Research progress on the interactions between long non-coding RNAs and microRNAs in human cancer (Review)

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Abstract. Numerous types of molecular mechanisms mediate the development of cancer. Non-coding RNAs (ncRNAs) are being increasingly recognized to play important role in mediating the development of diseases, including cancer. Long non-coding RNAs (lncRNAs) and microRNAs (miRNAs) are the two most widely studied ncRNAs. Thus far, lncRNAs are known to have biological roles through a variety of mechanisms, including genetic imprinting, chromatin remodeling, cell cycle control, splicing regulation, mRNA decay and translational regulation, and miRNAs regulate gene expression through the degradation of mRNAs and lncRNAs. Although ncRNAs account for a major proportion of the total RNA, the mechanisms underlying the physiological or pathological processes mediated by various types of ncRNAs, and the specific interaction mechanisms between miRNAs and lncRNAs in various physiological and pathological processes, remain largely unknown. Thus, further research in this field is required. In general, the interaction mechanisms between miRNAs and lncRNAs in human cancer have become important research topics, and the study thereof has led to the recent development of related technologies. By providing examples and descriptions, and performing chart analysis, the present study aimed to review the interaction mechanisms and research approaches for these two types of ncRNAs, as well as their roles in the occurrence and development of cancer.

These details have far-reaching significance for the utilization of these molecules in the diagnosis and treatment of cancer.

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1. Introduction

In 1993, Lee et al (1) discovered the first microRNA (miRNA), lin-4, which by repressing the lin-14 gene is essential for controlling the timing of Caenorhabditis elegans larval development. In 2000, the miRNA let-7 was discovered to repress lin-41 to promote a later developmental transition in C. elegans (2). Since then, a number of evolutionarily conserved miRNAs have been identified, from plants and fungi to humans, and have been shown to play various roles in biological and pathophysiological processes. To date, thousands of studies on miRNAs using well-developed methods which are now performed routinely (3). Mature miRNAs are short, single-stranded RNA molecules, ~22 nucleotides in length, processed from well-characterized precursors through a highly accurate pathway involving a fold-back hairpin structure (4). The majority of miRNA genes are located in intergenic regions; however, a small portion are located in intron and exon sequences. miRNAs function via their seed sequence (5'-end 2-8 nucleotide sequence), which is completely complementary or partially complementary to the 3'untranslated region (3'UTR), or even the coding sequence and 5'UTR, of the target gene. A ribonucleoprotein complex, named the RNA-induced silencing complex (RISC), is involved in regulating diverse biological processes, with argonaute (AGO) being the catalytic component (5). Gene silencing occurs either through RNA cleavage promotion or translational inhibition. In addition, some miRNAs do not inhibit target gene expression, but rather bind to the 5'UTR of ribosomal protein mRNA and promote ribosomal protein synthesis (6).

The discovery of long non-coding RNAs (lncRNAs) occurred earlier than that of miRNAs: The first lncRNA,
H19, was discovered by Brannan et al (7) in 1990. However, defining lncRNAs based simply on the size and the absence of protein-coding capability is insufficient. Thus far, miRNAs which greatly expand the functional genome from a large-scale regulatory network are well understood, while the lncRNA counterpart of the transcriptome has been relatively neglected. Nonetheless, the evolution and functions of lncRNAs have recently piqued interest among researchers due to the availability of sensitive detection techniques. lncRNAs are most commonly defined as non-protein-coding RNA molecules (>200 nucleotides) transcribed by RNA polymerase that may or may not be polyadenylated, and can be present within the nucleus or cytoplasm (8). lncRNAs share a similar conserved structure with mRNAs (9,10) and are considered sense, antisense, bidirectional, intronic or intergenic mRNAs, according to their location in the gene sequence. Some lncRNAs tend to be transcribed away from the 5' or the 3'ends of the gene and are concentrated near promoters. The initial exons and introns of these genes suggest that the transcription of these lncRNAs comprises a potential regulatory aspect (11). lncRNAs also participate in a wide variety of biological processes (12,13), such as post-transcriptional regulation (14). In general, weak conservation of lncRNAs exists due to evolution, and due to selective pressure, several local highly conserved sequences are often distributed in fragile chromosome sites. A number of studies on lncRNAs have focused on their regulation of protein-coding genes, and little is known about interactions between RNA classes. In addition, recent reports (15) suggest that lncRNAs may interact with other RNA classes, including miRNAs. Thus, non-coding RNAs (ncRNAs) are not mere evolutionary relics; rather, they provide a ‘Rosetta Stone’, facilitating the interpretation of much of the genomic repertoire of non-coding transcripts.

