TOPIC : EPIGENETICS
SUBJECT : BOTANY
SEMESTER : M.Sc. Botany Semester IV
PAPER/COURSE : MBOTEC–1 (Unit III)
Cytogenetic & Crop Improvement

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EPIGENOMICS

Introduction

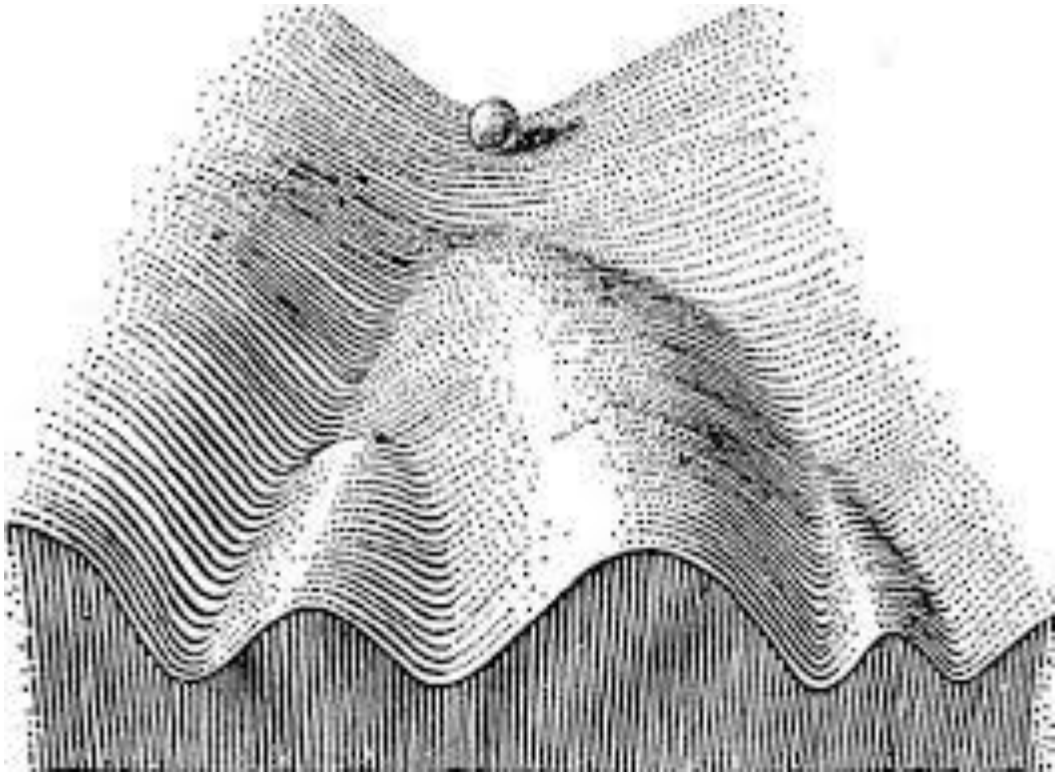
- An epigenome consists of a record of chemical changes to the DNA and the histone protein of an organism.
- These changes can be passed down to the offspring of an organism.

➢ How are epigenetics and Epigenomics different?

- Epigenetics focuses on process that regulates gene expression.
- Epigenomics focuses on the analysis of epigenetic changes across the entire genome

FATHER OF EPIGENETICS

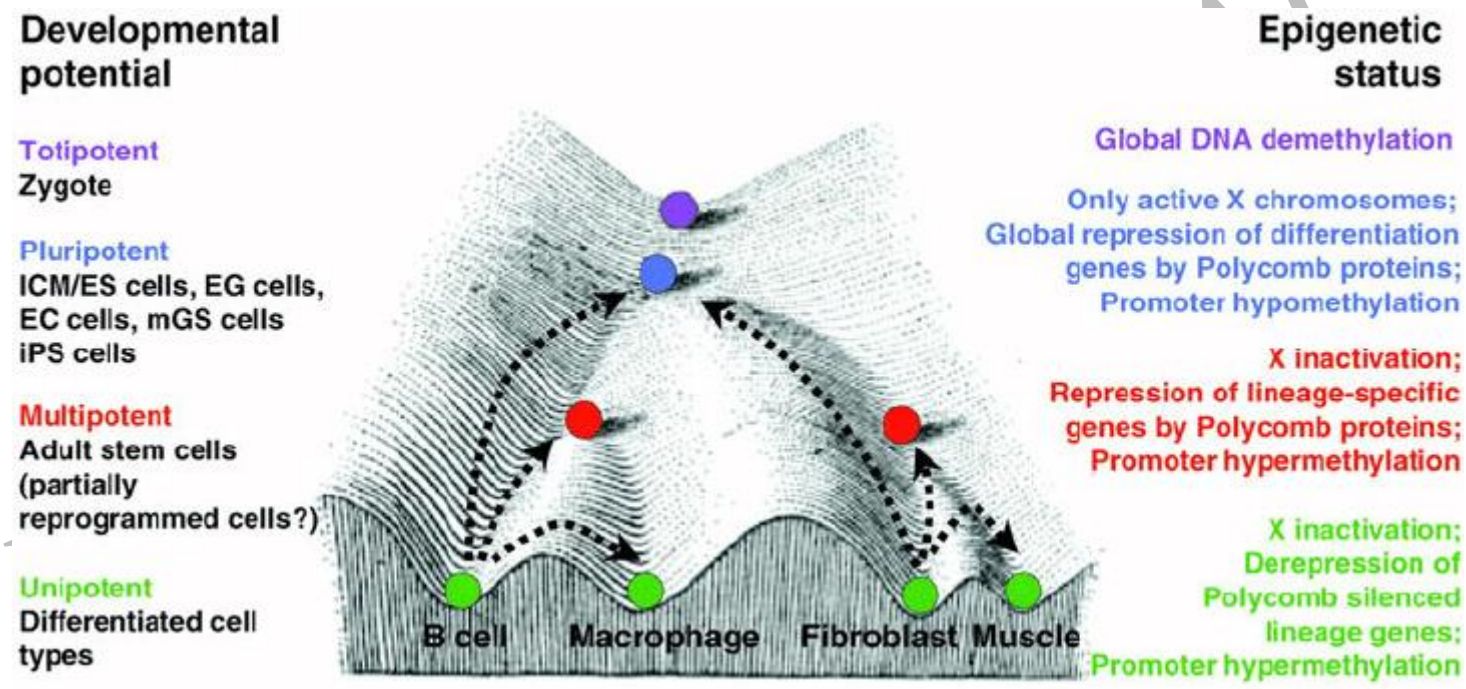
Waddington(1942)



The image created by Waddington to represent the epigenetic landscape.

