

Some Information in this lecture may not be mentioned by the Dr. as thoroughly as this sheet. But they cannot be overlooked for a better understanding, so bear with this lecture :) and sorry for any inconveniences.

# **DNA Structure**

The DNA structure of **Prokaryotes** is similar to that of **Eukaryotes**. The building blocks of DNA are **nucleotides**, which are made up of three parts: a **deoxyribose** (5-carbon sugar), a **phosphate group**, and a **nitrogenous base**.

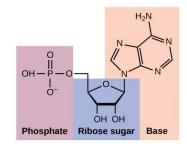
## There are four types of nitrogenous bases in DNA :

- Adenine (A) and thymine (T) are connected by 2 hydrogen bonds.
   Cytosine (C) and guanine (G) are connected by 3 hydrogen bonds.
- The **phosphate group** of one **nucleotide** bonds covalently with the **sugar molecule** of the **next** nucleotide, and so on, forming a **long polymer** of nucleotide monomers.
- The **sugar-phosphate groups** line up in a *"backbone"* for each single strand of DNA, and the nucleotide bases stick out from this backbone.
- Naturally, each DNA molecule is composed of two single strands held together with hydrogen bonds between the bases.

<u>Note:</u> When DNA is **heated**, the hydrogen bonds holding the 2 strands together **break**, and the 2 strands **fall apart**. Since G-C base pair are connected by **3 H-bonds**, A DNA with more G-C base pairs would need **more heat** to be broken.

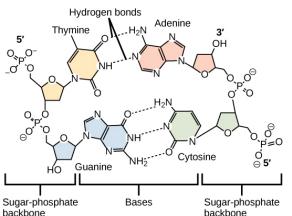
- The 2 **complementary strands** of a DNA double helix run in **opposite directions** alongside each other.
- The **antiparallel orientation** allows for the base pairs to complement one another. Antiparallel DNA is also **more structurally stable** than parallel DNA.

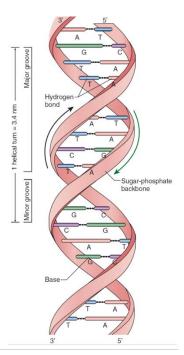
<u>Note:</u> This orientation affects the **DNA replication**, since certain enzymes only functions in the **3'- 5' direction**. (discussed more later in this sheet)



A and G are purines

C and T are pyrimidines





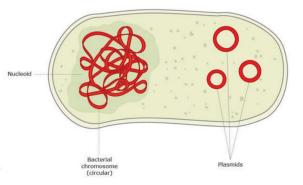
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## **Measuring DNA Size**

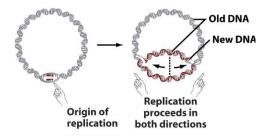
We can **measure the size** of the DNA molecule in **kilobase pair** (Kbp). In bacteria, a single DNA molecular size can be from **100s to 1000s Kilobase pairs**.

## **Bacterial Chromosome**

- A haploid, double stranded circular DNA with no free ends are characteristics of most bacterial chromosomes. Unlike the linear DNA of most eukaryotes.
- Many bacteria also contain **extra looped bits** of DNA known as **plasmids**.



- The genetic information of the plasmid is usually **not essential** for the survival of the host bacteria, however it carries multiple **antibiotic resistance genes**. (discussed later in the next lecture)
- A **Replicon** is any genetic material that replicates itself in a bidirectional manner from a single origin. For **most** prokaryotes, the replicon is the **entire chromosome** and the **plasmids**.



- Bacterial chromosome if **untangled** is almost **1mm long**, while the **bacterium** is about a **micrometer** in size. Thus, **supercoiling** of the bacterial chromosome is **needed** for **packaging** and **storing** purposes inside the bacterium.

In **Eukaryotes**, the chromosomes are tangled using **histones** which are not present in bacteria. **Bacteria** uses other compounds to promote supercoiling (*e.g. Polyamines*).

- **Haploid** Bacteria, with only **one copy** of each vital gene, are always **threatened** by mutations more than **diploid** Eukaryotes.

In Eukaryotes, the **complementation** in **diploids** compensate the **deficiencies** of **mutated genes** by other normal genes.

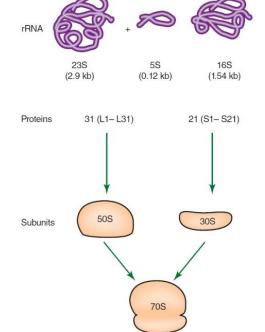
# **DNA Replication Process**

Important terms for further understanding before carrying on, also study thoroughly the following table of enzymes used in DNA replication:

- Sedimentation Rate (S): is a measurement of the rate of sedimentation in centrifugation, used to describe the ribosomal subunits and the rRNA fragments -but not the size of them- that's why they don't add up since it's a measurement of rate not size.
- 2) **Ribosomes:** Are complexes found within all living cells, that serves as the site of biological protein synthesis (translation) in the cytoplasm, where tRNA carries AAs from the cytoplasm into the ribosome. Ribosomes then link amino acids together in the order specified by the mRNA molecules.

