Nanobiotechnology and Nanomedicine
Course code: 601104

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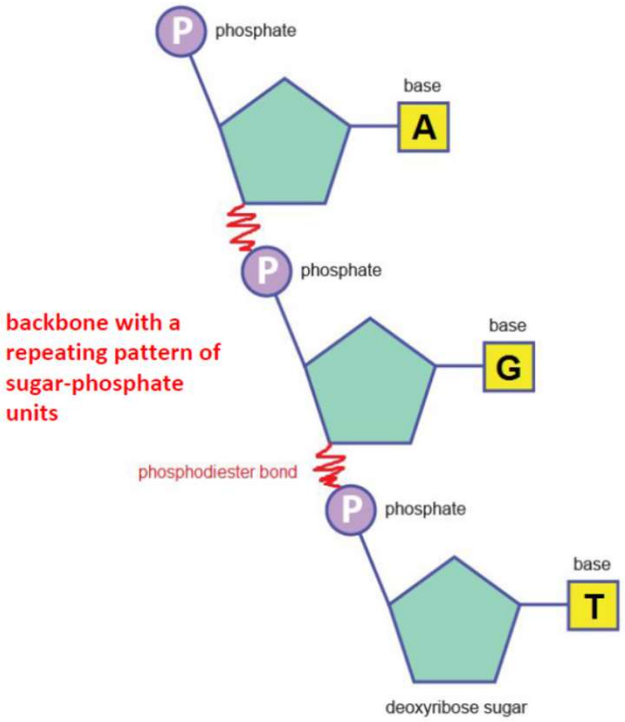
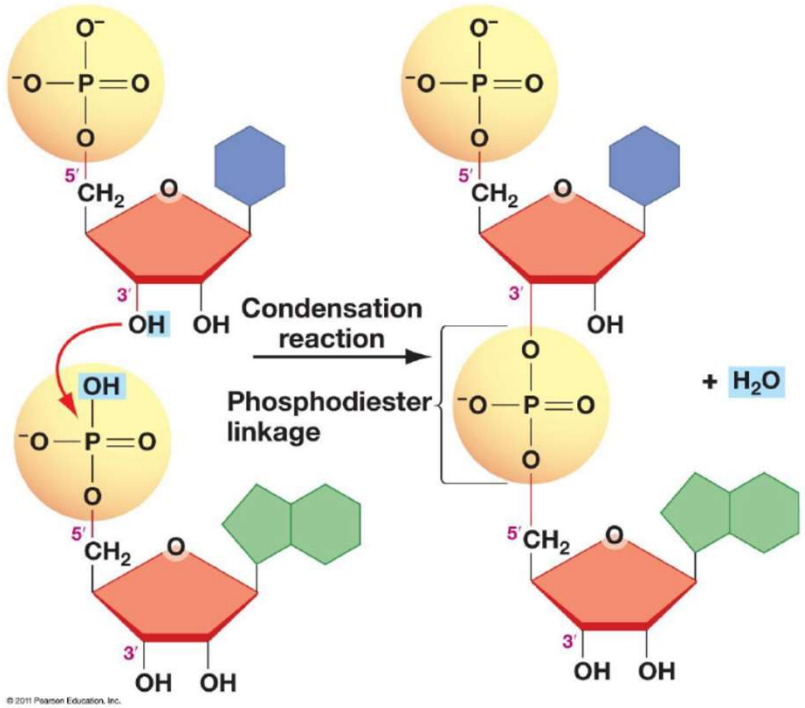
Phosphodiester Bond links two bases





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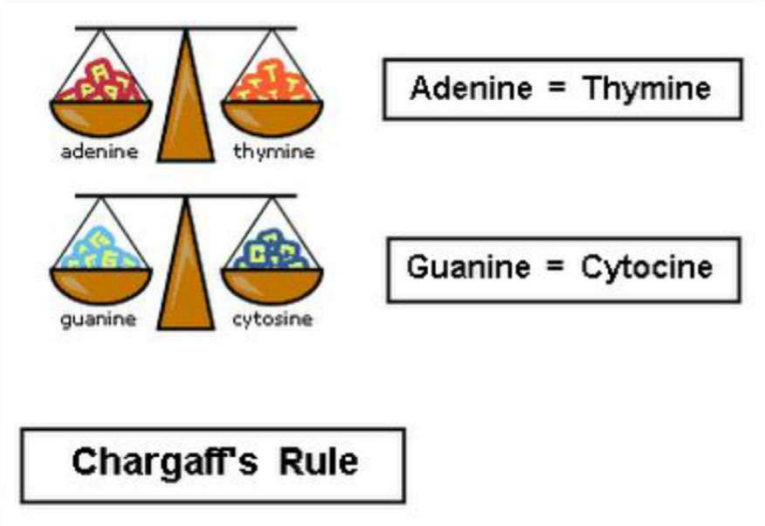
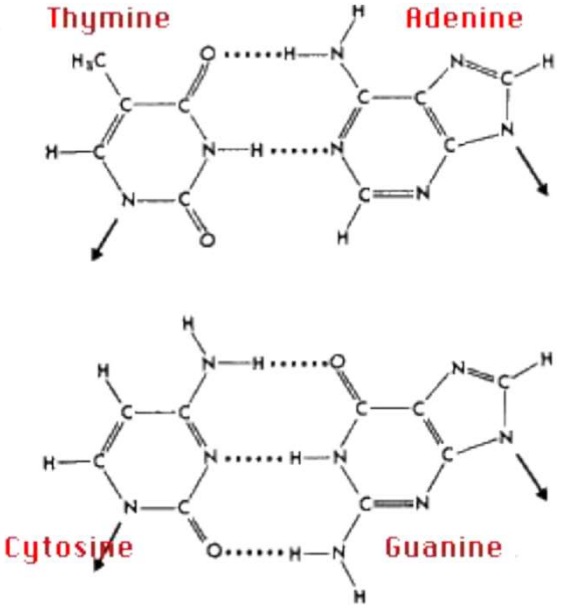
Chargaff ‘s Rule

