

Fighting the Enemy Within

Basic Life Science and Issues : Presentation

Group 4

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Fighting the Enemy Within

11th chapter of *The Epigenetics Revolution*

"Epigenetic perspective of Cancer and its treatment"



Healthy cells, have two types of genes:

- proto-oncogenes for cell proliferation
- tumor suppressor genes for regulation



Introduction: Cancer

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However, cancer cells lost balance of these, For example,

- proto-oncogenes is over-activated
- tumor suppressor genes is inactivated



Introduction: Cancer

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Epigenetic Approach for Oncogenesis

- DNA Methylation

Hypermethylation of CpG island

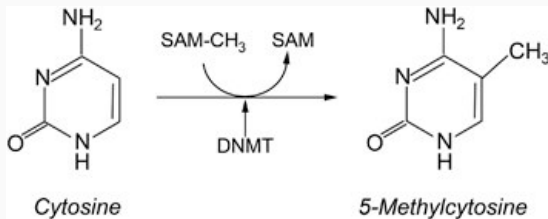
- Repressive Histone Modification

Histone deacetylation



DNA Methylation

Cytosine before Guanine can be methylated

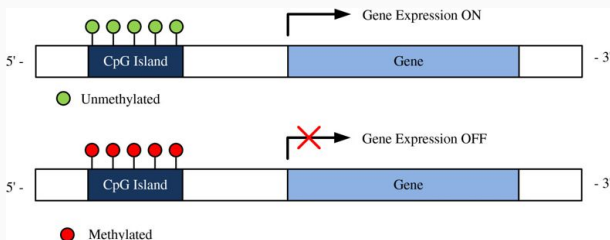


Methyl group is bond on 5' carbon atom



DNA Methylation

CpG dinucleotide cluster (CpG island, CGI) are usually located in the promoter regions of genes in a DNA sequence.



Hypermethylated CGI disables specific gene expression.



Histone deacetylation



Characteristics of Oncogenesis

- Multi-step process
- Defections must be accumulated

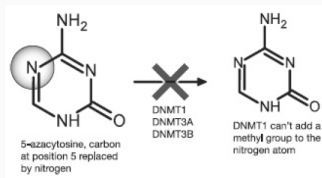
Inherited oncogenes are slowly expressed
e.g.) BRCA1 mutation

- Tumour suppressor gene - Switched off
- Alteration with epigenetic access



Approach for Treatment

- DNMT enzyme inhibitors
5-azacytidine, 2-aza-5'-deoxycytidine



methylation inhibited by 5-azacytidine



Approach for Treatment

- HDAC inhibitor
SAHA, Romidepsin



No easy wins

- Oncogenesis has numerous mechanisms

Case by case, person by person

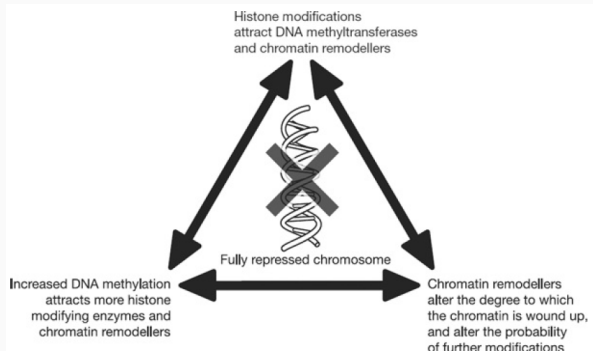
- The solutions are preferable for haematological cancer
- Also these solutions should be used in different fields

DMNT inhibitors for bone marrow, HDAC inhibitors for T-cell lymphoma



Alternative Approach

There are many enzymes that involved in histone alteration

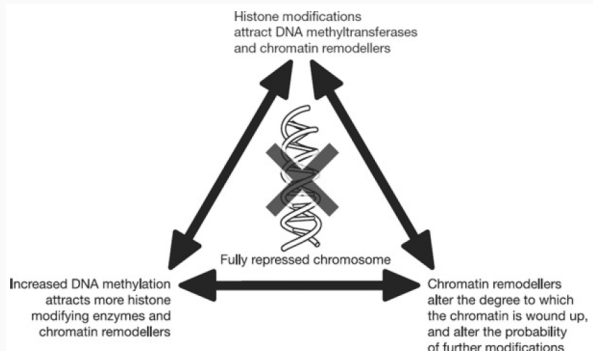


And these interact each other, forms vicious cycle.



Alternative Approach

There are many enzymes that involved in histone alteration



And these interact each other, forms vicious cycle.



Conclusion



References

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- [2] Kakumani, R.; et al. (2012). *Identification of CpG islands in DNA sequences using statistically optimal null filters*, EURASIP Journal on Bioinformatics and Systems Biology
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Q & A

Thank you!