Student Research Conference Abstract
Wingyin Lo

Diagnostic implications of microRNA expression profile in thyroid cancer

Each year, more than 1,500 Americans die from thyroid cancer. The current limited resources for thyroid cancer diagnosis indicate a need for more efficient and accurate modes of diagnosis. MicroRNAs (miRNAs) are groups of small non-coding RNA that play a role in gene expression. MiRNAs are known to be expressed differently in cancerous cells than in normal cells. There is potential in miRNA found in serum to be used as a simple, effective diagnostic tool for thyroid cancer. The significance of miRNA expression in serum has yet to be explored or compared to miRNA expression in tumor cells. The objective of this project is to use miRNA from benign and cancerous thyroid cells from their respective conditioned media as a model simulating miRNA expression in tumor cells and serum, and to study a profile for miRNA expression levels expressed in cells and in the media. Several targets were identified from literature as related to thyroid carcinoma. Eleven cell lines representing benign thyroid, papillary thyroid carcinoma (PTC), follicular thyroid carcinoma (FTC), and anaplastic thyroid carcinoma (ATC) were grown in pure cultures and harvested along with the media. MiRNA was extracted and purified from both cell and media samples using the miRNeasy kit from Qiagen. MiScript Reverse Transcription Kit from Qiagen was used to complete cDNA synthesis. MiScript SYBR Green PCR Kit in combination with miRNA-specific primer was used for detection of mature miRNAs. To calculate ΔCT values for the $\Delta\Delta$CT method, ncRNA snord25_1 was used for the control endogenous reference. Through preliminary analysis of a subset group, results have indicated a difference between miRNA expression in media compared to cells. Additional samples are currently being processed for a more significant study. These findings are important to understand and advance the potential to clinically diagnose thyroid carcinoma in serum through miRNA expression.