

Overview and concept

EPIGENETICS

- Epigenetics literally means "above" or "on top of" genetics. It refers to external modifications to DNA that turn genes "on" or "off." These modifications do not change the DNA sequence, but instead, *they affect how cells "read" genes*.
- The term epigenetics refers to heritable changes in gene expression that does not involve changes to the underlying DNA sequence; *a change in phenotype without a change in genotype*.

Conrad Waddington (1942) coined the term, "epigenetic". He is known as father of epigenetics.



Conrad Hal Waddington (1905 to 1975)

> Epigenome

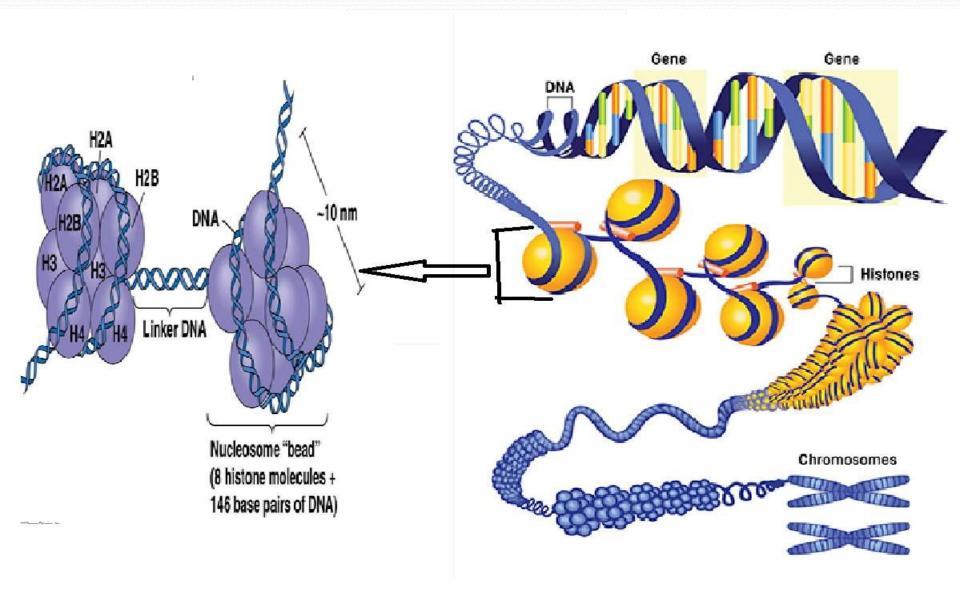
- An epigenome consists of a record of the chemical changes to the DNA and histone proteins of an organism.
- These changes can be passed down to an organism's offspring.
- Changes in the *epigenome* can result in changes to the structure of chromatin and changes to the function of the genome.
- The *epigenome* is a multitude of chemical compounds that can tell the genome what to do.

Epialleles

Alleles of a locus which have identical DNA sequences but display different epigenetic states and which have been proposed to influence a variety of phenotypes in plants and animals.

Molecular epigenetic mechanisms

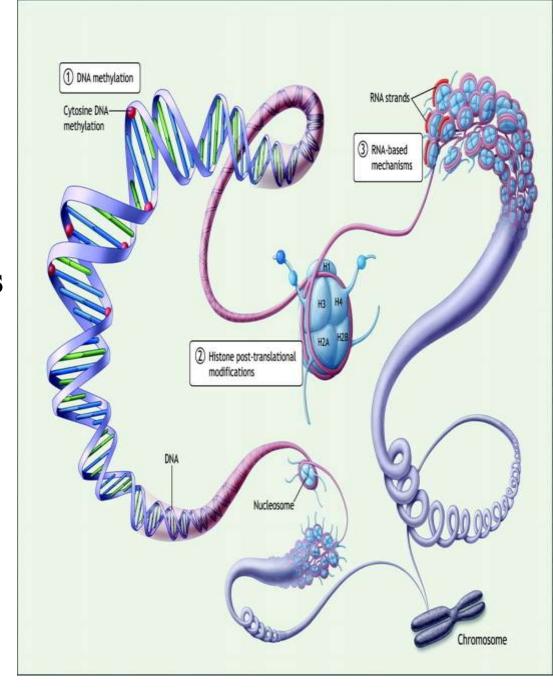
DNA PACKAGING



MECHANISMS

1. DNA methylation

- 2. Histone modifications
 - Acetylation
 - Methylation
 - Phosphorylation,
- 3. RNA mediated interference



