

F21S: genes

Transcription

- ① DNA Helicase unzips DNA and breaks the hydrogen bonds; DNA acts as a template
- ② RNA polymerase binds to DNA
- ③ Moves along it from 5' end to 3' end
- ④ Free RNA nucleotides are bound onto the exposed bases according to the complementary base-pairing rule [A-U; C-G]; the bases are hydrogen bonded on
- ⑤ RNA peels off strand of DNA and passes out through the nuclear pore

Translation

- ⑥ mRNA binds to a ribosome; the first codon is always AUG
- ⑦ The ribosome reads it from 5' to 3' end
- ⑧ 2 codons are exposed at once
- ⑨ tRNA molecules have a complementary anticodon and carry a specific amino acid (translating by hydrogen bonding)
- ⑩ -AA is transported to a ribosome
-When 2 amino acids are adjacent, a peptide bond forms between them
- ⑪ Translation stops at a stop codon

How DNA codes for a protein

- ^{def} gene = a length of DNA that codes for one or more polypeptides
- ① 1° structure determines the order of bases (one AA = 3 bases)
 - ② which determines the specific order of amino acids
 - ③ this then determines the projecting side groups
 - ④ leading to the 2° structure, involving H bonding / α -helix or β -pleated sheets
 - ⑤ which determines the 3° structure, bound by disulfide bonds; ionic bonds etc
 - ⑥ this determines the specific 3D shape which is vital for function
 - ⑦ If 3° structure altered, the shape will change & it can't function

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Apoptosis

Programmed cell death

- ① The cytoplasm is broken down by enzymes and the cell becomes densely packed with organelles
- ② The nucleus breaks down and fragments. Chromatin condenses & the nuclear envelope breaks down
- ③ "Blebs" form at the cell membrane
- ④ Organeller move into blebs and form vesicles
- ⑤ Phagocytes digest the vesicles by phagocytosis

Benefits:

- * very fast
 - * no toxic chemicals & hydrolytic enzymes like with necrosis
- uses:
- * controls limb & digit development
 - * destroys ineffective T lymphocytes in the immune system
 - * prevents all cells from dying in a viral attack

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Hardy-Weinberg principle

A model to calculate allele freq in populations with dominant + recessive alleles

How?

e.g. Take cystic fibrosis

To be a sufferer, you must be homozygous recessive.
* One in 2000 suffer from this.

Let's assign some symbols:

P = The frequency of the dominant allele, CF

q = The freq of the recessive allele cf

so, the possible genotypes are:

| | | |
|---|----|----|
| | P | q |
| P | PP | Pq |
| q | Pq | qq |

$\Rightarrow P^2 + 2Pq + q^2$

* since there is only either P (dominant allele) or q (a recessive allele)

$$P+q=1$$

* since the recessive sufferer probability is
 $1/2000$:

$$\text{so } q^2 = \frac{1}{2000} = 0.0005, \text{ so } q = 0.022 \text{ (square root it)}$$

* Thus:

$$\text{since } p+q=1,$$

$$p+0.022=1 \quad p=0.978$$

* so the % of carriers are:

$$2pq = 2 \times 0.978 \times 0.022 = 0.043 = 4.3\% \text{ of people}$$