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Tharini a/p Ravindra Kumar was born on 26th December 1997 in Subang Jaya. She received the entirety of her formal education in Subang Jaya, where she now resides. She has recently graduated from the University of Malaya with a Bsc. in Genetics with a final CGPA of 3.84. Her interest in genetics started before her undergraduate years, making it her goal to pursue a Genetics degree at the University of Malaya. During her time formally studying genetics, she developed a keen interest in epigenetics and developmental genetics. She completed her industrial training at the Center of Biomedical Physics, Sunway University, working on a colorectal cancer screening project during the duration. Besides being awarded Best Oral Presentation for her final year project during the Institute of Biological Sciences, UM Virtual Biosymposium 2020 for the Genetics and Molecular Biology Programme, she received the Dean's List Award (GPA > 3.7) for six semesters.

VALIDATION OF EPSTEIN-BARR VIRUS ENCODED CIRCRNA CANDIDATES FROM NASOPHARYNGEAL CARCINOMA CELL LINES

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ABSTRACT

Nasopharyngeal carcinoma (NPC) is a head and neck cancer that is endemic in certain regions of Southern China and South East Asia. A factor that contributes to the pathogenesis of NPC is the gamma herpesvirus Epstein-Barr virus (EBV). Circular RNAs (circRNAs) are non-coding RNAs that are characterized by its circular closed looped structure compared to its linear counterpart. Cellular circRNAs have a variety of functions namely in the regulation of gene function and expression. In recent years, viruses including EBV have been reported to produce circRNAs in several EBV-associated diseases. However, its expression in NPC remains largely unexplored. Previous in silico circRNA analysis of NPC cell line and xenograft transcriptomes has identified three EBV genes (BHLF1, LF3 and RPMS1) encoding circRNAs with the highest read counts. This study aims to validate and compare the expression of these EBV encoded circRNA candidates in different NPC cell lines. Divergent primers were designed to detect the backsplice junction of circRNAs candidates using RT-PCR and follow by Sanger sequencing validation. The expression of these candidate circRNA and its linear counterparts were then compared using semi-quantitative RT-PCR in both latent and lytic state of different NPC cell lines. The results show that in parallel to its linear counterpart, circBHLF1 level was up-regulated while circRPMS1 were down-regulated upon lytic reactivation. In contrast, although LF3 mRNA is expressed and increased upon lytic reactivation, the backsplice junction for circLF3 could not be detected for neither lytic nor latent state. Further studies are required to verify the predicted circLF3.