<u>Ribosomes in prokaryotes consist of two major</u> <u>components:</u>

- *a-* A small ribosomal subunit (30S), which reads the mRNA.
- *b-* A large subunit (50S), which join amino acids to form a polypeptide chain.



Each subunit is made up of rRNA molecules and a variety of ribosomal proteins.

Table 1. The Molecular Machinery Involved in Bacterial DNA Replication	
Enzyme or Factor	Function
DNA pol I	Exonuclease activity removes RNA primer and replaces it with newly synthesized DNA
DNA pol III	Main enzyme that adds nucleotides in the 5' to 3' direction
Helicase	Opens the DNA helix by breaking hydrogen bonds between the nitrogenous bases
Ligase	Seals the gaps between the Okazaki fragments on the lagging strand to create one continuous DNA strand
Primase	Synthesizes RNA primers needed to start replication
Single-stranded binding proteins	Bind to single-stranded DNA to prevent hydrogen bonding between DNA strands, reforming double-stranded DNA
Sliding clamp	Helps hold DNA pol III in place when nucleotides are being added
Topoisomerase II (DNA gyrase)	Relaxes supercoiled chromosome to make DNA more accessible for the initiation of replication; helps relieve the stress on DNA when unwinding, by causing breaks and then resealing the DNA
Topoisomerase IV	Introduces single-stranded break into concatenated chromosomes to release them from each other, and then reseals the DNA

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## **Step 1: Replication Fork Formation**

Before DNA can be replicated, the double stranded molecule must be "untangled" by an enzyme called <u>Topoisomerase</u>, then it is "unzipped" into two single strands by an enzyme known as <u>DNA helicase</u>. DNA helicase disrupts the hydrogen bonding between base pairs to separate the strands into a Y shape known as the replication fork. This area will be the template for replication to begin.

<u>Note:</u> One strand is oriented in the 3' - 5' direction (leading strand) while the other is oriented 5' - 3' (lagging strand). The two sides are therefore replicated by two different processes to accommodate the directional difference, each discussed below.

## **Step 2: Primer Binding**

 Once the DNA strands have been separated, a short piece of RNA called a primer generated by the <u>DNA primase enzyme</u> binds to the 3' end of the strand on the leading strand.

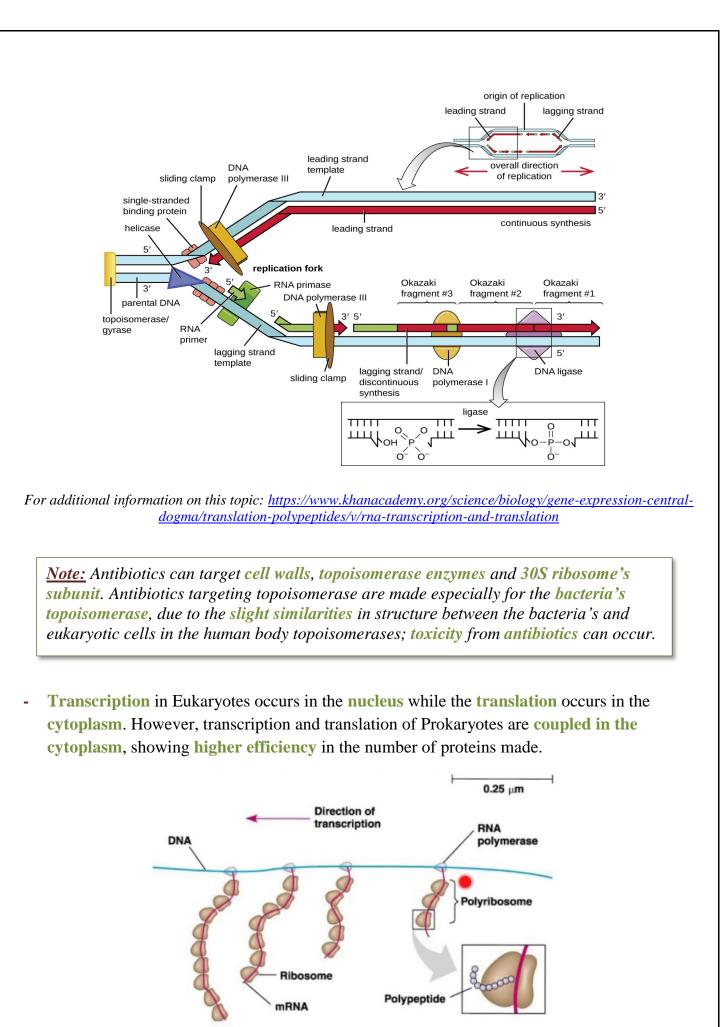
## **Step 3: Elongation**

- **DNA polymerase III** binds at the **site of the primer** and begins adding new base pairs **complementary** to the **template strand**. *Note that the template strand is read in the 3'-5' direction, while the new strand is added in the 5'-3' direction.*
- The lagging strand begins replication by binding with multiple primers. Each primer is only several bases apart. DNA polymerase then adds pieces of DNA, called Okazaki fragments, to the strand between primers.

