Progressing Targeted Cancer Therapy and Diagnosis: Analyzing the Role of MiRNA Target Interactions and Expression Signatures for Glioblastoma Progression

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Short non-coding RNAs, microRNAs (miRNAs) regulate gene expression by silencing their target mRNAs through degradation. Because miRNA dysregulation is linked with tumorigenesis, expression signatures of dysregulated miRNAs can be used as indicators of glioblastoma, the most malignant and aggressive type of brain cancer. The objective of my project is to design and create an innovative computational model to discover miRNA expression signatures and target interactions, to provide early and accurate diagnosis for glioblastoma. MiRNA and mRNA expression values for 426 glioblastoma patients were obtained from the Cancer Genome Atlas database. 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 innovative statistical techniques, to develop a novel method to analyze patient data and discover miRNA expression signatures and interactions for glioblastoma. 164 miRNA-mRNA networks were identified.10 miRNA expression signatures, previously unassociated with glioblastoma, were discovered through my research. Mir221 and mir222 had the strongest correlation values and regulated the greatest number of mRNA networks, thereby best indicating glioblastoma. Because glioblastoma cells secrete large numbers of exosomes containing miRNAs into the blood, the miRNA profile for a patient 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, while it is still curable. My research will completely revolutionize glioblastoma diagnosis and may allow this disease to be cured completely.

Awards Won:

Fourth Award of $500