LncRNA–miRNA–mRNA Networks of Gastrointestinal Cancers Representing Common and Specific LncRNAs and mRNAs

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Gastrointestinal (GI) cancers are responsible for approximately half of cancer-related deaths, highlighting the need for the identification of distinct and common features in their clinicopathological characteristics. Long ncRNA (lncRNAs), which are involved in competitive endogenous RNA (ceRNA) networks with critical roles in biological processes, constitute a substantial number of non-coding RNAs. Therefore, our study aimed to investigate the similarities and differences in the ceRNA networks of The Cancer Genome Atlas (TCGA)-GI cancers. We performed a comprehensive bioinformatics analysis of ceRNA networks for TCGA-GI cancers in terms of the deferential mRNA, lncRNA, and miRNA expression levels, ceRNA networks, overall survival analysis, correlation analysis, pathological cancer stages, and gene set enrichment analysis. Our study revealed several common and distinct mRNAs and lncRNAs with prognostic values in these networks. It was specifically noteworthy that *MAGI2-AS3* lncRNA was found to be shared in almost all GI cancers. Moreover, the most common shared mRNAs between GI cancers were *MEIS1, PPP1R3C, ADAMTSL3, RIPOR2,* and *MYLK*. For each cancer ceRNA network, we found that the expression level of a number of lncRNAs and mRNAs was specific. Furthermore, our study provided compelling evidence that several genes, most notably *KDELC1*, can act as novel proto-oncogenes in cancers. This, in turn, can highlight their role as new prognostic and therapeutic targets. Moreover, we found cell cycle and extracellular matrix structural constituent as the top shared KEGG and molecular function, respectively, among GI cancers. Our study revealed several known lncRNAs and known and unknown mRNAs in GI cancers with diagnostic and prognostic values.

Keywords: tumor biomarkers, gastrointestinal cancers, long-non-coding RNA, The Cancer Genome Atlas (TCGA), competitive endogenous RNA (ceRNA)