2. Interactions between lncRNAs and miRNAs

With the development of gene networks, and differential expression and pathway analyses, lncRNAs are emerging as important regulators implicated in various biological processes (16). However, our understanding of the impact of miRNA-lncRNA regulatory networks remains limited.

‘Sponge effect’ of lncRNAs on miRNAs. Competing endogenous RNAs (ceRNAs) and microRNA response elements (MREs), two important components involved in the ‘sponge effect’, can act in almost all interaction mechanisms as lncRNAs and miRNAs (Fig. 1). ceRNAs were first proposed by Salmena et al (17), who hypothesized molecular regulation patterns, such as an lncRNA that competes with a miRNA to release the inhibition of other genes; this lncRNA was called a ceRNA. Lewis et al (18) described more fully the concept of an MRE in 2004; an MRE (miRNA response element) is a seed region that comprises nucleotides 2-8 of the 5'portion of the miRNA and is particularly crucial for mRNA recognition and silencing or interaction with ncRNAs. Moreover, MREs and ceRNAs play an irreplaceable role in the ‘sponge effect’ of lncRNAs and miRNAs. The characteristics of this ‘sponge effect’ can be observed via the following aspects.

At present, there are two modes used to describe the ‘sponge effect’ of lncRNAs and miRNAs, namely complete complementary mode and partial complementary mode. miRNAs that bind to target gene sequences are partially complementary, and this process is mediated by MREs that harbor conserved target sites. In 2009, Seitz (19) proposed that miRNA-binding sites identified via bioinformatics can titrate miRNAs and thereby impair their activity. Such ceRNAs regulate MREs on their targets, and thus play an important role in post-transcriptional regulation. When the sponging effect of an lncRNA and a miRNA occurs, it is usually complete complementation. However, when an miRNA negatively controls an lncRNA, the mature lncRNA usually has a hat and a poly(A) tail, that is, a 5'UTR and a 3'UTR. Therefore, miRNAs can also have partial complementation with an lncRNA, similar to an mRNA (11).

In general, an lncRNA has multiple MREs, and the more it has, the more the lncRNAs and miRNAs communicate with each other. This has an important effect on different physiological and pathological conditions. For instance, IncRNA-BGL3 functions as a ceRNA for miR-17, miR-93, miR-20a, miR-20b, miR-106a and miR-106b to prevent repression of the mRNA for phosphatase and tensin homolog (20). lncRNAs that share multiple MREs will cross talk effectively, which is also of great significance in a variety of biochemical processes (21).

Moreover, the same MREs on a ceRNA are not equal. For miRNA, all lncRNAs that do not contain an MRE will have a sponging effect with the corresponding miRNA, exhibiting a preference when several miRNAs are present at the same time (22). For instance, the IncRNA BC032469 contains elements complementary to the miR-1207-5p and miR-1266 seed regions; however, BC032469 functions as a ceRNA by impairing only miR-1207-5p-dependent target gene downregulation (23). It is proposed that the primary targets of a certain miRNA are preferentially affected, whereas the remainder are less affected Moreover, previous studies (24,25) have suggested that MREs in lncRNAs show a positional preference for the AGO binding sites in mid-regions and at the 3'ends of the IncRNAs (11). These sites harbor a possible pattern of regulatory elements across transcripts.

