CURRENT POSTGRADUATE STUDENT

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PROGRAM	PhD in Surgery
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FIELD OF RESEARCH / INTENDED THESIS TITLE	Difference and function of lncRNA profiles in Caucasian and Chinese glioblastoma multiforme patients
KEYWORDS FOR RESEARCH	lncRNA, sequencing, glioblastoma

RESEARCH STUDY:

Glioblastoma multiforme (GBM) is the most common form of primary brain tumors. Even treated with the integreted measures including maximal sugical resection, irradiation, and temozolomide (TMZ) chemotherapy, the outcome of GBM patients remains unsatisfactory. During the last two decades, researchers had made extreme effort on the molecular mechanisms, signal pathways and genetics to find out a cure clue for GBM. With the development of gene sequencing tech and microarray tech, large-scale multi-dimensional datasets had been generated on different platforms.

The funciton of long non-coding RNAs (lncRNAs) had been proved to play an important role in human cancer. lncRNAs are non-protein-coding transcripts ranging in length from 200 nucleotides to 10 kilobases (kb). The lncRNAs had been founded to be the key player in imprinting control, cell differentiation, immune response, tumour genenesis and other cell functions. Recent studies indicated that lncRNAs were important regulators for both oncogenic and tumor suppressive pathways in cancer development. lncRNAs can regulate gene expression at the transcriptional, post-transcriptional and epigenetic levels. The differential expressions of lncRNAs can also be served as the indicator of disease progression and the prognosis of disease. However, the predictive value of lncRNAs for GBM treatment outcomes remains unclear and need to be explored.

The lncRNA profiling will be achieved from the previously published database in TCGA, CGGA, as well as GEO etc. By analysing the lncRNA datasets, together with histological classification and grading, clinical treatment and outcomes, the study aims to determine the relationships between lncRNA expression signatures and treatment outcomes of GBM patients, also the difference of lncRNA profiling and outcome between Caucasian and Chinese groups.

CONFERENCE TITLE / ABSTRACT / POSTER: