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ALTERNATIVE SPLICING OF EXTENDED SYNAPTOTAGMIN-2 AS A PROGNOSTIC BIOMARKER IN RENAL CELL CARCINOMA

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The protein of gene ESYT2 Extended synaptotagmin-2 has been demonstrated to be interacted with the Fibroblast Groth Factor Receptor and activated FGF receptor. It plays an important role in growth factor signaling. However, the expression and function of the transcript variants of this gene is unclear in cancer. In this study, we observed a significant isoform switch of ESYT2 based on the RNA-seq data of the renal cell carcinoma (KIRC) samples downloaded from the TCGA database. Although the expression level of gene ESYT2 is higher in KIRC tumor samples, the expression ratio of the long ESYT2 isoform (ESYT2-L) which includes a cassette exon between exons 13 and 14 to the short isoform (ESYT2-S) is higher in kidney normal samples. The Kaplan-Meier survival curves showed that samples with higher expression ratio of ESYT2-L are associated with better survival (p=2.04e-06). Multivariate Cox proportional hazards regression revealed that the expression ratio of the ESYT2-L could be as an independent prognostic factor for patients with CRC (hazard ratio, 0.037; 95% confidence interval, 0.01-0.125; P=1.24e-07). In addition, the Gene set enrichment analysis (GSEA) revealed that genes correlated with the expression ratio of ESYT2-L is enriched in hallmark of the EMT and invasiveness signature from cancer cell. In conclusion, our findings show that the alternative splicing of ESYT2 could be a potential prognostic biomarker in KIRC and samples with lower expression ratio of the ESYT2-L isoform may be more likely to have the potential to become metastatic.

BIOGRAPHY

Dan Huang is a PhD candidate from The Chinese University of Hong Kong. She has been involved in the design, application, and evaluation of bioinformatics pipelines for transcriptome studies based on high throughput sequencing data. She mainly focus on the alternative splicing events that may be associated with cancer by studying large genetic and genomic datasets downloaded from The Cancer Genome Atlas (TCGA) database.

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