The Epigenetic Landscape

- Conrad Waddington was a hugely influential British polymath. He was born in 1903 in India.
- This image was created by Waddington to represent the epigenetic landscape. The position of the ball represents different cell fates. The image is incredibly powerful in helping to visualise what might be happening during cellular development.
- The ball at the top of the hill is the zygote, the single cell that results from the fusion of one egg and one sperm. As the various cells of the body begin to differentiate (become more specialised), each cell is like a ball that has rolled further down the hill and headed into one of the troughs.
- Once it has gone as far as it can go, it's going to stay there. Unless something extraordinarily dramatic happens, that cell is never going to turn into another cell type (jump across to another trough). Nor is it going to move back up to the top of the hill and then roll down again to give rise to all sorts of different cell types.



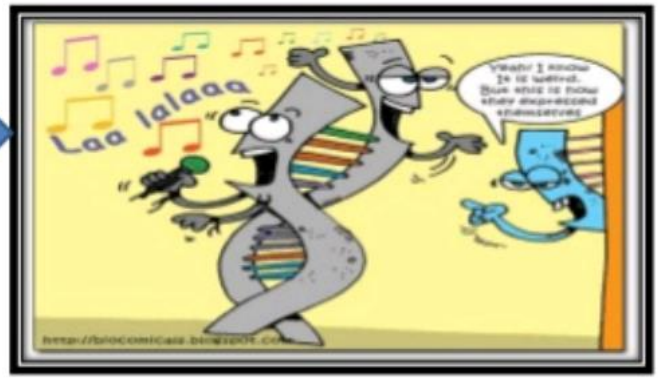
Explained form of Waddington's landscape

What is EPIGENETICS ?

Epigenetics literally means "above" Or " on top of" genetics: It refers to external modification to DNA that turns genes 'on' or 'off'.

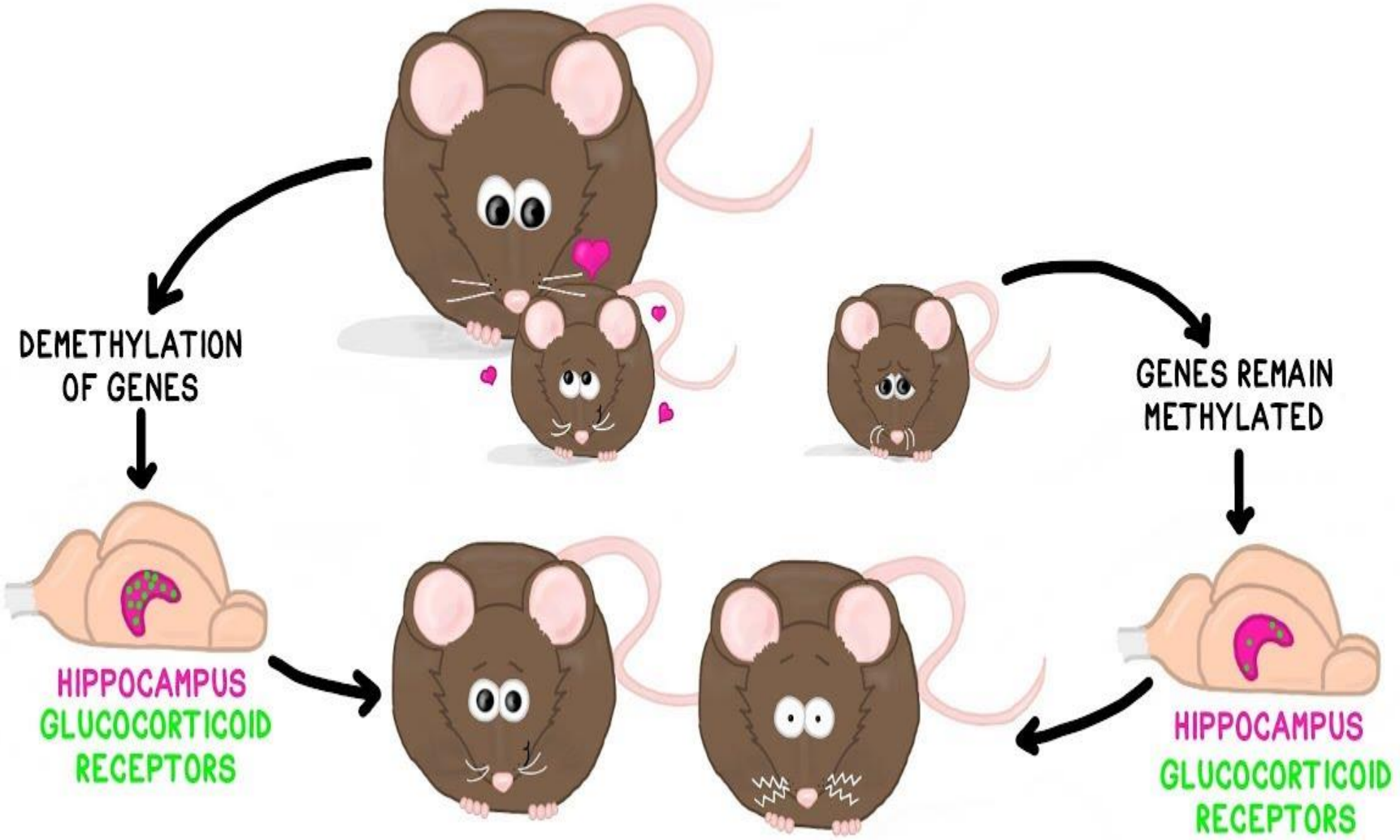
''The study of changes in gene function that are heritable and donot entail a change in DNA sequence''

- Corrent wu and morris(2001)



Epigenomics : Study of the complete set of epigenetic modifications on the genetic material of a cell .

