CALIFORNIA STATE SCIENCE FAIR
2015 PROJECT SUMMARY

Name(s)

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Project Number

S0513

Project Title

A Computer-Based Integrated Analysis of Genomic Signatures in Ovarian Cancer

Abstract

Objectives/Goals

Ovarian cancer is one of the deadliest gynecological cancers due to a lack of early detection methods and high rates of resistance to chemotherapy. As a result, the overall purpose of this project was to examine processes that may mediate the development of cancer. The objectives consisted of three main components: 1) to discover and analyze signatures for various types of genomic and epigenomic data, 2) to identify biological pathways that are altered in ovarian cancer based on these signatures, and 3) to utilize these signatures and other multidimensional genomic data in integrative analyses to determine possible mechanisms of aberrant gene expression in ovarian cancer.

Methods/Materials

Using data from The Cancer Genome Atlas and R programming language, the predictive potential of genomic signatures for abnormal mRNA expression, miRNA expression, and DNA methylation were determined and cross-validated. Pathway enrichment analysis was then performed on these signatures using an algorithm based on a hypergeometric function distribution. Finally, the signatures were utilized in conjunction with data collected from cBioPortal, DAVID, and published studies, as well as a number of statistical tests and algorithms implemented in R, to propose mechanisms of aberrant gene expression in ovarian cancer.

Results

Six robust genomic signatures that differentiate between tumor and normal ovarian tissue samples were generated and used in integrated analyses of ovarian cancer. Furthermore, six smaller signatures were discovered that could be used as diagnostic tools for this disease, each yielding a predictive accuracy of 90% or greater. The results also produced multiple pathways altered in this disease, in particular cell cycle-related pathways and FOXM1 signaling, and determined many processes, notably aberrant expression of miRNAs and transcription factors, that may contribute to abnormal gene expression.

Conclusions/Discussion

Various features have been proposed that could serve as diagnostic biomarkers in ovarian cancer. Moreover, the data from the integrated analyses provide important information on pathways and gene expression regulatory mechanisms in ovarian cancer that can further our understanding of the carcinogenesis process. Although the results presented here still remain to be experimentally validated, these results nevertheless hold important implications in diagnostic and therapeutic applications.

Summary Statement

Using online data and bioinformatics tools, genomic signatures were identified and used in integrated analyses to determine predictive features, altered pathways, and biological mechanisms causing aberrant gene expression in ovarian cancer.

Help Received

My mother offered advice for my project and edited my writing and my sister helped with the layout of my board.