CALIFORNIA STATE SCIENCE FAIR
2014 PROJECT SUMMARY

Name(s)

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Project Number

S0524

Project Title

Targeted Cancer Therapy and Diagnosis: Analyzing miRNA Expression Signatures & Interactions for Glioblastoma Progression

Abstract

Objectives/Goals

Short noncoding RNAs, microRNAs (miRNAs) regulate gene expression by silencing mRNAs through degradation. Since miRNA dysregulation is linked with tumorigenesis, expression signatures of dysregulated miRNAs can be used as indicators to provide an early and accurate diagnosis of glioblastoma, the most malignant and aggressive type of brain cancer. The objective of my research is to create an innovative computational model to analyze glioblastoma data, and to apply my model to miRNA and mRNA expression data from glioblastoma patients to discover miRNA expression signatures and miRNA-mRNA network interactions.

Methods/Materials

MiRNA and mRNA expression values for 426 glioblastoma patients were obtained from the Cancer Genome Atlas. The data was screened for mRNAs with variable expression values to find the 4454 mRNAs most likely linked with glioblastoma development. Using R-programming, I created an original computational model, which utilized clustering and correlation among several other statistical techniques, to develop a novel method to analyze patient data and discover miRNA expression signatures and interactions for glioblastoma.

Results

164 miRNA-mRNA network interactions were identified. 10 of the discovered miRNA expression signatures were uniquely identified in my research and were previously unassociated with glioblastoma in literature. Mir221 and mir222 had the strongest correlation values and regulated the greatest number of mRNA networks, thereby best indicating glioblastoma. The discovered results were cross-validated from the literature to establish their accuracy. This computational model can be used to screen miRNA profiles of patients for the discovered expression signatures, to accurately diagnose glioblastoma in its early stages.

Conclusions/Discussion

Imaging techniques used in glioblastoma diagnosis today are flawed because they cannot image small tumors or multifocal lesions. Because glioblastoma cells secrete large numbers of exosomes containing miRNAs into the blood, a patient#s miRNA profile can be generated using a blood test. Using my model to screen this profile for the discovered miRNA signatures, I can diagnose glioblastoma in its early stages. Since glioblastoma does not metastasize outside of the brain, it can be cured if it is diagnosed early on using the methods proposed. My research will revolutionize glioblastoma diagnosis and allow this disease to be cured completely.

Summary Statement

I created an innovative computational model to discover miRNA expression signatures and interactions for glioblastoma, and screen the miRNA profiles of patients to accurately diagnose this disease in its early stages, when it curable.

Help Received

Dr. Olivier Gevaert of Stanford University helped me finalize my research idea and answered any questions I had during the research.