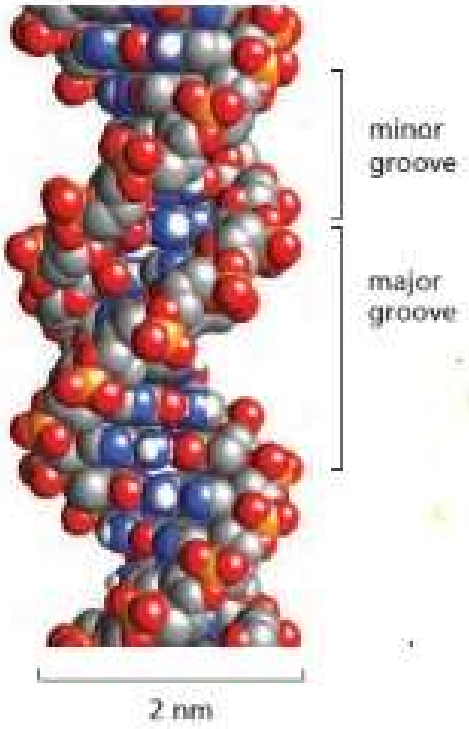




Chargaff's rules demonstrate that DNA from any cell of any organisms have a 1:1 ratio (base Pair Rule) of pyrimidines and purine bases. It means that the amount of guanine should be equal to cytosine and the amount of adenine should be equal to thymine. This pattern is found in both strands of the DNA. Discovered by Austrian born chemist Erwin Chargaff in the late 1940s.

DNA space filling model

Figure (right): **The DNA double helix space-filling model of 1.5 turns of the DNA double helix. Each turn of DNA is made up of 10.4 nucleotide pairs, and the centre-to-centre distance between adjacent nucleotide pairs is 0.34 nm. The coiling of the two strands around each other creates two grooves in the double helix. The wider groove is called the major groove, and the smaller the minor groove, as indicated.**



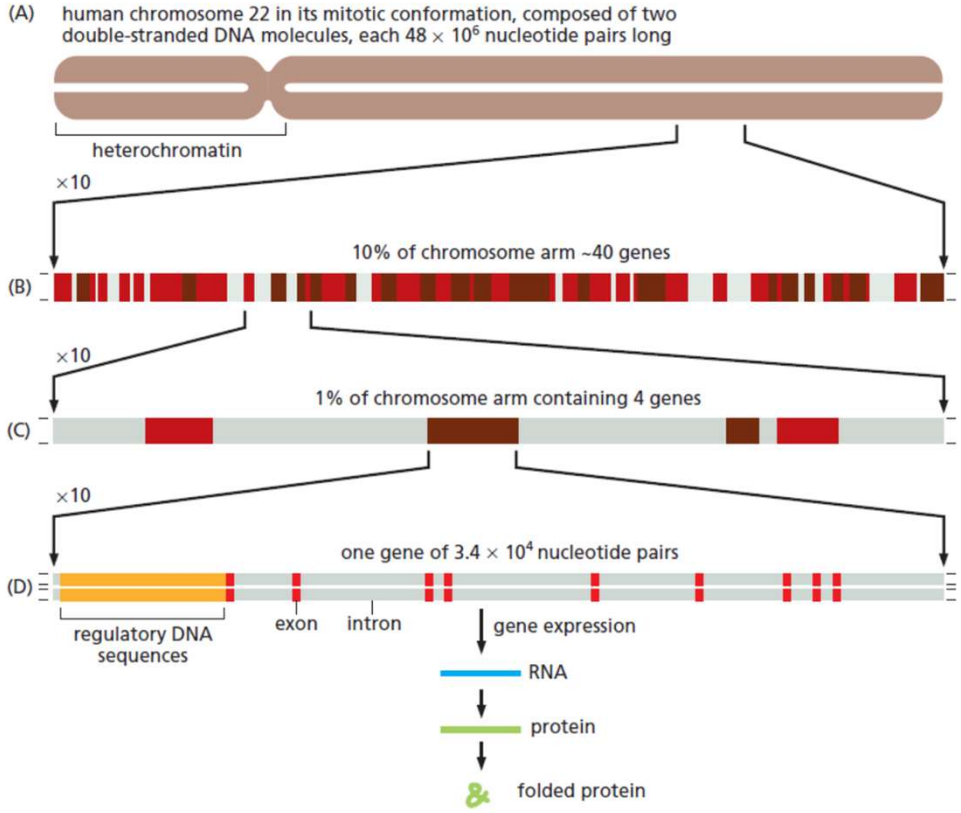
- **Ligand and proteins binds to either minor or major grooves.**

