ABSTRACT

Background: Liver cancer starts in the liver and often develops in the context of cirrhosis and chronic liver disease. For early diagnosis identification of biomarkers **is** necessary.

Aim: To elucidate the miRNA-based mechanism of liver cancer and to identify potential biomarkers to predict liver cancer.

Methods: Comprehensive bioinformatics analysis was performed on two GEO datasets “GSE20077” and “GSE164760”. DIANA Tool-mir path v.3, STRING, Cytoscape 3.6.0, Enrichr and Tarbase v8 were used for the identification and analysis of miRNAs and their targets in liver cancer.

Results: Four miRNAs; hsa-miR-200b-3p, hsa-miR-130a-3p, and hsa-miR-122-5p and has-miR-122-5p were identified in the current study. These miRNAs were differentially regulated in liver cancer. Further bioinformatics analysis identified KRAS regulated by has-miR-200-3p, CDKN1A regulated by has-miR-1301-3p, TP53 regulated by has-miR-122-5p and CDK6 regulated by has-miR-10-5p.

Conclusion: This study identified a set of miRNAs which should be studied further to confirm experimentally as biomarkers.

Keywords: liver cancer; miRNA; differential expression; KRAS; CDKN1A; TP53;CDK6; proliferation.