

## **Article 5**

### **Evaluation of serum long noncoding RNA NEAT and MiR-129-5p in hepatocellular carcinoma**

#### **Abstract:**

Hepatocellular carcinoma (HCC) is one of the most prevalent form of cancer. Various long non coding RNA (lncRNAs) and micro RNA have been confirmed to have a role in the progression of HCC. Our aim was to investigate for the first time the expression profile of serum level of LNC NEAT (nuclear enrich abundant transcript) and MiR-129-5p in HCC patients and their relations with patient's clinical and biochemical investigations rather than previous studies on tissue cell lines. Our study includes 72 subjects divided into 36 as control subjects and 36 patients with HCC. Complete physical and laboratory investigations were done on all subjects. RNAs were extracted from sera of all subjects. RNAs were reversed transcribed into cDNAs using Qiagen, Valenica, CA. Quantitative PCR (qPCR) was performed using Rotor gene Q System (Qiagen). Relative NEAT1 expression level was significantly increased in serum of HCC patients 4.7 (1.31–6.82) ( $p < .0001$ ). Meanwhile MiR-129-5p relative expression level was significantly decreased in serum of HCC patients 0.17 (0.14–20) ( $p < .0001$ ). Also there was negative significant correlation between the expression level of LNC NEAT and MiR-129-5p in HCC group ( $p < .0001$ ). ROC curve analysis revealed that LNC NEAT; AUC = 0.981,  $p < .0001$ , cutoff value (1.02), sensitivity 100%, specificity 88.9%. MiR-129-5p; AUC = 0.997,  $p < .0001$ , cutoff value (0.43), sensitivity 100%, specificity 97.2%.

**Conclusion** Serum LNC NEAT and MiR-129-5p could be used as potential biomarkers for HCC cancer diagnosis and prognosis.