Modulation of POTE-2 Expression by ncRNAs in Hepatocellular Carcinoma

Anilkumar A[1,2,5], Lopez S[1,2,5], Doxtater K[2,5], Chauhan N[2,5], Kotnala S[2,5], Yallapu M[2,5], Dhevan V[3,4], Chauhan SC[2,5], Tripathi MK[2,5]

[1]Department of Biology, College of Sciences, The University of Texas Rio Grande Valley, McAllen, TX 78539, USA.

[2]South Texas Center of Excellence in Cancer Research, School of Medicine, University of Texas Rio Grande Valley, McAllen TX 78504, USA.

[3]Valley Baptist Hospital, Harlingen, TX 78550, USA.

[4]Department of Surgery, School of Medicine, University of Texas Rio Grande Valley, Edinburg, TX 78501, USA.

[5]Department of Immunology and Microbiology, School of Medicine, University of Texas Rio Grande Valley, McAllen, TX 78504, USA.

Background: Hepatocellular carcinoma (HCC) has one of the highest incidents and mortality rates within the Hispanic population of South Texas. The Surveillance, Epidemiology, and End Results (SEER) cancer registry reports a 20.3% 5-year relative survival rate upon HCC diagnoses, which decreases in advanced stage cancers. The disproportionate impact on the Hispanic community and poor prognostics makes the search for better diagnostic measures imperative. A major step in bridging the disparity in HCC occurrence is the identification of potential biomarkers aiding in HCC diagnosis, surveillance, and treatment. POTE ankyrin domain members have been recognized as key promotors of tumorigenesis. POTE-2, a novel protein, has shown to be differentially regulated in liver cancer. Micro-RNAs (miRNAs) regulate protein expression through translational inhibition or mRNA degradation. This study aims to investigate possible role of miRNA-3662 in POTE-2 expression regulation in HCC cell lines.

Methods: POTE-2 mRNA and protein were analyzed using RT-PCR and western blot respectively in liver cancer cell lines, SK-HEP1, C3A, HEPG2, and HEP-3B. POTE-2 mRNA was analyzed for potential miRNA binding sites using miRNAdb.org. Identified miRNAs were verified using miRNA specific RT-PCR.

Results: SK-HEP1 yielded relatively low mRNA with high protein, and the opposite was observed in C3A cells. SK-HEP1 cells showed higher proliferation, migration, and invasion. Analysis of POTE-2 mRNA using miRNA database identified potential miRNAs binding sites. MiRNA-3662 being the top candidate is being analyzed for its role in POTE-2 regulation.

Conclusions: Regulation of POTE-2 mRNA by miRNA-3662 makes it a potential candidate for miRNA-based therapeutics in HCC.