NORTHERN HEALTH RESEARCH CONFERENCE

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Elucidation of Tumour Suppressor Genes Using the CGL1 Radiation Induced Tumorigenesis Model

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ABSTRACT:
The CGL1 cell line is a powerful somatic hybrid cell system for quantitative analysis of neoplastic transformation frequency. This system has been extensively utilized to elucidate the mechanisms underlying radiation induced neoplastic transformation. The CGL1 cell line was derived from fusion of normal human male fibroblast skin cells and cervical cancer HeLa cells. Irradiation of CGL1 with 7Gy of gamma radiation produced tumorigenic segregates called gamma induced mutants (GIM), and non-tumorigenic cells called gamma irradiated control (CON). Our lab recently published a whole transcriptome study between CGL1, GIM, and CON cells, and identified 1067 differentially expressed genes (DEGs) between the GIM and CON cell lines. Previously, GIM were characterised by the loss of chromosome 11, and transfer of chromosome 11 into GIM reduced their neoplastic transformation frequency. Similarly, removal of chromosome 11 from CON cells increased their transformation frequency. We hypothesize that chromosome 11 may contain potential tumour suppressor genes that prevent the CGL1 cell line from transforming into a tumour cell. The objective of this study is to determine whether the DEGs identified in GIMs compared to CONs on chromosome 11 are tumor suppressor genes. We hypothesize that deletion of candidate tumor suppressor genes in the CGL1 cells using CRISPR/Cas9 gene editing technology will promote radiation induced transformation frequency. Likewise, overexpression of candidate tumor suppressor genes will decrease the transformation frequency. This research will provide novel tumor suppressor gene targets that can be used by the pharmaceutical industry to develop pharmacological tools to prevent neoplastic transformation.