## Early Genetics

| | |
|---|---|
| - biochemical group first thought to contain genetic information = | proteins |
| **Griffith bacterium experiment~** | |
| smooth strain (S) | outer capsule; pathogenic |
| rough strain (R) | NO capsule; NOT pathogenic |
| *Conclusion~* | |
| R cells combined w/ killed S cells transformed into living S cells | |
| **Avery bacterium experiment~** | |
| - deactivated parts of dead S cells to find what transformed the cells | |
| *Conclusion~* | |
| DNA transforms the bacteria | |
| **Hershey & Chase DNA experiment~** | |
| phages reproduced in presence of DNA (not proteins) | |
| *Conclusion~* | |
| DNA is the genetic material | |
| **Chargaff nucleotide experiment~** | |
| *Conclusions~* | |

## Early Genetics (cont)

| |
|---|
| base composition varies between each species (diff. % nucleotides) |
| # of nitrogenous bases equaled (A=T G=C) |

## DNA Structure

| | |
|---|---|
| - x-ray crystallography images of DNA by: | Rosalind Franklin |
| ↳ DNA is a helical shape | |
| - construction of the double helix model by: | Watson & Crick |
| - purines (2 rings) | A & G |
| - pyrimidines (1 ring) | T & C |
| - A pairs with T by... | 2 H bonds |
| - C pairs with G by... | 3 H bonds |
| - base pairs present in 1 helix turn = | 10 |
| **antiparallel:** | subunits run in opposite directions |

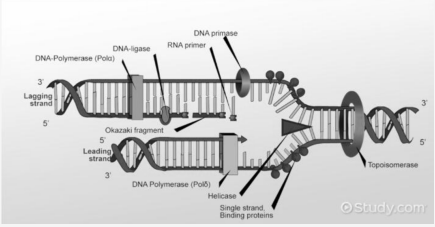
## DNA Replication Experiment

| | | |
|---|---|---|
| - experiment done by: | Meselson & Stahl | |
| ***Prediction*** | | |
| **replication style** | **# bands 1st rep.** | **# bands 2nd rep.** |
| *conservative* | 2 | 2 |
| *semiconservative* | 1 | 2 |
| *dispersive* | 1 | 1 |
| ***Results*** | | |
| # bands 1st rep. | 1 | |
| # bands 2nd rep. | 2 | |
| conclusion = | semiconservative | |

## Replication Process

| | |
|---|---|
| **origin of replication:** | site where the replication of DNA molecules begins |
| **replication fork:** | Y-shaped region on the replicating DNA molecule |
| **- E. coli** | |
| ↳ 1 replication origin | |
| ↳ 500 nucleotides/sec | |
| **- human** | |
| ↳ 100s-1000s of replication origins | |
| ↳ 50 nucleotides/sec | |
| **- 2 items required to start replication:** | |
| 1. primer | 2. DNA template strand |
| **- how added nucleotides bring energy:** | |
| ↳ nucleotides carried by triphosphate | |
| ↳ DNA polymerase catalyzes triphosphate | |
| ↳ 2 phosphates are released | |
| - DNA polymerase adds to the... | 3' end |
| | (elongates from 5' to 3') |
| - lagging strand created from series of... | Okazaki fragments |

## Replication




**helicase:** enzyme that unwinds & separates the DNA strands
**topoisomerase:** enzyme that breaks, swivels, & rejoins the DNA
**primase:** enzyme that synthesizes RNA primers
**primer:** a short sequence of RNA that starts Okazaki fragments
**polymerase III:** enzyme that adds nucleotides
**polymerase I:** enzyme that removes the primer and replaces the nucleotides
**ligase:** enzyme that forms the final bonds between the fragments and nucleotides

## Errors in DNA

- as replication occurs, DNA polymerase finds & corrects any mistakes ---- *reducing the error rate*

- change in the DNA nucleotide is *permanent/mutation* when ---- *the pair is replicated*

- changes in DNA nucleotides due to...

↳ **1.** replication errors **2.** chemicals **3.** x-rays **4.** spontaneously

**telomeres:** multiple repetitions of a short nucleotide sequence at the end of a chromosome

↳ buffer zone to delay erosion of the genes as they get replicated

**telomerase:** enzyme that catalyzes the lengthening of telomeres (restore original length)

**histone:** protein responsible for the first level of packing of chromosomes

**nucleosome:** segment of DNA wound around a protein unit

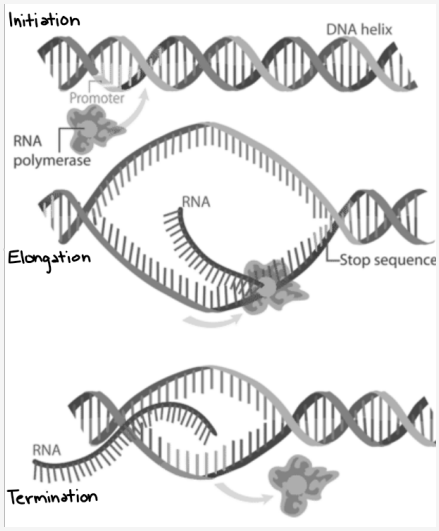
## Gene Expression Background

| | |
|---|---|
| **gene:** | region of DNA expressed to produce a functional product (polypeptide/RNA molecule) |
| **transcription:** | synthesis of RNA from DNA template |
| **translation:** | synthesis of proteins from encoded mRNA |
| **primary transcript:** | initial RNA transcript from any gene (pre-mRNA) |
| **codon:** | 3 nucleotide sequence that specifies a particular amino acid |
| *- eukaryotes~* | transcribe DNA to pre-mRNA |
| | from nucleus to ribosome |
| *- prokaryotes~* | transcribe DNA to mRNA |
| | from cytoplasm to ribosome |

## Transcription

| | |
|---|---|
| **RNA polymerase:** | enzyme that controls the transcription of DNA to RNA |
| ↳ pries DNA strands apart & joins the RNA nucleotides | |
| ↳ moves 3' to 5' | (strand formed 5' to 3') |
| ↳ attaches at the **promoter** | |
| **3 STAGES OF TRANSCRIPTION** | |
| ***1. Initiation*** | |
| *- transcription factors:* | protein that allows for polymerase to attach to DNA and transcribe |
| - 3 items to make up transcription initiation complex = | transcription factors, RNA polymerase, & promoter |
| *- TATA box:* | promoter that is 20-25 nucleotide from the starting point |
| * prokaryotes have NO transcription factors | |
| ***2. Elongation*** | |
| a. *10-20* nucleotides exposed at a time | |
| b. nucleotides added to the *3' end* of the RNA molecule | |
| - difference between RNA & DNA nucleotides = | different sugars |
| - nucleotide RNA that DNA doesn't have... | *uracil* |
| - RNA & DNA nucleotides held together by... | *hydrogen bonds* |
| ***3. Termination*** | |
| a. transcription of the *polyadenylation signal* adds nucleotides of AAUAAA to RNA | |
| b. protein cuts the pre-mRNA from polymerase = end of process! | |

## Transcription Diagram




## Pre-mRNA Modification

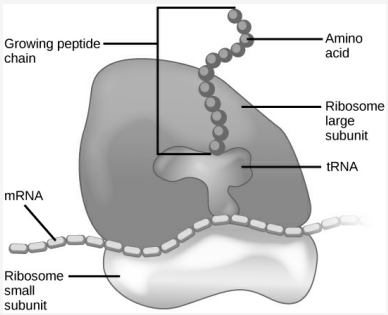
- 5' end receives **5' cap**
- 3' end receives **poly-A tail** (enzyme adds 50-250 more A nucleotides)
  - ↳ *facilitate export* from nucleus
  - ↳ *protect mRNA* from hydrolytic enzymes
  - ↳ *help ribosomes attach* to end of mRNA

| | |
|---|---|
| **RNA splicing:** | process of removing RNA sections from pre-mRNA |
| *- introns:* | noncoding sequences of pre-mRNA |
| *- exons:* | sequences of pre-mRNA used for translation |

- 3 benefits of introns:
  - ↳ make many differnet polypeptides
  - ↳ discrete structural/functional regions
  - ↳ increase exon shuffling (new protein function)

| | |
|---|---|
| **ribozymes:** | RNA molecule that functions as an enzyme (create 3D structure; contain functional groups; H bond w/ DNA or RNA) |

## Ribosome Structure




**tRNA:** transfers amino acids from cytoplasm to ribosomes (& contain anticodon)

↳ **anticodon:** nucleotide triplet on tRNA molecule

↳**'wobble':** flexible base pairing at the 3rd codon position

- # of amino acids used= *20*

**-makeup of a ribosome:**

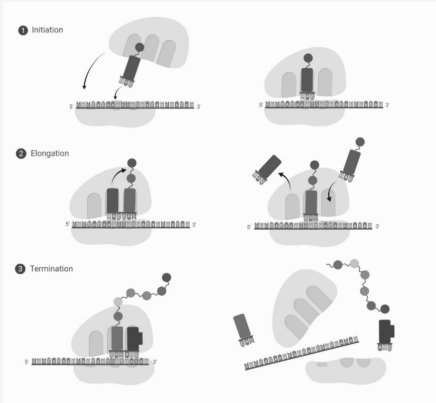
- *large & small subunit*~ made of proteins and rRNAs (eukaryotes in nucleolus & prokaryotes in cytoplasm)

## Translation

*3 STAGES OF TRANSLATION*

| | |
|---|---|
| **1. Initiation** | |
| a. small subunit binds to mRNA & initiator tRNA | |
| b. *translation initiator complex=* | attachment of large subunit (& initiation factors) |
| **2. Elongation** | |
| a. codon recognition- | anticodon of tRNA pairs w. mRNA codon |
| b. peptide bond formation- | removes polypeptide from tRNA by forming peptide bond |
| c. translocation- | empty tRNA released |
| * ribosome moves 5' to 3' | |
| **3. Termination** | |
| a. stop codon- | "release" factor accepted |
| b. hydrolysis of bond- | freeing polypeptide |
| c. subunits dissociate- | mRNA can be used again |

## Translation Diagram

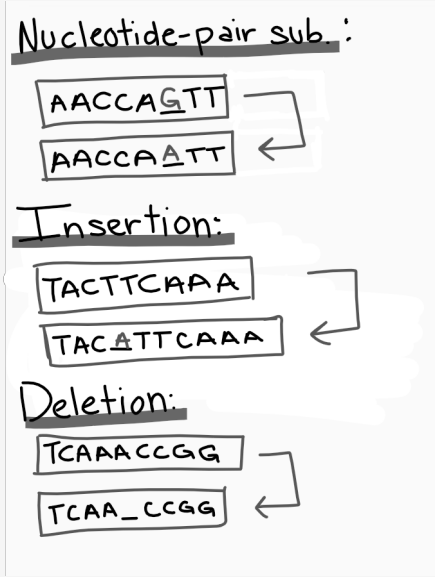



**polyribosomes:** series of ribosomes moving over an mRNA at the same time

**chaperone protein:** proteins that assist polypeptides in forming 3D structures

**signal peptides:** sequence of amino acids at beginning of polypeptide tagging it to where it will go

## Nucleotide Mutations




**point mutation:** change in a single nucleotide

**frameshift mutation:** change in nucleotide # to not be a multiple of 3

↳ may still code for same amino acid

↳ may code for stop codon early

↳ may result in protein not functioning properly

## Regulation of Gene Expression

- responds to changes in environmental conditions

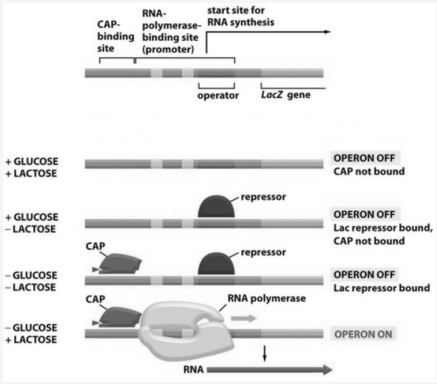
- either adjusts **activity** of enzymes present or **production** of enzymes

| | |
|---|---|
| - 3 things to make up an *operon*: | operator; promoter; genes |
| **operator:** | segment of DNA within promoter that controls the access of RNA polymerase to the genes |
| **repressor:** | protein that binds to operator to block attachment of RNA polymerase |

↳ made by activity of *regulatory gene*

| | |
|---|---|
| **repressible operon:** | transcription is inhibited by small molecule binding to regulatory protein |
| **inducible operon:** | stimulated when small molecule binds to regulatory protein |

## Lac Operon




- *high lactose* = allolactose bind to repressor to change shape & no longer attach
- *low glucose* = high levels of cAMP combine with CAP

## Differential Gene Expression

- differential gene expression = different cell types

- 3 processes of development:

**1.** cell division **2.** cell differentiation **3.** morphogenesis

**cytoplasmic determinants:** substances in the egg that influence the course of early development

**induction:** embryonic cells influence the development of another (change in gene expression)

**homeotic genes:** genes that control pattern formation as an organism develops

## Biotechnology

**Gel electrophoresis**

- separates DNA by size and charge

- DNA negatively charges

↳ smaller segments = farther to bottom

**Polymerase Chain Reaction (PCR)**

- create many copies of DNA segment

↳ DNA denatured → primers added → DNA replicated

**Recombinant DNA**

- DNA segment put into plasmid to be reproduced

**DNA Sequencing**

- establish the order of nucleotides

↳ labeled with dye