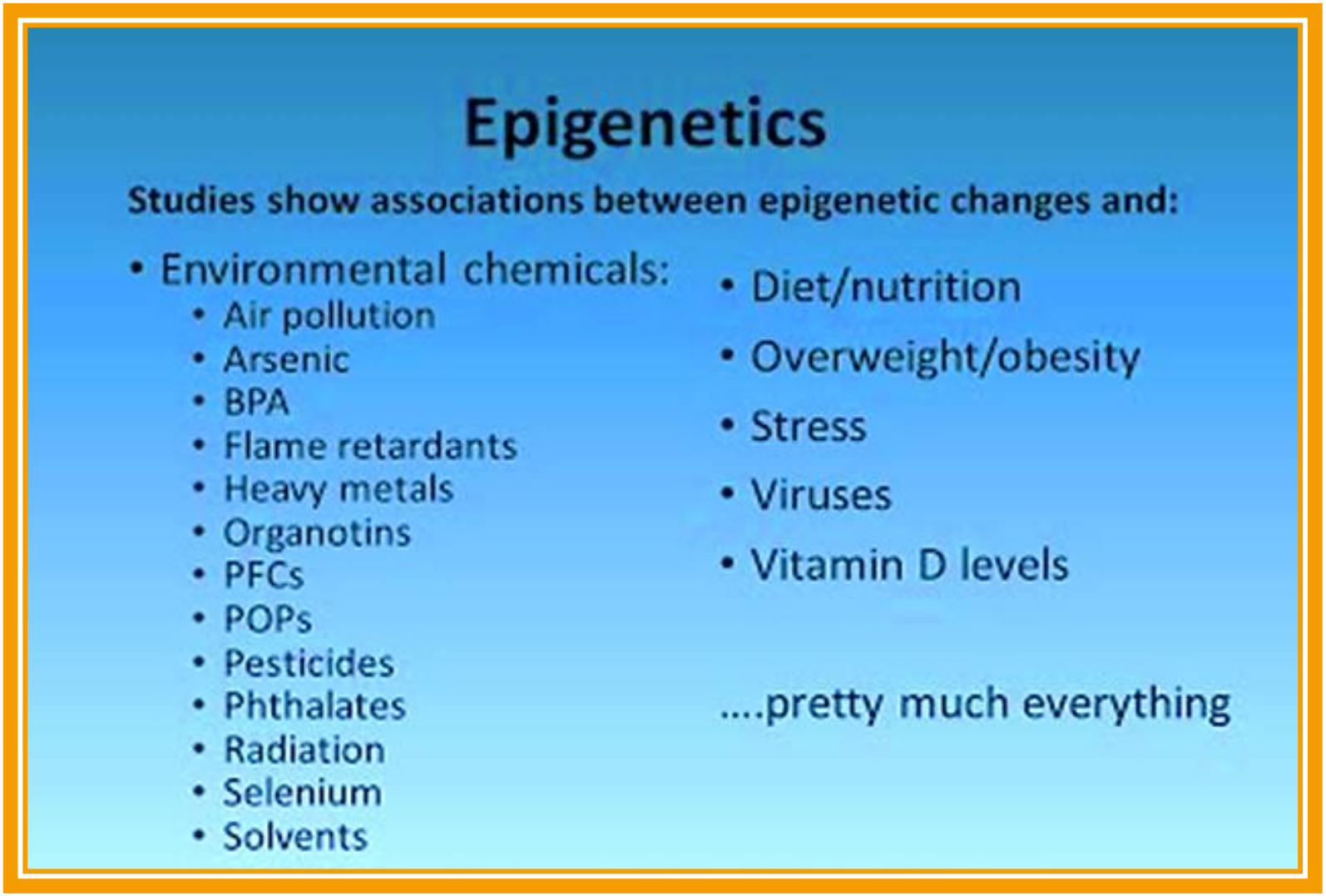
EPIGENETICS:



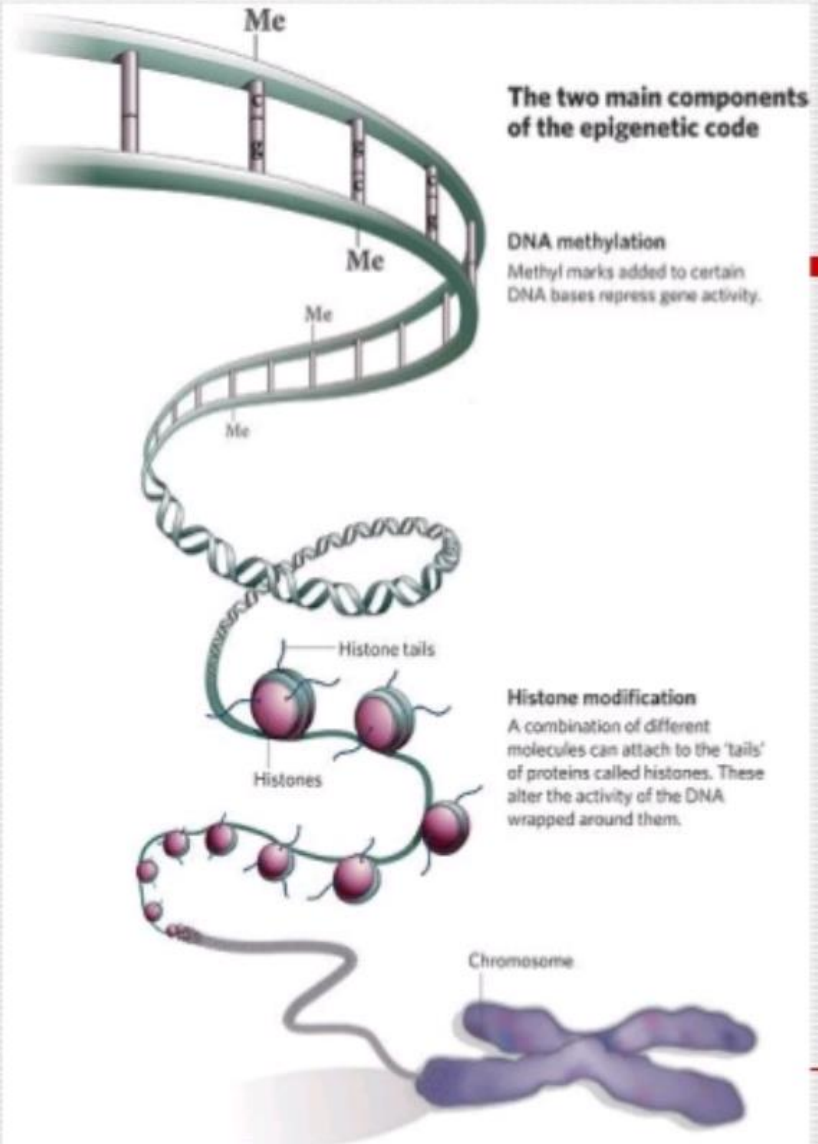
NATURE VS. NURTURE?

EPIGENETICS…

Genome is identical, Yet looks different –Epigenetics



RELATION OF EPIGENETIC CHANGES WITH DIFFERENT FACTORS



Epigenomics

Epi (Greek for above) -***genetics*** refers to changes in the phenotype or gene expression caused by mechanisms other than changes in the underlying DNA sequence.

