Sentence Outline

IB Subject: Biology
Topic: Epigenetic mechanisms and gene expression

Geoffery Lewis

Research Question:

I. What are epigenetics and its influence on gene expression?
   A. Epigenetics is the study of changes in organisms caused by modification of gene expression rather than alteration of the genetic code itself.
      1. Environmental factors can play a vital role in epigenetics.
   B. Chromatin is the complex of chromosomal DNA associated with proteins in the nucleus and is where gene expression is regulated.
      1. DNA in chromatin is packaged around histones creating nucleosomes that inhibit transcription and it's factors.
      2. Nucleosome spacing determines chromatin structure which can be broadly divided into heterochromatin and euchromatin.
      3. Chromatin structure and gene accessibility to transcriptional machinery are regulated by modifications to both DNA and histone tails.
   C. There are multiple mechanisms of epigenetics that affect gene expression in multiple ways.
      1. DNA-methylation is one mechanism of epigenetics that is prevalent.
      2. Histone modifications, such as methylation and acetylation are prevalent to gene expression.

II. What is the mechanism of DNA-methylation in epigenetics?
   A. DNA methylation is a process by which methyl groups are added to DNA.
      1. Methylation modifies the function of the DNA. When located in a gene promoter, DNA methylation typically acts to repress gene transcription.
      2. Methylation in differentiated mammalian cells, the principal epigenetic tag found in DNA is that of covalent attachment of a methyl group to the C5 position of cytosine residues in CpG dinucleotide sequences (referred to as CpG).
   B. DNA methylation is a long-term and more stable epigenetic modification.

III. What is the mechanism of Histone modifications in epigenetics?

A. Histone modification is when N-terminal histone tails protrude from nucleosomes and contain amino acids that are subject to a vast array of chemical modifications.
B. Methylation is a type of histone modification that can both suppress or express a gene.
C. Acetylation is another type of histone modification that promotes gene expression.
    1. Acetylation can allow transcriptional repressors to be found.
    2. Deacetylation is the opposite and correlates to CpG methylation binding sites.
D. Histone modification is a short-term epigenetic modification.

IV. How do these mechanisms compare to each other?
A. Cell differentiation is affected by both of these epigenetic mechanisms and actually influences lineage to, meaning it's heritable.
B. Both impact gene expression and thus phenotypes, however where one mechanism is a much longer-termed one, the other is shorter.
    1. Diseases and other health issues are influenced by gene expression.
C. It's found that both mechanisms might link to each other or rely upon each other in some way, however the process behind that is complex.

V. Conclusion
A. Future directions include methods of sex determination and dosage compensation in mammals.
B. The mechanism of histone modifications is better expressing genes and shorter time period.
C. The mechanism of DNA methylation is better for repression of expression and longer term.

Bibliography

Cedar, H., & Bergman, Y. (2009, May). Linking DNA methylation and histone modification: patterns and paradigms. Retrieved September 19, 2019, from Nature.com website: https://www.nature.com/articles/nrg2540

This article talks about how both DNA methylation and histone modification are involved in establishing patterns of gene repression during development. Certain forms of histone methylation cause local formation of heterochromatin, which is readily reversible, whereas DNA methylation leads to stable long-term repression. It has recently become apparent that DNA methylation and histone modification pathways can be dependent on one another, and that this crosstalk can be mediated by biochemical interactions between SET domain histone methyltransferases and DNA methyltransferases. Relationships between DNA methylation and histone modification have implications for understanding normal development as well as somatic cell reprogramming and tumorigenesis.

Constanze, B., & Cockerill, P. N. (n.d.). Chromatin Mechanisms Regulating Gene Expression In Health And Disease. Retrieved September 18, 2019, from NCBI website: https://www.ncbi.nlm.nih.gov/books/NBK45032/

This article discusses the chromatin mechanisms that effect the gene expression of heart diseases and other health issues. The article begins with the role of transcription factors and thus the chromatin structure on gene expression patterns. The basic features of chromatin structure are defined and then and the role of epigenetics in cell differentiation is explained. DNA-methylation, is a huge process involved in epigenetics and often the key to understanding the effect of epigenetics on gene expression related to environmental factors. The article then goes into the topic of discussing the chronic diseases and health aspects, and how expression plays a vital role in this.

Eichten, S. R., Schmitz, R. J., & Springer, N. M. (n.d.). Epigenetics: Beyond Chromatin Modifications and Complex Genetic Regulation. Retrieved from JSTOR database.

