Epigenetics Matin Amani – Biomedical Engineering – University of Rhode Island

When the human genome project was completed many scientists thought that genetic disease would become a thing of the past; however, the geneticists did not find answers only more problems. The issue is that there are only thirty thousand genes in humans. Original expectations were around one hundred thousand and were as high as two million. This was a massive shock and signified that something was missing.

The solution to this problem was found in twins. The expectation with identical twins is that they are and always will be exactly the same since they are genetically identical, but cases have been seen where one twin develops a disease such as cancer or autism and another does not. Much study has resulted in the conclusion that the genetic code can be read in different ways, meaning that parts of the code can be blocked and others can be promoted.

Epigenetics is the study of modifications that occur in DNA that cause certain genes to be suppressed. The mechanism for this is the bonding of many methyl groups to the chromatin, preventing RNA polymerase to read the code and create a transcription. By blocking certain segments of DNA cells can differentiate. and create different tissues. Furthermore, unlike the genome which is stable the epigenome changes constantly. The implications of this are huge, by understanding how the epigenome behaves therapies can be developed for once incurable illnesses furthermore the epigenome leaves a huge burden on humans, since it is hereditary and is easily changed by outside influences.

The epigenome plays a critical role

in gene suppression, a recent MIT study found that 80 % of rats genetically engineered to have a deficient methylating enzyme died due to cancer. Further study showed that humans as well as many other animals contain genes that cause tumors as well as one that prevent them, and as the epigenome deteriorates over time risk of expressing such genes or suppressing necessary genes increases.

Reasons for the deterioration of the epigenome are still unknown; however, several conclusions have been made. The first is that environment, diet, and personal habits affect the epigenome (which is inherited). The implication of this is that the expression of your genes is changing and effected by not only what you do but also what your parents did. For example, a recent analysis of the very detailed records of northern European town shows very distinct relationships between famine and the life expectancy's of children born years after the famine. Recently several projects have been started to map methyl bonding sites in the epigenome, which will hopefully take us one step closer to finding a cure to genetic disease.

References:

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