- DNA methylation
- Histone modifications

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Epigenomics and stress relation

High handling, low stress mom

Low handling, high stress mom

Switch offspring

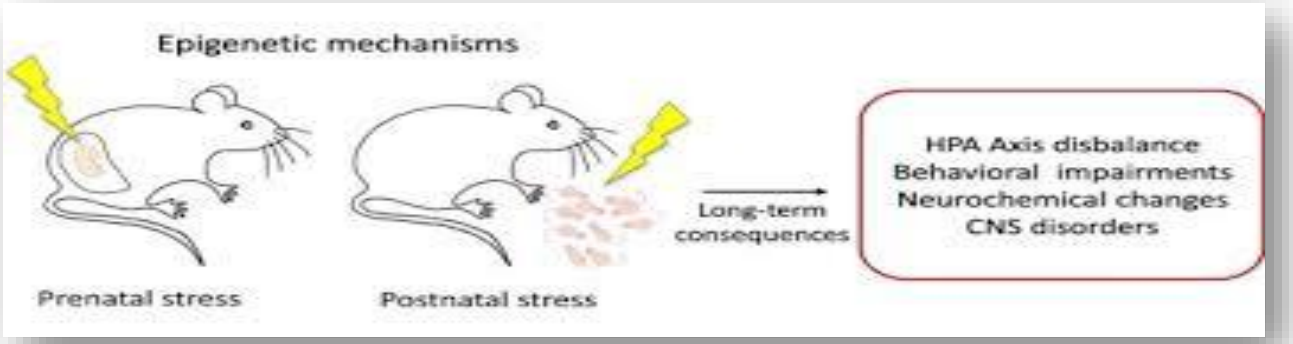
~~If stress is genetic, offspring will have same stress level as biological parent~~

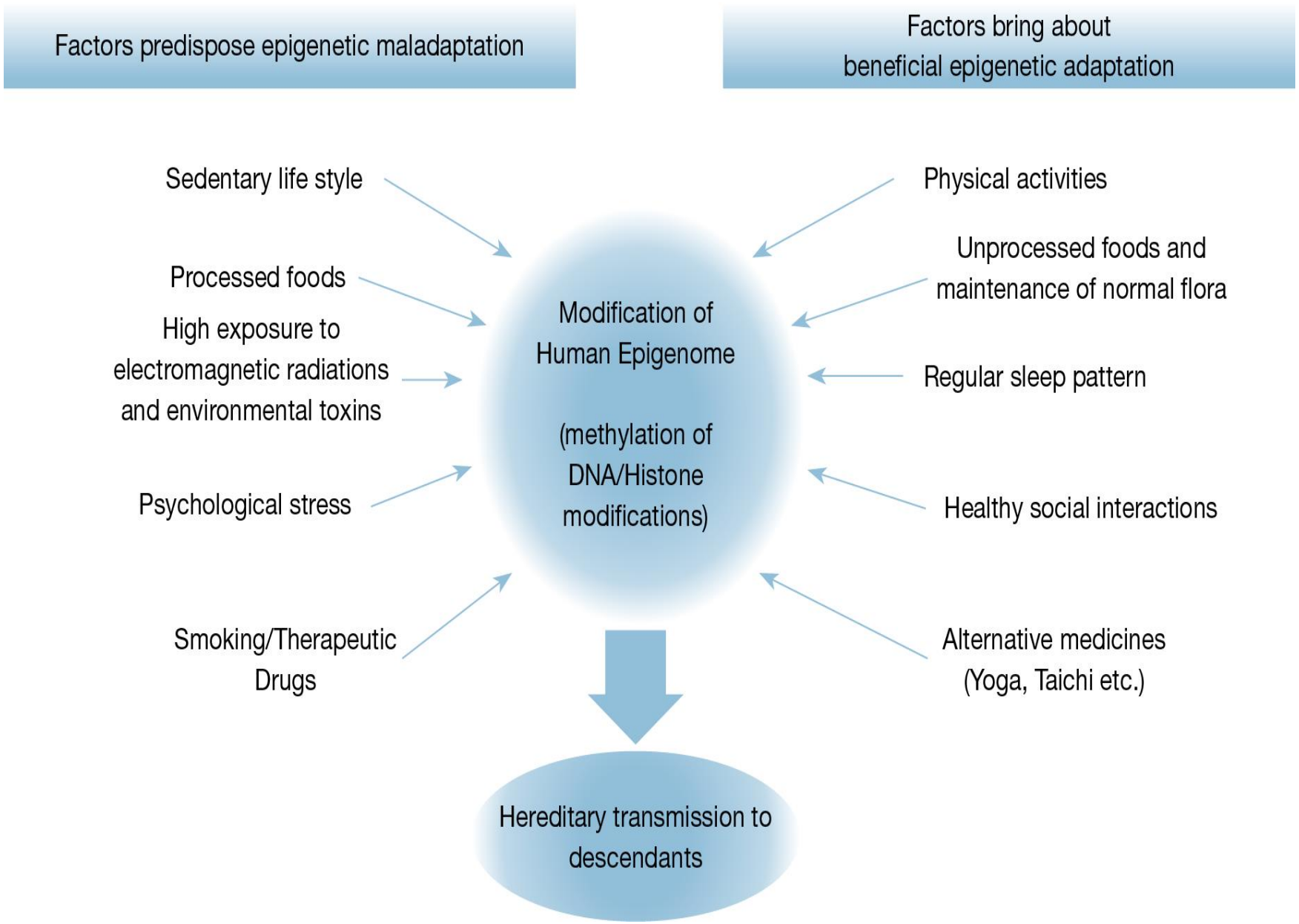
If stress is environmental, offspring will have same stress level as foster parent

Stress Gene Experiment

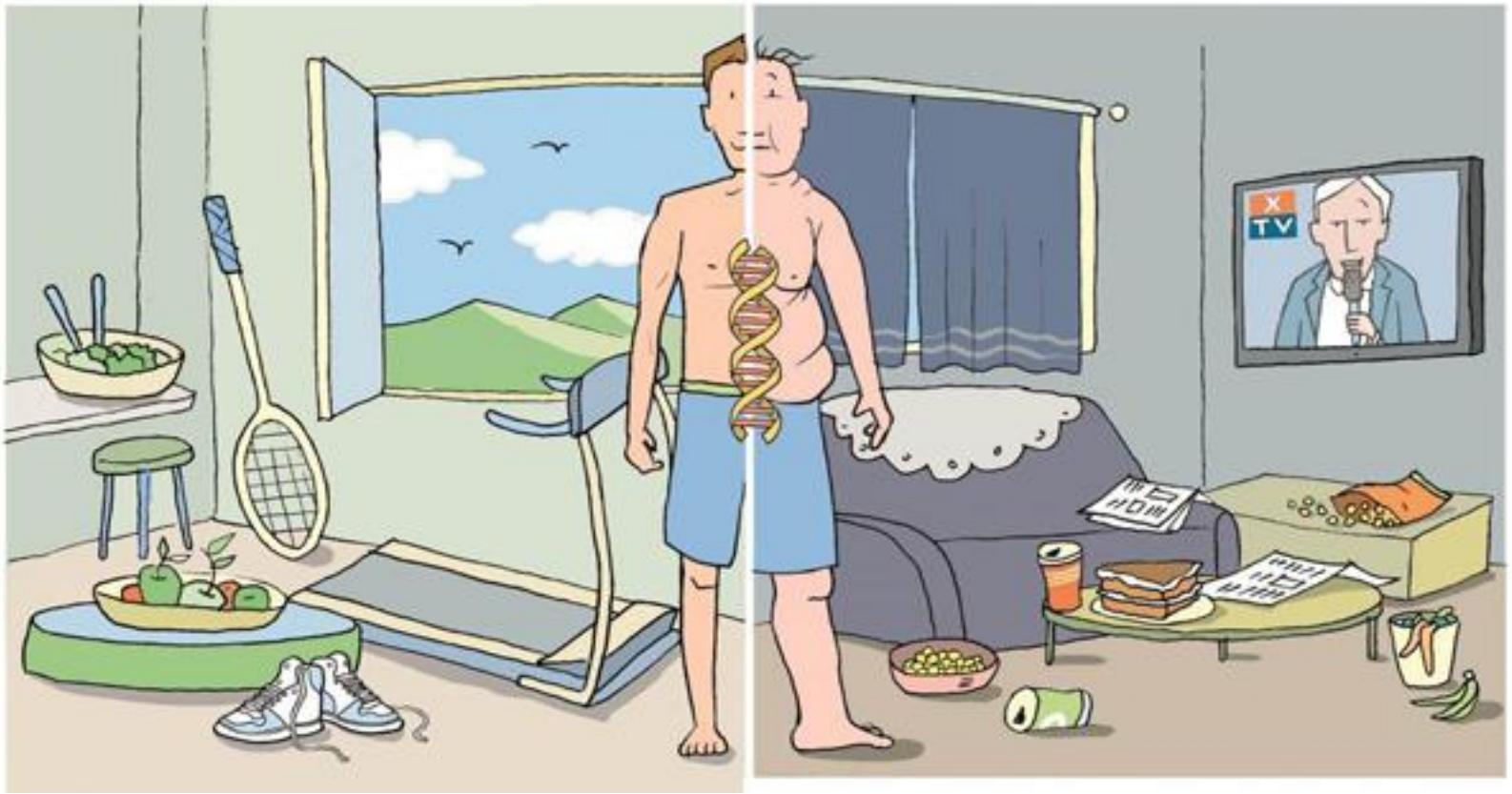
Group 1:
The babies' DNA is tested and epigenetic tags are visible on the stress response gene, turing it "on." These rats respond very well in stressful situations for the rest of their lives.

