

LncRNA malat1 as a novel stress related factor in Hepatocellular Carcinoma

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LncRNA Malat1 as a novel stress-related factor in Hepatocellular Carcinoma

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As a result of the fast life pace, stress, and a major dietary shift toward preserved food, hepatocellular carcinoma (HCC) incidence and mortality are on rising trend, thus posing severe concerns. Texas is expected to have the second highest number of deaths related to liver cancer, with Hispanics having the highest mortality rate. HCC accounts for 85% to 90% of liver cancers. The Rio Grande Valley (RGV) region, where a predominantly (~90%) Latino/Hispanic population resides, has ~4-fold higher prevalence of liver cirrhosis and is a major hotspot of HCC in the nation. In addition, it was found to be positively correlated with diabetes and obesity. Thus, the RGV region is severely affected by the disproportionate burden of HCC incidence and mortality. As per recent SEER data, the five-year survival rate in this disease drops from 35% to 2% of patients diagnosed with regional and distant stages. Unfortunately, no adequate and specific molecular markers are available that can detect HCC at the early onset of disease. Additionally, how different socio-behavioral, dietary, and stress factors influence the molecular drivers of HCC are not fully understood. It has been demonstrated that, apart from family history, different socio-behavioral factors, certain diets, alcohol, and smoking are associated with *dysregulated functioning of a major endocrine* (HPA; Hypothalamus-Pituitary-Adrenal) axis and higher levels of biochemical stressors (cortisol, cytokines, leptin). These are active areas of research in the HCC field to aid the discovery of new early diagnostic molecular markers and define molecular triggers of the disease. *Recently, we have observed that a Long noncoding RNA (LncRNA), Metastasis Associated Lung Adenocarcinoma Transcript 1 (LncRNA MALAT1), is involved in HCC pathogenesis. It is regulated by the transcription factor Nuclear Factor of Activated T cell 1 (NFATc1), a poor survival indicator of cancer patients. We have developed a novel, clinically applicable Z-Probe-based RNAScope Technology for detecting LncRNAs (such as MALAT1) on tumor tissues just like immunohistochemistry. This will allow us to investigate MALAT1 expression about NFATc1 and establish the association of these two distinct class of molecular markers (LncRNA and NFATC1 protein) in HCC samples. We are investigating how biochemical stress factors can influence the expression of these two oncogenic drivers.*