The organization of genes on human a chromosome

Chromosomes contain long string of genes:

Chromosomes carry genes—the functional units of heredity. A gene is defined as a segment of DNA, It contains the instructions for making a particular protein.

(A) Chromosome 22, one of the smallest human chromosomes, contains 48 × 10^6 nucleotide pairs. It is makes up approximately 1.5% of the human genome. The left arm of chromosome 22 consists of short repeated sequences of DNA that are packaged in a particularly compact form of chromatin (heterochromatin). (B) A tenfold expansion of a portion of chromosome 22, with about 40 genes indicated. Those in *dark brown* are known genes and those in *red* are predicted genes. (C) An expanded portion of (B) showing four genes. (D) The intron–exon arrangement of a typical gene is shown after a further tenfold expansion. Each exon *(red)* codes for a portion of the protein, while the DNA sequence of the introns *(gray)* is relatively unimportant. The human genome (3.2 × 10^9 nucleotide pairs) is the totality of genetic information belonging to our species.



DNA Molecules Are Highly Condensed in Chromosomes

- All eukaryotic organisms has a unique packaging mechanism of DNA into chromosomes.
- For example, if the 48 million nucleotide pairs of DNA in human chromosome 22 could be laid out as one long perfect double helix, the molecule would extend for about 1.5 cm if stretched out end to end. But chromosome 22 measures only about 2 μm in length. The end to- end compaction ratio of over 7000-fold.
- The DNA of human interphase chromosomes is still tightly packed.
- The chromosome structure is dynamic. The each chromosome condenses to an extreme degree in the M- phase of the cell cycle.

- Nucleosomes are a basic unit of eukaryotic Chromosome structure.
- The proteins that bind to the DNA to form eukaryotic chromosomes are two types: the histones and the *non-histone chromosomal proteins*, each contributing about the same mass to a chromosome as the DNA.
- The complex of both classes of protein with the nuclear DNA of eukaryotic cells is known as chromatin.

The Condensation is less visible, but of vital importance, specific regions of interphase chromosomes decondense to allow access to specific DNA sequences for gene expression, DNA repair, and replication—and then recondense when these processes are completed.

Structure of Nucleosome core particles and DNA packing

The interface between DNA and histone is extensive: 142 hydrogen bonds are formed between DNA and the histone core in each nucleosome. Nearly half of these bonds form between the amino acid backbone of the histones and the sugar-phosphate backbone of the DNA. Numerous hydrophobic interactions and salt linkages also hold DNA and protein together in the nucleosome.

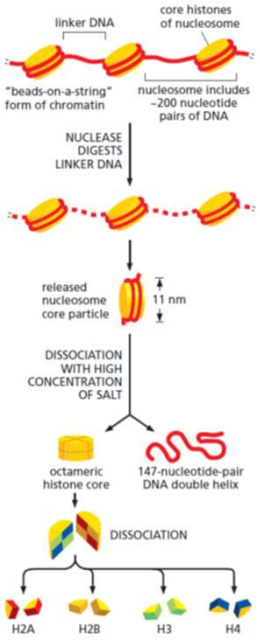


Figure first right: Structural organization of the nucleosome.
A nucleosome contains a protein core made of eight histone molecules. In biochemical experiments, the nucleosome core particle can be released from isolated chromatin by digestion of the linker DNA with a nuclease, an enzyme that breaks down DNA. (The nuclease can degrade the exposed linker DNA but cannot attack the DNA wound tightly around the nucleosome core.) After dissociation of the isolated nucleosome into its protein core and DNA, the length of the DNA that was wound around the core can be determined.
This length of 147 nucleotide pairs is sufficient to wrap 1.7 times around the histone core.

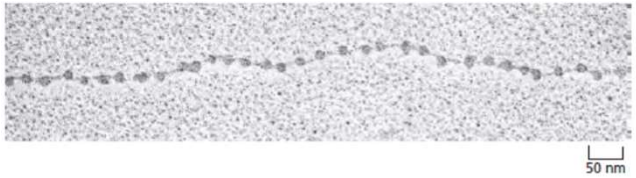


Fig: Transmission electron micrograph of Bead and string type arrangement of DNA

To be continued in next lecture

References

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