Group 2:
The babies' DNA is tested and epigenetic tags are NOT present on the stress response gene, keeping it "off." These rats do NOT respond well in stressful situations for the rest of their lives.

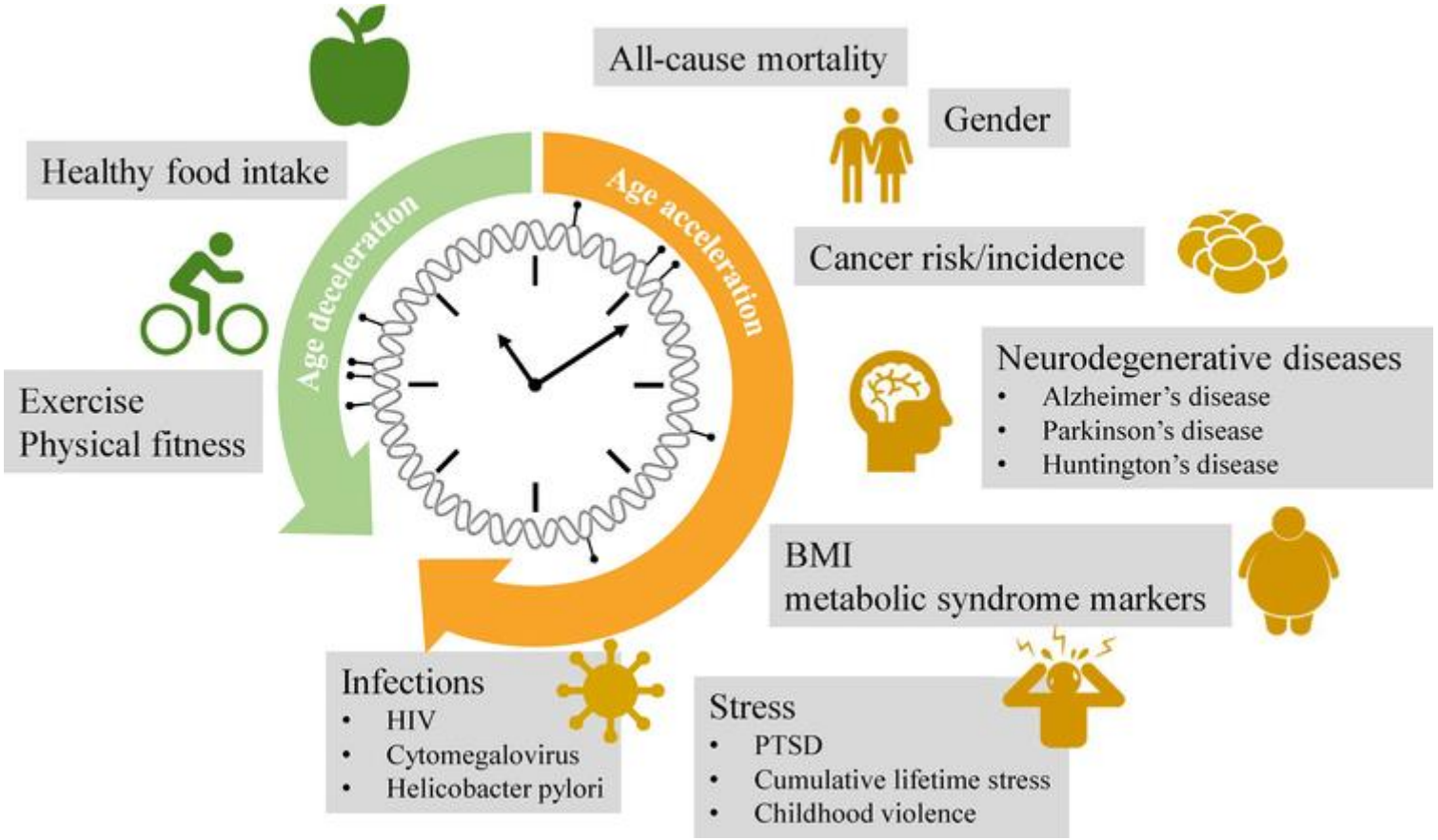



Factors predispose epigenetic maladaptation
Factors bring about beneficial epigenetic adaptation
Sedentary life style
Processed foods
High exposure to electromagnetic radiations and environmental toxins
Psychological stress
Smoking/Therapeutic Drugs
Physical activities
Unprocessed foods and maintenance of normal flora
Regular sleep pattern
Healthy social interactions
Alternative medicines (Yoga, Taichi etc.)
Modification of Human Epigenome
(methylation of DNA/Histone modifications)
Hereditary transmission to descendants