This process of replication is **discontinuous** and **slower** than the leading strand thus calling it a lagging strand.

## **Step 4: Termination**

- Once both the continuous and discontinuous strands are formed, an enzyme called DNA pol I (*Exonuclease*) removes all RNA primers from the original strands. These primers are then replaced with appropriate bases.
- Another enzyme called **DNA ligase** joins **Okazaki fragments** together forming a single unified strand.
- In the end, replication produces **two DNA molecules**, each with one strand from the parent molecule and one new strand.



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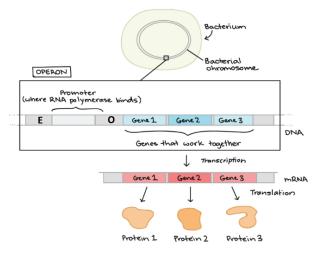
# **Regulation of Transcription in Prokaryotes**

There are various forms of **gene regulation**, that is, **mechanisms for controlling** which **genes get expressed** and at what levels (*e.g. Attenuation*). Bacteria have specific regulatory molecules that control whether a particular gene will be **transcribed into mRNA** or not.

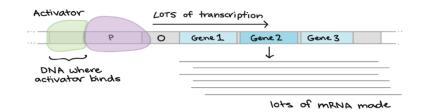
## **Operons**

- In bacteria, genes are **often** found in **operons**. An operon is a cluster of genes under control of a **single promoter**.
- Operons are **common** in **bacteria**, but they are **rare** in **eukaryotes**.

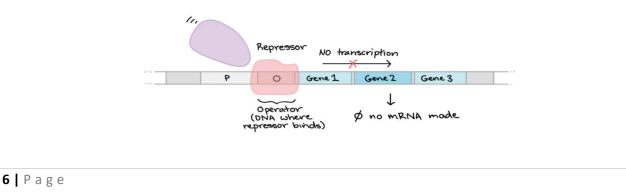
They have **3** regulatory regions: **Promoter**, **operator** (*O*) and the **enhancer** (*E*).



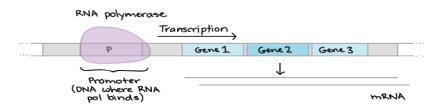
- Operons contain **regulatory DNA sequences** (*Promoter where RNA polymerase binds*) that **control transcription** of the operon's genes.



- Also, **most operons** have **regulatory DNA sequences** in addition to the promoter. These sequences (*called operators*) are **binding sites** for **regulatory proteins** that either **induces** or **reduces transcription**. *Types of regulatory proteins:* 
  - 1) **Repressor** binds on an **operator**. When bound to its operator, it **reduces transcription** (*e.g. By blocking RNA polymerase from moving forward on the DNA*).

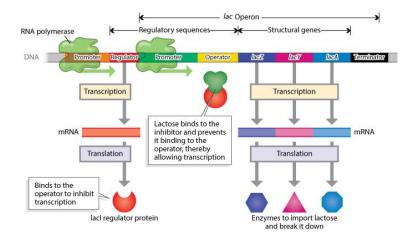


2) Activator, when bound to its DNA binding site (enhancer), it increases transcription of the operon (e.g. By helping RNA polymerase bind to the promoter).



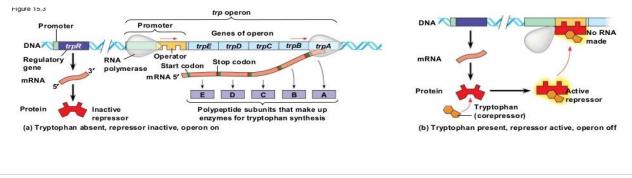
- Operons can either be **inducible** or **repressible**.
- 1) **Inducible operon** means that they are **usually Off** and doesn't turn on unless its **induced** by **small molecules** (*inducer*).

**Example:** Lac Operon which encodes enzymes for the metabolism of lactose, is usually off repressed by a lac regulatory protein. It's On only when lactose (inducer) is present which inhibits the repressor. So, its activated to break down that lactose.



2) **Repressible operon** means that they are **usually On** unless it gets turned Off by a **small molecule** (*corepressor*).