This article discusses the chromatin structure in depth, specifically the histones that make up the chromatin. The article questions whether or not the histone modifications done are able to be passed on generation to generation. They distinguish between epigenetic variations and genetic variations, and how the line between those begin to blur when discussing the epialleles and the factors that play into each of those things. The article then takes a look at epigenetics in plant development and how

that can relate and compare to humans.

Furey, T. S., & Sethupathy, P. (n.d.). Genetics Driving Epigenetics. Retrieved from JSTOR database.

This article discusses recent discoveries about how gene expression works. It talks about how the proteins that don't code for anything in DNA actually do more then that, including controlling which genes are expressed. They do this in chromatin where nucleosomes (which compose of DNA and Histones) contain transcription factors. Dependent upon histone tails and transcription factors binding to chromatin DNA the gene will be expressed or not.

Kondo, Y. (2009, August 19). Epigenetic Cross-Talk between DNA Methylation and Histone Modifications in Human Cancers. Retrieved September 19, 2019, from NCBI website: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2730606/

This article reviews examples of studies that demonstrated the relationship between histone modifications and DNA methylation in human cancers presented and the potential implications of these epigenetic mechanisms in human neoplasia are discussed.

Landecker, H., & Panofsky, A. (2013, May 15). From Social Structure to Gene Regulation, and Back: A Critical Introduction to Environmental Epigenetics for Sociology. Retrieved from JSTOR database.

This article takes a look not only at epigenetics but also in particular the environmental aspect of the epigenetic influencers. Environmental epigenetic research tracks mechanisms by which social forces-from pollution to nutrition to mothering to traumatic experience-become molecularly embodied, affect gene expression, and induce durable changes in health and behavior. Sociologists find this very interesting and believe it is the key to solving a lot of our social interaction problems today. The article looks at how epigenetics offers opportunities and challenges for sociological research on both empirical and theoretical grounds.

Loscalzo, J., Handy, D. E., & Castro, R. (2011, May 17). Epigenetic Modifications: Basic Mechanisms and Role in Cardiovascular Disease. Retrieved September 19, 2019, from NCBI website: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3107542/

This article compared the two major mechanisms of epigenetics, DNA methylation (long term version) and Histone modification (short term version) in their processes and effect on gene expression. Where in DNA methylation the presence of methylation at CpG sites was repressive

toward gene expression, Histone methylation as well as acetylation was permissive toward gene expression. The processes that go into why and how that is are thoroughly explained in this article. These mechanisms are then used to analyze how both types of mechanisms go into effecting the epigenetic expression of cardiac disease.

Meymandi, A. (2010, March). The Science of Epigenetics. Retrieved September 19, 2019, from NCBI website: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2861525/

This article discusses living and exemplar proof of epigenetics in real time based off of environmental factors. In Northern Sweden, famine of crops erupted for 7 whole years. Overtime, it was found that those people who didn't eat much due to the famine and reproduced, produced children that were scrawnier and more prone to mental illness, versus if parents ate more and were healthier, they're children grew up healthier. Epigenetics acts like a switch and is apparent all throughout. What's interesting is that this proves that evolution doesn't necessarily need to take place over a time frame of millions of years and in fact can happen within generations.

Turner, B. M. (2007). *Chromatin and Gene Regulation: Molecular Mechanisms in Epigenetics*. Chichester: John Wiley & Sons.

This book goes into great depth on the subject of chromatin and gene regulation. It begins with an introduction of how the author tried to format his book and detailed the importance of genetics in our evolutionary tale as a species. It dives in, beginning with controlling transcription, defining the process and it's effect in eukaryotes versus prokaryotes. The chromatin, and it's structure is then described and how it's packaged up in chromosomes. Histones are a vital part of the "packaging process", and so the book continues to describe the mechanisms behind histone proteins and their overall role in gene expression. The book discusses more about transcription in chromatin and it's role in environment. The final part of the book discusses the future of epigenetics and the possibilities of how the controlling of gene expression could affect the world.

Wolffe, A. P., & Matzke, M. A. (n.d.). Epigenetics: Regulation Through Repression. Retrieved from JSTOR database.

This article goes in depth upon the epigenetic effects more so then the processes and mechanisms of it. The article begins by talking about epigenetic control and how DNA-based mechanisms are important to that. Repetition of DNA can trigger the formation and the transmission of

inactive genetic states and DNA modifications. Methylation as a genome defense is discussed in that methylated groups bind to the histone N-terminal tails which act as a suppressor to gene expression. The article then takes a look at epigenetic heritability and how it effects lineage and cell differentiation. Epigenetics also play a vital role in diseases and how the suppression or rather the permissiveness of a gene can cause a major disease in human health.