In addition, the overall influence of the sponging effect depends on the specific spatial-temporal distribution. For example, during embryonic development, an miRNA has been proven to be an important post-transcriptional regulator that can promote the rapid clearance of core transcription factors (TFs) during human embryonic stem cell (hESC) differentiation (26). Long intergenic non-coding RNA, regulator of reprogramming (Linc-RoR) can serve as the endogenous ‘sponge’ for differentiation-related miRNAs. In hESC self-renewal, Linc-RoR suppresses miRNAs at a certain stage when highly expressed or under treatment with various agents. However, in hESCs with strong differentiation ability, the relevant miRNA is highly transcribed, and Linc-RoR levels decrease. Linc-RoR is important for suppressing miRNA expression in the early stage of hESC differentiation, which may facilitate further hESC differentiation (26). Moreover, these results may provide an insight into miRNA-lncRNA interactions occurring in multiple stem cells.

In summary, the sponging effect is the basis of the molecular mechanism of the network involved in various biochemical processes mediated by miRNAs, lncRNAs and related molecules.
Main mechanisms of regulation between lncRNAs and miRNAs. There are two aspects of regulatory factors and regulatory targets: One is the regulation of lncRNAs by miRNAs, and the other is the regulation of miRNAs by lncRNAs (Fig. 2). Regarding the former, miRNAs can indirectly regulate the expression of lncRNAs. lncRNAs and miRNAs interact to form the transcriptome of regulatory networks, an interaction that is sometimes similar to an enhancer function, influencing the expression of flanking genes (27). An interesting example of the interaction between an miRNA and an lncRNA is the DLK1-MEG3 imprinted domain, which includes the tumor suppressor factor MEG3 lncRNA, and an miRNA, such as miR-29, which is involved in a number of cancer types (28). miR-29 negatively regulates DNA methylase and indirectly regulates the expression of MEG3 in liver cancer. In addition, miRNAs degrade lncRNAs in an AGO-dependent manner. Within the RISC, miRNA binds to the target lncRNA 3'UTR, leading to full mRNA degradation or blockade of the ribosomal machinery, both of which result in gene silencing (29). lncRNAs also regulate miRNAs in further ways. The most common involves lncRNA-mediated inhibition of miRNA expression via the sponging effect. lncRNAs can be used as precursors of miRNAs to directly affect miRNA regulation; some differences between the two sequences may exist (30). Guo et al (31) examined H19 and the product of miR-675 sequencing analysis, and found that the H19 main base is G, with miR-675 having a G or C. These two types of mature miRNA sequences are reversed in miR-675-3p/5p, and this structure ensures the stability of the pre-miRNA stem-loop structure. Differences in nucleotide composition tend to indicate that different lengths are required for functioning. Although miR-675 and H19 belong to the ncRNA family, they exhibit different conservation and nucleotide mutation frequencies. Additionally, lncRNAs bind competitively with miRNA targets (some miRNAs), and lncRNAs compete with the 3'UTR of the target miRNA, which indirectly inhibits the negative regulation of the target mRNA by the miRNA (18,31). For example, lncRNA FEZF1-AS1 can competitively inhibit miRNA-30a, leading to Nanog silencing in breast cancer (32). lncRNAs also bind to several proteins in complex to regulate miRNA expression, such as H19, which can act on PCAF/hnRNP/Pol RNA II and enhance the histone acetylation of the region upstream of miR-200 (33), and lncRNAs can affect the expression of miRNAs via other chromatin modifications (34).

miRNAs and lncRNAs constitute a negative feedback loop. Another important mechanism of interaction between miRNAs and lncRNAs is that they can function together to form a negative feedback regulation pathway. A relatively

