Epigenetic Analysis for Diabetes Risk and Resiliency

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Diabetes mellitus is one of the various types of major metabolic diseases that affect over 800 million people worldwide, according to the World Health Organization. The number of people living with the disease is significantly increasing, particularly in low and middle-income countries, leading to significant public health concerns due to its complications and associated healthcare costs. While there are many risk factors like overweight and obesity, known to contribute to the non-genetic type 2 form of diabetes mellitus (T2D), there are some people with these risks who do not develop T2D. I plan to study non-genetic factors (epigenetic changes) that may contribute to this resiliency. QUESTION: Are people with diabetes risk prevented from it due to their epigenetics and DNA methylation in specific genes? HYPOTHESIS: DNA methylation in relevant genes for T2D may prevent certain at-risk shows from developing T2D. EXPECTED OUTCOME: There are changes in DNA methylation in T2D risk genes in people who are overweight/obese, which are risk factors for T2D. MATERIALS: Data sets from Kaggle, CDC NHANES, and other publicly available datasets. Anaconda, Jupyter Notebook, Python, GraphPad Prism, SAS, Excel, ROC classifiers. PROCEDURE: 1. Kaggle data is used to determine the correlations in healthy controls vs patients with T2D. 2. CDC NHANES datasets (demographics, fasting blood glucose and body mass index or BMI) of 4000 subjects were used to determine if family income or BMI correlated with fasting blood glucose. 3. Publicly available datasets in healthy control vs. T2D are used to determine the changes in the DNA methylation of commonly known T2D-associated genes in data with higher BMI but lower blood glucose/A1c, and the opposite is analyzed.

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