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IN-SILICO ANALYSIS OF SIRT1 GENETIC POLYMORPHISMS AND THEIR POTENTIAL ROLE IN INFLAMMATORY RESPONSE

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In-Silico Analysis of SIRT1 Genetic Polymorphisms and Their Potential Role in Inflammatory Response

Synopsis:

This research project aims to investigate how genetic polymorphisms within African Americans predispose them to inflammatory diseases such as cancer when coupled with a violent/traumatic environment.

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Introduction: Inflammation is crucial in the body's immune response and has been shown to increase susceptibility to disease. The protein encoded by *SIRT1*, located on chromosome 10, modulates proteins that function as inflammation regulators such as NFkB transcription factor. *In silico* analysis helps to identify SNPs in candidate genes implicated in health and disease. The goal of this research is to implement bioinformatics tools to identify SNPs in the *SIRT1* gene and determine the most significant differences in allele distribution between African-American (AA) and European American (EA) populations as ideal targets for further experimentation.

Methods: For this study, four databases for *in silico* analysis were used to identify differences between allele frequencies in both populations. 1000 Genome Browser, was used to identify all SNPs in the *SIRT1* gene, while NCBI Gene Viewer, the University of California Santa Cruz Genome Browser, and DNAsp, identified the functionality and location of the SNPs. In an effort to filter through the vast search results, only SNPs within region (chr10:67874669..67928390) carrying missense, synonymous, or exonic mutations were observed. In addition to this, SNPs with allele frequency differences less than 30% were filtered out from the search results and only SNPs at above 60% were considered significant.

Results/Conclusion: *In silico* analysis within the UCSC Genome Browser database, yielded no significant allele frequency differences found within the exonic region of the chromosome. In using the 1000 Genome Browser, UCSC Gene Viewer, DNAsp program, seven SNPs, rs35620729, rs1467568, rs2273773, rs2394445, rs2394446, rs36107781, and rs35620729 were found to be significant based on their allele frequency differences and functionality. Although these SNPs were intronic rather than exonic, they should still be targeted for further study due to the regulatory role they play in determining gene expression.