



The Role of ceRNA Networks in the Development and Progression of Gastric Cancer

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Abstract

MicroRNAs or miRNAs bind to miRNA Response Elements (MREs), a location on target transcripts, causing either transcript destruction or translational inhibition. ncRNAs with MREs can compete with mRNA as a miRNA sponge and are involved in a complex regulatory network that regulates the transcription of mRNAs through miRNAs competitive binding. According to the ceRNA hypothesis, ncRNAs, including lncRNAs, circRNAs, and pseudogenes, contend against mRNAs in binding to miRNAs *via* miRNAs' MRE. MicroRNA is the most important part of the ceRNA network and ncRNAs and mRNAs are other components of the ceRNA network. LncRNAs, circRNAs, and pseudogenes have been demonstrated to play a key role in cellular processes like cell proliferation, cell growth, apoptosis, and differentiation. CeRNA networks are involved in many cancers, including liver, breast, lung, and Gastric Cancer (GC). Therefore, the study of the ceRNA network in GC will help to understand how the disease develops and progresses, as well as identify new therapeutic approaches.

Keywords: Apoptosis, Cell proliferation, MicroRNAs, Pseudogenes, Response elements, Circular, Competitive endogenous, Long noncoding, Stomach neoplasms

regulated by miR-106b and miR-93 in GC cells (76).

Conclusion

In summary, few studies have been done on the role of ceRNA in the diagnosis and treatment of GC. In this study, the role of non-coding RNAs (ncRNAs), including microRNA, long non-coding RNAs (lncRNAs), circular RNAs (circRNAs), and pseudogenes as a network of competing internal RNAs in regulating gene expression at the transcriptional level in GC, were presented. Non-coding RNAs, as ceRNAs, are involved in various biological processes, such as cell proliferation, apoptosis, invasion, and migration.

CeRNAs networks play a significant regulatory role in the progression of GC, and in the ceRNAs networks, ncRNAs competitively target miRNAs and play a role in the regulation of gastric cancer-related genes. Altogether, the study of the ceRNA network in GC can improve our knowledge on the disease

development and progression, molecular signaling, prognosis, and diagnosis, as well as for identifying new therapeutic strategies for treating GC patients.

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Conflict of Interest

The authors declare that they have no conflicts of interest.

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