EPIGENOMICS: DECIPHERING THE OTHER GENETIC CODE

GENOMICS 2019/2020
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**EPIGENETIC VS EPIGENOMIC**

**EPIGENETICS**

The study of all changes in gene expression and chromatin organization that are independent of the DNA sequence.

**EPIGENOMICS**

The science that study the epigenome: a set of compounds including proteins that can join to the genome and control gene expression.
Epigenetics is focused on processes that mediate gene expression, epigenomics on the analysis of the epigenetic changes in the whole genome.
GENETIC CODE VS EPGENETIC CODE

Same genome in every cells of the same organism.

Static code.

Variable epigenome across different cell types and in the same cells at different developmental stages.

Dynamic code.
COMPONENTS OF THE EPIGENETIC CODE

COMPONENTS OF THE EPIGENETIC CODE

DNA METHYLATION

Maintaining the conformation and integrity of chromosomes

Repression of gene transcription

Methylation in repeat regions (centromeres): chromosome stability

COMPONENTS OF THE EPIGENETIC CODE

DNA METHYLATION

DNMT3 and DNMT3b

COMPONENTS OF THE EPIGENETIC CODE

HISTONE MODIFICATION

HATs

HMTs

COMPONENTS OF THE EPIGENETIC CODE

HISTONE MODIFICATION

HATs
HMTs


REVERSIBLE CHANGES

ADP
rybosylation

Ubiquitination

Acetyl Group

Methyl Group

DNA

Phosphate Group

Histone Tail

Histone Octamer

Glycosilation

Citrullination
COMPONENTS OF THE EPIGENETIC CODE

NUCLEOSOME POSITIONING

## Components of the Epigenetic Code

**Non Coding RNA**

### Table I.

Main non-coding RNAs in regulation of epigenetics.

<table>
<thead>
<tr>
<th>Name</th>
<th>Size</th>
<th>Source</th>
<th>Main functions</th>
</tr>
</thead>
<tbody>
<tr>
<td>siRNA</td>
<td>19–24 bp</td>
<td>Double stranded RNA</td>
<td>Silent transcription gene</td>
</tr>
<tr>
<td>miRNA</td>
<td>19–24 bp</td>
<td>pri-miRNA</td>
<td>Silent transcription gene</td>
</tr>
<tr>
<td>piRNA</td>
<td>26–31 bp</td>
<td>Long single chain precursor</td>
<td>Transposon repression DNA methylation</td>
</tr>
<tr>
<td>IncRNA</td>
<td>&gt;200 bp</td>
<td>Multiple ways</td>
<td>Genomic imprinting X-chromosome inactivation</td>
</tr>
</tbody>
</table>

TO DECIPHER THE EPIGENETIC CODE

HUMAN EPIGENOME PROJECT

Aims to identify and catalogue MVPs in the human genome and their corresponding effect on gene activity.

As SNPs they promise to significantly advance our ability to understand and diagnose human disease.

It will link genetics, disease and the environment for knowing the aetiology of human pathologies.
TO DECIPHER THE EPIGENETIC CODE

ENCODE PROJECT

Aims to develop technologies for generating extensive, high-resolution maps of functional and structural features of the human genome.
TO DECIPHER THE EPIGENETIC CODE

ENCODE PROJECT

Project

Biosample Type

15388

15388

ENCODE
Roadmap
modERN
modENCODE
GGR
community
cell line
tissue
whole organisms
primary cell
in vitro differentiated cells
cell-free sample
single cell
TO DECIPHER THE EPIGENETIC CODE

Aims to characterize epigenomic landscapes in primary human tissues and cells with a public resource of human epigenomic data.

Collection of normal epigenomes as a reference for comparison of future studies.
TO DECIPHER THE EPIGENETIC CODE

Genomics of Gene Regulation

The Genomics of Gene Regulation (GGR) project develops better methods to construct predictive, accurate gene regulatory network models using genomic data.
The goal is to build a comprehensive public resource to study tissue-specific gene expression and regulation.

- Samples from 54 non-diseased tissue sites across 1000 individuals
- Molecular assays such as RNA-seq.

GTex Portal
CONCLUSIONS

- The total knowledge of the epigenetic code will improve the detection, prevention and treatment of human diseases.

- The epigenetic code is currently unknown but there are a lot of projects in process to decipher it.
THANKS FOR YOUR ATTENTION