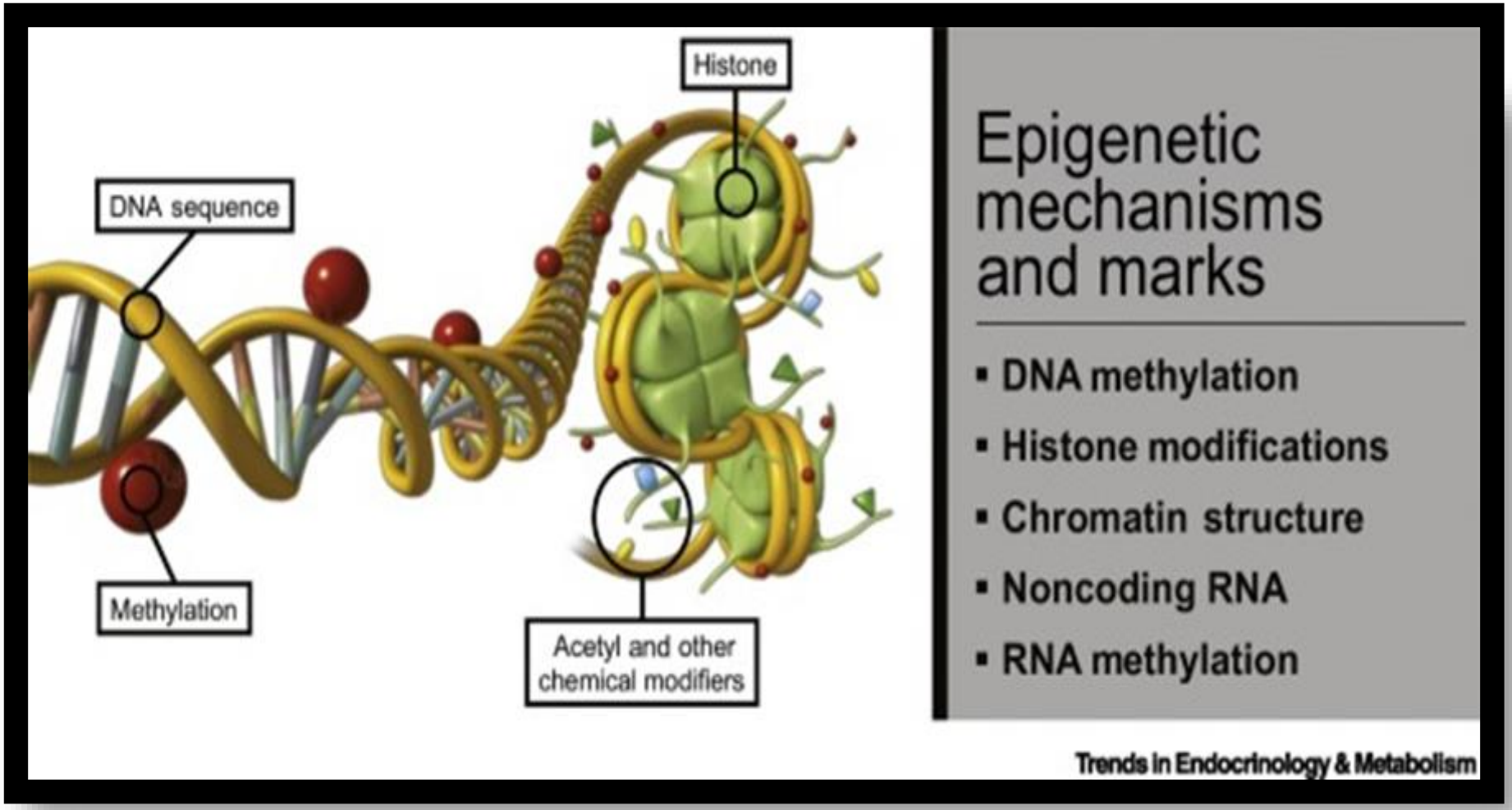
MODIFICATION OF HUMAN EPIGENOME



HUMAN EPIGENOME...

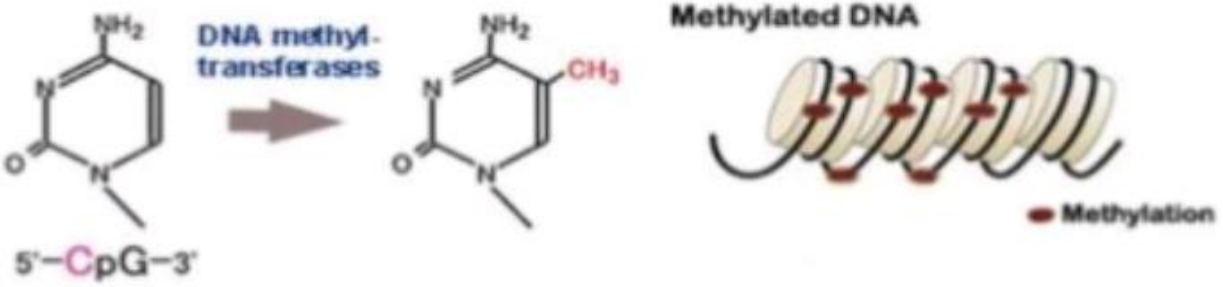


Epigenetics mechanism



DNA METHYLATION

- The methylation reaction is catalyzed by the enzyme *DNA methyltransferases* (DNMTs).
- The most frequent positions for methylation in eukaryotic DNA are C residues that are present next to G (CpG) islands Murrell *et al*, 2005.



METHYLATION

Stimulates binding of some proteins on chromosome

Binding of Histone Deacetylases(HDACs)

