Long non-coding RNA (lncRNA) as a new biomarker for hepatocellular carcinoma (HCC) drug resistance

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Background

Hepatocellular carcinoma (HCC) is the 4th leading cause of cancer-related deaths worldwide and the 6th most common cancer worldwide. When HCC progresses to advanced stages, drug resistance becomes a major hurdle and leaves clinicians with limited therapeutic options. Long non-coding RNAs (lncRNAs) have shown to promote drug resistance in various cancers. The goal of our research is to explain the molecular role of lncRNAs in HCC drug resistance and compile a comprehensive list of studied lncRNAs involved in HCC drug resistance.

Methods

To compile a list of lncRNA involved in HCC drug resistance we performed an advanced search on Lnc2Cancer, a database that provides experimentally supported associations between lncRNA and human cancer, using the following filters: “hepatocellular carcinoma”, “drug clinical application”, “lncRNA”, “all biological function”, and “all regulatory mechanism.”

Results

We identified 12 lncRNAs that are involved in HCC drug resistance: Metastasis Associated Lung Adenocarcinoma Transcript 1 (MALAT 1), Keap1 Regulation-Associated LncRNA (KRAL), Transcribed Ultra-conserved Region 338 (TUC338), Long intergenic non-protein coding RNA, regulator of reprogramming (linc-ROR), Linc-VLDLR, Highly Upregulated in Liver Cancer (HULC), HCC associated long non-coding RNA (HANR), LncRNA Regulator of AKT Signaling Associated with HCC and RCC (LncARSR), Taurine up-regulated gene 1 (TUG1), H19, NR2F1 Antisense RNA 1 (NR2F1-AS1), and HOX Transcript Antisense RNA (HOTAIR).

Conclusions

Our review demonstrates that lncRNAs involved in HCC drug resistance participate in various mechanistic categories such as autophagy, epithelial-mesenchymal transition, and efflux pump upregulation. There is a need to uncover novel lncRNA biomarkers for both the early detection of HCC and to create drug strategies for clinicians when predicting chemoresistance.