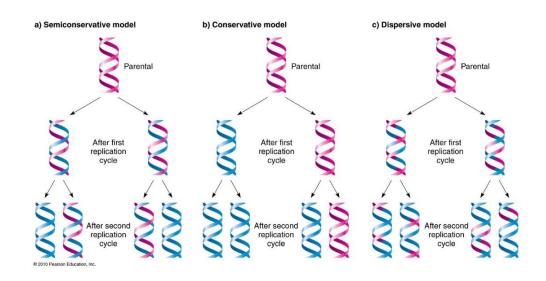
**<u>Example</u>:** Trp Operon which encodes enzymes to synthesize the amino acid tryptophan. This operon is On by default, but can be repressed when high levels of the amino acid tryptophan (corepressor) are present to stop any further synthesis of Trp.



**Note:** These gene regulations allows bacteria to **respond to environmental changes**, by altering **gene expression** and thus, changing the set of proteins present in the cell.

I strongly recommend this site for any further understanding of operons, but it may not be required: https://www.khanacademy.org/science/biology/gene-regulation/gene-regulation-in-bacteria/v/operons-and-generegulation-in-bacteria

# **Models of DNA replication**



- **a- Semi-conservative model:** The two parental strands **separate** and each makes a **copy of itself**. After one round of replication, the two daughter molecules each have **one old and one new strand**.
- **b- Conservative model:** The parental molecule directs synthesis of **an entirely new double-stranded molecule**, such that after one round of replication, one molecule is conserved as two old strands. This is repeated in the second replication.
- **c- Dispersive model**: The material in the two parental strands is **distributed randomly** between two daughter molecules.

→ The semi-conservative model is the correct/most appealing model.

		<b>Types of Mutations</b>
Substitution	Silent	If a <b>single base substitution</b> occurs and the resulting codon is a <b>synonymous codon</b> . Thus, the amino acid sequence encoded by the gene is <b>not changed</b> and the mutation is said to be <b>silent</b> .
	Missense	<ul> <li>When a single base substitution results in the generation of a codon that gives a different amino acid and hence leads to a different protein. It can be:</li> <li>a- Conservative If the structure and properties of the substituted amino acid is very similar to the original amino. </li> <li>b- Nonconservative If the substitution leads to an amino acid with very different structure and properties. </li> </ul>
	Nonsense	When a <b>single base substitution</b> results in a <b>stop codon</b> ultimately cutting off translation and most likely leading to <b>a nonfunctional protein</b> . Mutated template DNA strand UUUUUAAGCACGU Mutated mRNA Phe STOP Polypeptide synthesis ceases
Frameshift	Deletion	A base or more is deleted changing the AAs sequence from that point forward.
	Insertion	A base or more is inserted, changing the AAs sequence from that point forward.

<u>Note:</u> Mutations can be a result of many causes, for example: A defect in DNA polymerase, UV radiations, etc.

# **DNA Repair Mechanisms**

### 1) Direct DNA repair

It is used for **reversal cell damages** (e.g. pyrimidine dimers and alkylated bases), the damaged area is repaired directly by **specialized proteins** in our body. It is the **simplest** form of DNA repair and it does not require a **reference template** unlike the other mechanism.

#### 2) Excision repair

Damaged bases are **removed/cut** out and replaced directly (*By DNA poly. III*) using the other **undamaged** strand as a **template**, and finally it gets **ligated**.

#### 3) Post replication recombinational repair

If a DNA strand contain **lesions** (*sites of damage*), it will **prevent** base pairing thus **creating a gap** in the daughter strand during replication. In this repair mechanism, the gap is **filled** by a sequence of information from a **parent strand** of a **sister chromosome** (*not by DNA poly. III*).

#### 4) SOS response

SOS response is induced when DNA is **damaged** or when replication of DNA stops and single stranded DNA accumulates. When induced, a group of genes are **transcribed** to **repair the damage**.

#### 5) Error prone repair

Is the **last resort** of a bacterial cell before it dies. An error prone polymerase is used to fill in gaps with a **random sequence** when a DNA template is **not available** for directing an accurate repair. However, a **higher risk** of **mutations** will arise due to the randomly mismatched base pairs. The following table is only an additional revision of some points

prences
is <b>faster in Prokaryotes</b> .
enzymes are slightly different in structure.
Bacteria have a single circular, double stranded, haploid chromosome. (one copy of each gene)
Most bacteria have only <b>a single origin of replication</b> per circular chromosome.
Transcription and translation are almost simultaneous in a prokaryotic cell as it <b>doesn't</b> <b>require</b> post transcriptional modification
70s ribosomes
larities

# The DNA strand is **read** from **the 3'-5' direction** while the new strand is **synthesized** from the **5'- 3' direction**.

Continues synthesis of the leading strand and discontinuous synthesis of the lagging strand.

Good luck @ and don't hesitate to discuss anything