Genes become non-accessible to RNA polymerase

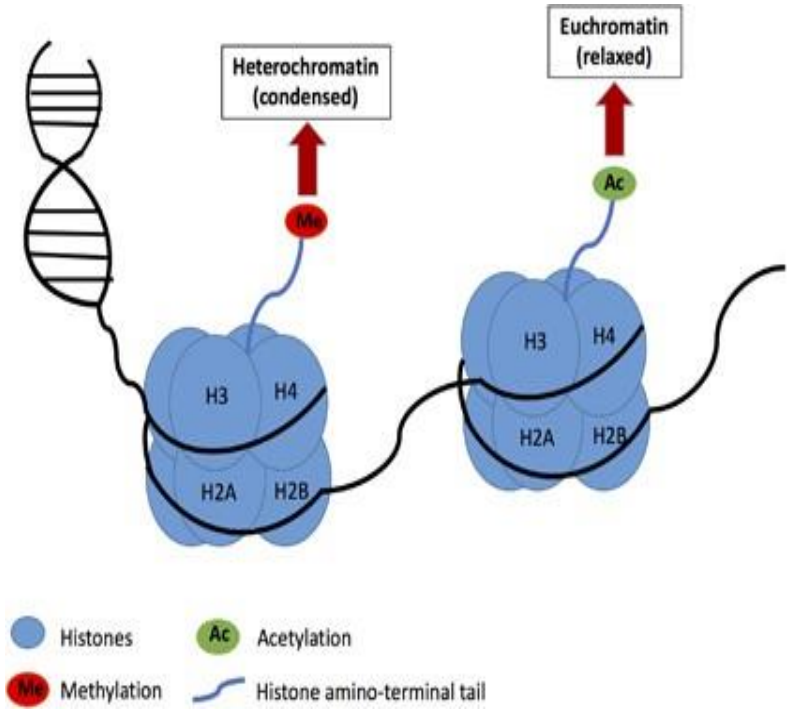
HISTONE MODIFICATIONS

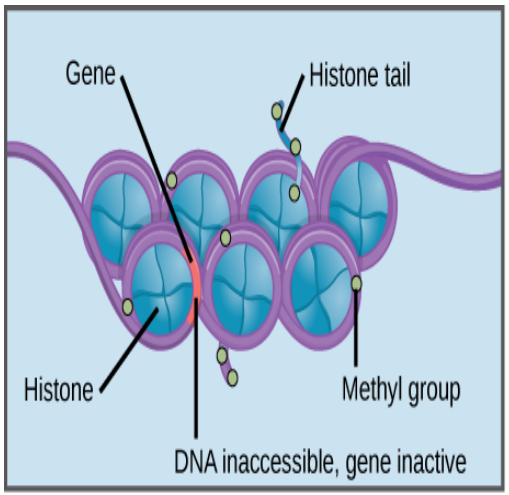
The unwrapping of DNA from histones is necessary for expression of genes. Hence, change in the structure of chromatin leads to variation in the gene expression. This is called as chromatin-remodelling.

TYPES OF HISTONE MODIFICATION

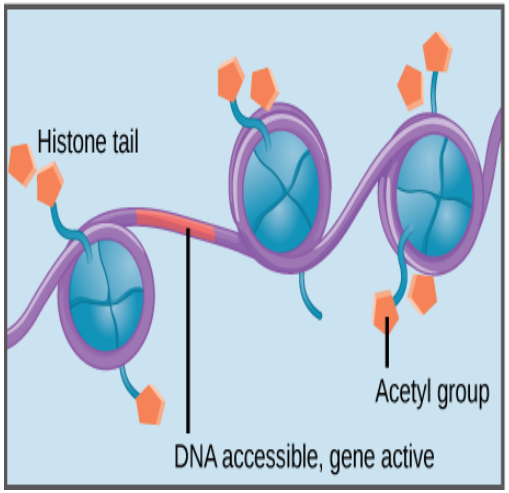
- Methylation
- Acetylation and Deacetylation
- Phosphorylation
- Ubiquitylation

METHYLATION OF DNA & ACETYLATION OF HISTONE





Methylation of DNA and histones causes nucleosomes to pack tightly together. Transcription factors cannot bind the DNA, and genes are not expressed.



Histone acetylation results in loose packing of nucleo-somes. Transcription factors can bind the DNA and genes are expressed.

HISTONE PHOSPHORYLATION

- Occurs at S, T & Y residues.

- Unlike acetylation and methylation, histone phosphorylation seems to function by establishing interactions between other histone modifications and serving as a platform for effector proteins.