1.DNA METHYLATION

- **DNA**methylation mechanism used by
- is an epigenetic cells control

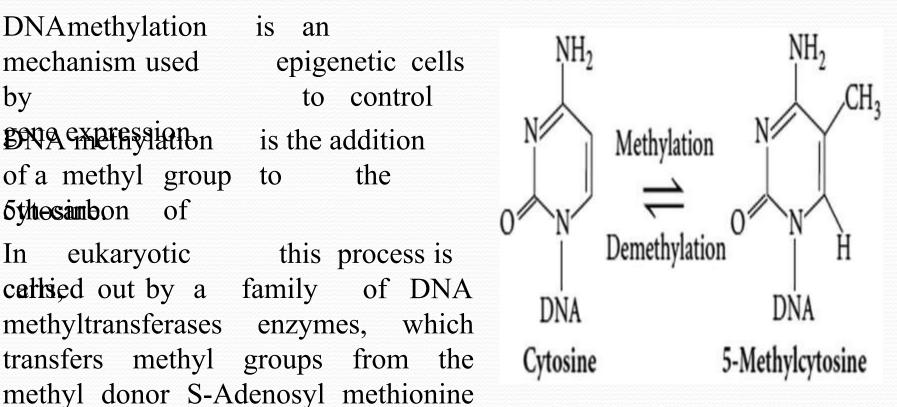
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BNA GRAPHANION is the addition of a methyl group to 5thesambon of

(SAM) to the cytosine.

In eukaryotic this process is cethied out by a family of DNA methyltransferases enzymes, which transfers methyl groups from

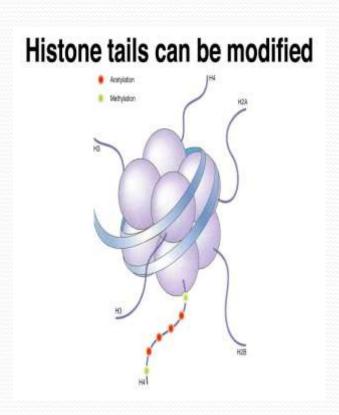
 \Box The resulting 5-methyl cytosine (5mC) is often repressive.



The repressive nature of 5mC is thought to inhibit the binding of DNA by transcription factors thus it is inaccessible for transcription

2. Histone modification

- ☐ They are the chief protein components of chromatin, acting as spools around which DNA winds, and playing a role in gene regulation.
- Histone modifications occur primarily on histone tails by three methods-
- Methylation
- Acetylation
- Phosphorylation



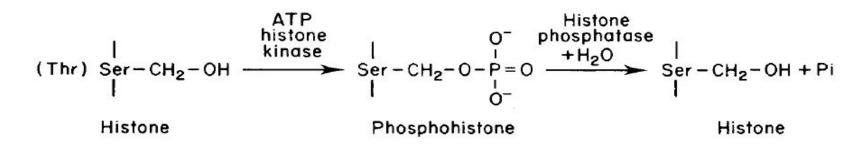
a. Histone Methylation

- **□** Enzyme required
- ☐ Histone methytransferases (HMTs)
- ☐ KMT- Lysine methyl transferase
- ☐ Methylation can result in activation or repression of genes.

b. Histone Acetylation &

- Reacetylation
 - Histone acetyl transferases (HATs)
 - Adds acetyl groups to histone tails.
 - Reduces positive charge and weakens interaction of histories with DNA
 - ☐ Facilitates transcription by making DNA more accessible to RNA polymerase II
- **☐** Histone deacetylation
 - Histone deacetylases (HDACs)
 - ☐ Removes acetyl groups from histone tails
- Increases interaction of DNA and histones
- ☐ Represses transcription

C. Histone Phosphorylation



■ Phosphorylation

- ☐ Enzyme required Protein kinase
- ☐ Phosphorylation increase the negative charge on Histone as a result less interaction between DNA and histones that leads to chromatin de-condensation.

Dephosphorylation

- ☐ Enzyme required phosphatase
- ☐ increase positive charge followed by chromatin condensation.

3. RNA interference

Also called post transcriptional gene silencing (PTGS)

CONCLUSION

- The field of epigenetics has rapidly developed into one of the most influential areas of scientific research.
- Recent advances in analytical methodology have allowed for a significant expansion of what is known about genome wide mapping of DNA methylation and histone modifications.
- Good knowledge of epigenetic mechanisms leads to better understanding of regulation of gene expression at transcriptional and post-transcriptional levels.
- Epigenetic mechanisms such as DNA methylation and histone modification play a key role in development and stress response.

THANK YOU YOU