a central 5-carbon sugar, which can be a ribose or deoxyribose. Attached to one end is a phosphate (acid), and on the other side there is a nucleotide base (NBs).

(2) There are 5 different NBs, so there are 5 different NTs. They are named in the image. A & G are purines, C, U & T are pyrimidines.

(3) We form the polymer via dehydration synthesis. We end up with a sugar-phosphate backbone with NBs exposed (they are now free to interact).

Notice that the NBs are charged.

(4) We end up with a single alpha helix NA, which is a very stable molecule. This is the most basic NA.
Concept 1 Continued

Nucleotides polymerize into Nucleic Acids, of which there is more than one type.

(5) The NB can bond to each other. Interestingly, however, they can only do SPECIFIC BASE PARINGS (shown on image).

(6) One consequence of this is that NA chains can begin to interact with each other, giving us different forms of NAs which will have different chemical characteristics and therefore different functions (see later).

(7) Another consequence of this is that NAs can act as a template, whether this is for production of another NA, replication, or protein synthesis (see later concepts: TRANSCRIPTION and TRANSLATION)

Remember....this only works because there is a "reader molecule" for the sequence of nucleotide bases (see transcription & translation overviews).

(8) The 2 main types of NAs are DNA & RNA.

Four big differences between DNA and RNA:

1. The sugar in DNA is deoxyribose; in RNA it is ribose

2. The nitrogenous base uracil (U) is used in RNA in place of T (they are very similar bases; in RNA U= A just like T = A.)

3. DNA is a double helix, found in the nucleus.

RNA is single stranded

4: In our cells - DNA is the HEREDITARY INFO (passed through generations).

Codon: sequence of 3 nucleotide bases ("Triplet") contains information for 1 AA in primary sequence of protein (see later).

Gene: (alternate way of looking at a gene): sequence of codons that code for 1 polypeptide (start to finish).

Mutation: Change in sequence. Most do not matter. Some are deleterious.
Concept 2 – The “Transcription Overview”

Follow the numbers in blue circles:

1. Gene = stretch of DNA used to code for 1 polypeptide. Of course, it is what is used to make 1 mRNA (2) during the process of transcription (3).

* Therefore, a “gene” is a sequence of bases found on the DNA molecule. They have a “start” and a “stop” sequence (4 & 5).

Concept 3 – The “Transcription Small Detail”

Follow the numbers in blue circles:

1. When DNA is not being used, we have a tight “double alpha helix” shape that is very stable.

2. A binds to T, and G binds to G.

- New Info (3): however, only one side of the double helix will be used to make an mRNA. This is the “sense strand”.

4. In order to use the DNA, the helix must be unwound, making the sense strand available to use!

5. A molecule (polypeptide, of course!) called RNA polymerase lays down nucleotide bases following the “instructions” on the sense strand of the DNA. However, it uses “U” instead of “C”, so we end up with a single-stranded RNA molecule called mRNA, which can be used later in protein synthesis!

6. We now have a molecule that will drift out of the nucleus into the cytoplasm and be used directly for protein synthesis.

7. Every 3 nucleotide bases is a codon, which tells the cell “which AA comes next in the polypeptide”
Concept 4 – The “Translation Small Detail”

Follow the numbers in blue circles:

(1) In the cytoplasm, a ribosome attaches to the mRNA. It sits over a “codon”.

NOTE: I did not tell you how it does this

(2) It attaches an AA according the Genetic Code (3)

NOTE: I did not tell you how it does this

New Info: (4) For all of our proteins, the “start” is always AUG which codes for the AA methionine, so all our proteins begin with this AA!

(5) The ribosome then slides down the mRNA strand to the next triplet (codon), and attaches the next AA following the code (3 again!).

NOTE: I did not tell you how it does this

Of course, this is done via dehydration synthesis, forming a peptide bond (not shown)

(6) The ribosome keeps doing this, forming a polymer of AAs (polypeptide).
Concept 5 – The “Translation Big Picture”

Follow the numbers in blue circles:

(1) The ribosome continues to move down the mRNA strand.

Interesting note: Actually, many ribosome will attach at the beginning and slide down. So this image can be 1 ribosome over time, or a “polyribosome” at one snapshot of time.

(2) The ribosome lengthens the polypeptide chain following the information in the mRNA (sequence of codons).

NOTE: Dehydration synthesis!

(3) The ribosome comes to one of several “stop codons”. This causes the ribosome to let go of the mRNA and the polypeptide chain.

NOTE: I did not tell you how it does this

(4) We now have the primary sequence of the polypeptide chain.