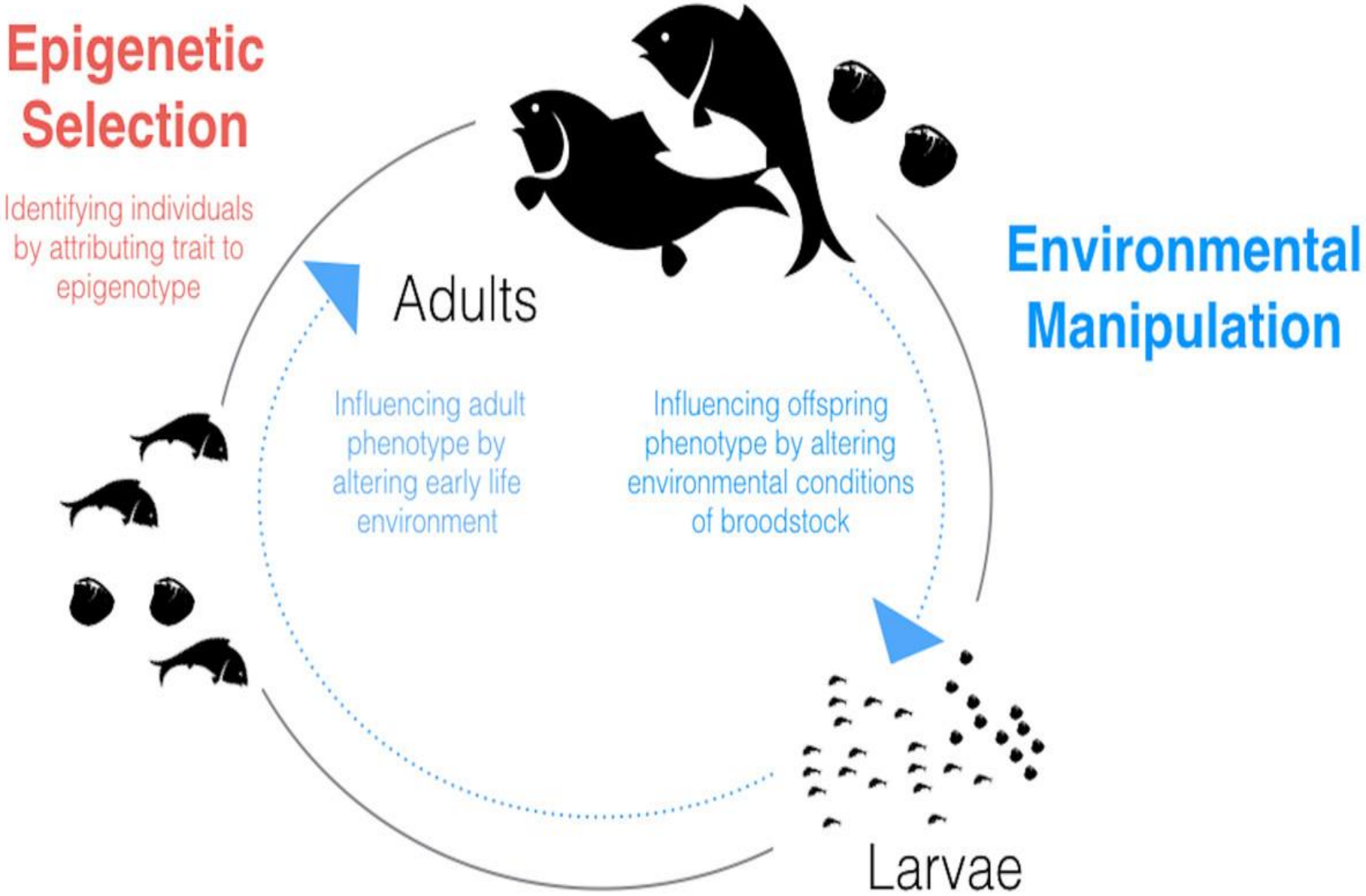
HISTONE UBIQUITYLATION

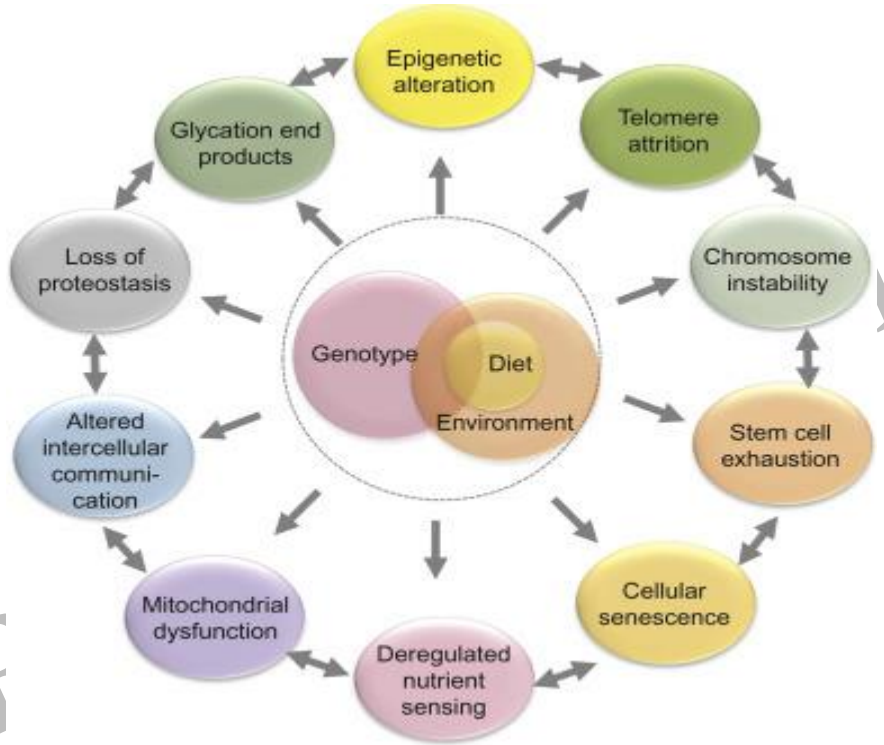
- Histone H2A and H2B are two of the most highly ubiquitylated proteins found in the nucleus.
- The most abundant forms are monoubiquitylated H2A on K119 and monoubiquitylated H2B on K123
- Ubiquitylated H2B is associated with transcription activation.
- Ubiquitylation of H2A and H2B is reversible, and is tightly regulated by histone ubiquitin ligases and deubiquitylating enzymes.

NON-CODING RNAs

- About 90% of the eukaryotic genome is transcribed. Interestingly, only 1 – 2% of these transcripts encode for proteins; the majority are transcribed as non-coding RNAs (ncRNAs).

1. MicroRNA (miRNA)
2. Piwi-interacting RNA (piRNA)
3. Small-interacting RNA (siRNA)
4. Long non-coding RNA (lncRNA)

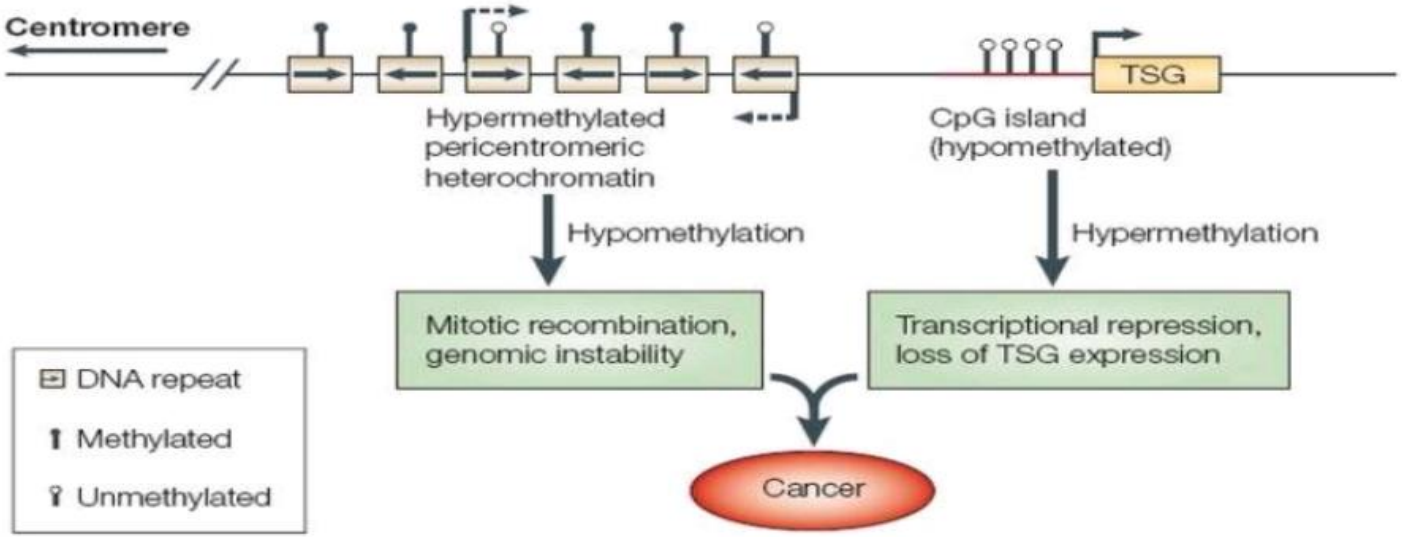

Epigenetic Selection
Identifying individuals by attributing trait to epigenotype
Adults
Environmental Manipulation
Influencing adult phenotype by altering early life environment
Influencing offspring phenotype by altering environmental conditions of broodstock
Larvae



RELATION OF EPIGENOMIC CHANGES WITH DIFFERENT FACTORS

DEVELOPMENT OF EPIGENOMICS IN CROP RESEARCH

- Initially, the epigenomics based researches were mostly contributed towards the understanding the phenomena of various human diseases, mainly cancer Murell *et al*, 2005: Thakur *et al*, 2013.



Plant Biotechnology Journal

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Small RNA and degradome deep sequencing reveals drought-and tissue-specific micrornas and their important roles in drought-sensitive and drought-tolerant tomato genotypes

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Objective:

To know the role of **"Epigenetic regulation"** for drought tolerance in Tomato by miRNA analysis in drought tolerant and drought sensitive tomato root and up ground tissues.

Advantages of Epigenomics

- Inheritable over many generations.
- New source of polymorphism.
- Basis for selection and plant breeding.
- Produce new source of variation and response to stressfull environment.
- It could emerge at high frequency in a single generation.
- DNA methylation is generator of epiallel and permanent mutant allele.

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THANKYOU