(5) Chaperone molecules then guide the twisting, turning and attaching necessary to have the secondary, tertiary and quaternary structures of the completed protein.
Concept 6 – Genetic Material:

The relationship between Nucleic Acid, Nucleotide, Chromatin, Chromosome, Sister Chromatid

Follow the numbers in blue circles:

DNA (1) – a NUCLEIC ACID (macromolecule)
- Polymer of Nucleotides, which have Nucleotide Bases (NBs): A, T, C, & G
- Contains GENES (2 - Gs): segments that code for a polypeptide. Must be “opened” to be used.
- Hereditary material
- EXTREMELY LONG & Fragile
- Must be “unwound” to be used.

Chromatin (3) – DNA + protein
- protect the long fragile DNA
- Wrap it around histone proteins (4)
- This is the form your genetic material is in while not in use. To use it, must unwind it and open it (5).

Chromosomes (6): Giant organization of duplicated chromatin!

Related terms:
HOMOLOGOUS chromosomes
HOMOZYGOUS: you have the same copy from each parent
HETEROZYGOUS: you have a different copy from each parent
DOMINANT TRAIT
RECESSIVE TRAIT
Concept 7 – Mutations & Somatic Mutations

- Nucleic acids can replicate itself, and act as a template (transcription / translation).

But during these processes, there is error.

- MUTATION: Random change in the sequence of the DNA might lead to a change in the codon on the mRNA, and therefore a change in the sequence of the AAs in the protein.

- Small change in AA sequence can have one of 3 consequences:
  1. No effect. New AA doesn’t change overall shape of the polypeptide very much. MOST COMMON. We all have small genetic differences between us that do not matter.
     
     Redundancy in genetic code (no change in AA sequence), or they do not significantly change resulting polypeptide, maybe do not affect active site, etc.

     Alleles: different versions of the same gene (or product of that gene – the protein)

     e.g.: there are 3 functioning alleles of Hemoglobin: HbA, HbA2, & HbF

  2. Bad effect: Mutation in code leads to AA sequence change, which changes the shape of the protein in such a way that the resulting protein loses its function. Might lead to a PATHOLOGY. The mutation is "deleterious".

     * About 20% of all mutations are deleterious. Average human has an estimated 2000 mutations that would lead to a pathology.

- Somatic Mutations: Changes in the genetic code of existing cells. Estimated that we have trillions of these mutations daily. Most do not matter, as we have trillions of cells.

Exceptions: Some cancers (minority), some other diseases BUT RARE..
Concept 8 – Mutations & Heredity Basics

- Inherited mutations are more likely to cause a genetic disease. But still unlikely as we have protections.

- If a gamete contains a mutation, then the zygote will have it, and all the body’s cell will have it.

- But, due to sexual reproduction, we have 2 sets of all our chromosomes, and therefore 2 sets of all our genes.

* Homologous pairs of chromosomes. Humans have 23 pairs (= 46 total). Maternal & paternal chromosomes have same genes on them, but usually different versions.

Heterozygote: the 2 versions are different (deleterious, or simply a different variant). This protects us from deleterious mutations, as we make both proteins (good & bad version).

Homozygote: the 2 versions are the same (rarest of the 2 cases). For most genetic diseases, the person has to be homozygous for the deleterious mutation (in other words, got a bad copy from both parents).

Not always true: dominant genes supercede recessive genes.

Dominant genes – person has the trait with only 1 copy. True of both deleterious and non-deleterious traits, like hair color.

Recessive genes: More common condition. You need 2 copies to show the trait.

If the deleterious mutation is dominant, only need one. Super rare because they are so deadly.
**Important terms and concepts for the exam**

- Your genetic material codes for proteins. It is the hereditary material (passed to you directly from your parents). So, the ability to make the correct proteins is passed from one generation to the next generation.

1. Gene (genetic info to make one polypeptide).
2. Chromosome and Chromatin - molecule carrying the Genetic info.
   * Genetic code is the sequence of bases on DNA
4. Nucleic Acids: DNA & RNA.
   * Know the differences between these 2 molecules.
5. Transcription: sequence of bases on DNA dictates sequence of mRNA in nucleus. Done by various enzymes in nucleus.
   * mRNA has "start sequence", then "codons (triplets), then a "stop sequence".
6. Translation: Sequence of bases on mRNA dictates primary sequence of Amino Acids, which thereby determines the proteins tertiary shape and therefore overall function (see protein section).
   * Done by various enzymes and ribosome in cytoplasm. Ribosome strings along the AAs, using dehydration synthesis, following the codons in the mRNA.
7. Genetic code - a listing of all the 3-nucleotide sequences on the mRNA (Codons) and their corresponding AAs on the polypeptide chain.
8. Mutation - change in nucleotide sequence.
9. Heterozygous = different on the 2 homologous chromosomes, homozygous = same on the 2 homologous chromosomes.
10. Carrier = a heterozygote that has a "bad copy" of a gene (="deleterious")