Figure 1. Different ‘Sponge’ effect of lncRNAs on miRNAs. (1) Complete complementarity between lncRNAs and miRNAs. (2) Partial complementarity between lncRNAs and miRNAs. (3) lncRNAs have multiple MREs for different miRNAs. (4) The overall influence of the sponging effect depends on the specific spatial-temporal distribution. (5) For different miRNAs containing the same MRE, lncRNAs will give priority to one of these miRNAs for binding. lncRNA, long non-coding RNA; miRNA, microRNA; MRE, microRNA response element.
A simple example is that miRNA-200a and histone deacetylase 4 (HDAC4) can form a negative feedback regulation loop in hepatocellular carcinoma; that is, HDAC4 overexpression can inhibit miR-200a (33). Other studies have confirmed that HDAC4 overexpression also inhibits H19, indicating that H19, miR-200A and HDAC4 together constitute a negative feedback regulation loop (33, 35). Another example involves the tumor formation process, whereby the enhancer of zeste homolog 2 (EZH2) gene participates in polycomb complex 2 core subunit inhibition, with epigenetic modification playing a crucial role. EZH2 has been confirmed to interact with a variety of miRNAs and has been accepted as a negative regulator of miRNAs (36). Some miRNAs can bind directly to the 3'UTR of EZH2, and EZH2 regulates miRNA expression at two transcriptional levels. By interacting with EZH2, miRNAs can affect H3K27 methylation and regulate cellular processes. Thus, miRNAs and EZH2 constitute an important regulatory and feedback pathway in which EZH2 is a stable factor. In addition, miR-26a-2 forms a negative feedback loop with miR-101 and EZH2 and is under the negative regulation of MYC and HIF-1α/1β (36, 37). EZH2 inhibits cell cycle regulatory factors and the tumor suppressor gene Rap1GAP, and participates in the epithelial-mesenchymal transition process via molecules such as E-cadherin (36). Moreover, EZH2 and IncRNAs are closely related, affecting both each other and the expression of target genes. Therefore, miRNA-101, miR-26a, EZH2 and HOTAIR IncRNA also comprise a negative feedback loop (38). Furthermore, IncRNAs and related molecules can form other negative feedback loops. In addition, MIR100HG, miR-100 and miR-125b overexpression has been observed in cetuximab-resistant colorectal cancer, head and neck squamous cell cancer cell lines, as well as in tumors from patients with colorectal cancer whose disease progressed on cetuximab, and miR-100 and miR-125b have been observed to coordinately repress five Wnt/β-catenin negative regulators (mitochondrial genome maintenance exonuclease 1, Dbf4-dependent kinase 3, ring finger protein 4, cell division cycle 27 and nuclear factor, erythroid 2 like 2). These results describe a double-negative feedback loop between MIR100HG and the TF GATA6: GATA6 represses MIR100HG; however, this repression is relieved through targeting of GATA6 by miR-125b, which results in increased Wnt signaling, and Wnt inhibition in cetuximab-resistant cells restores cetuximab responsiveness (39). Thus, the IncRNA MIR100HG, miR-100, miR-125b and GATA6 form a double-negative feedback loop. These examples also indicate that IncRNAs and miRNAs may be involved in the diversity of the negative feedback loop (Fig. 3).

3. Methods of research into IncRNAs and miRNAs

Databases for studying interactions between miRNAs and IncRNAs. In recent years, a number of IncRNA/miRNA-related databases have been established by researchers in combination with bioinformatics technology (Table I) (40–50). The establishment of these databases not only provides comprehensive information on various types of IncRNAs, but also a very important platform for studying the regulatory relationship between IncRNAs and miRNAs. Three representative databases (44, 46, 50) are discussed below. The DIANA-LncBase database (http://www.microrna.gr/LncBase) is a tool developed by the DIANA Laboratory for researchers to explore potential interactions between IncRNAs and miRNAs. The DIANA-LncBase database offers detailed information for each miRNA-IncRNA pair, such as graphical plots of the genomic location of the transcript, a representation of binding sites, IncRNA tissue expression, and MRE conservation and prediction scores. The CHIP database (http://rna.sysu.edu.cn/chipbase/) is an open database developed by Zhongshan University (Guangzhou, China). The CHIP database is mainly used for comprehensive annotation of ncRNAs, including TF binding sites and motifs, and for decoding the transcriptional regulatory networks of IncRNAs, miRNAs, other ncRNAs and protein-coding genes based on chromatin immunoprecipitation-sequencing (seq) data. By integrating experimental and predicted ncRNA-disease associations from manual literature curation and other resources under one common framework, the MNDR v2.0 database (http://www.microrna.gr/MNDR) is an open database developed by Zhongshan University (Guangzhou, China). The CHIP database is mainly used for comprehensive annotation of ncRNAs, including TF binding sites and motifs, and for decoding the transcriptional regulatory networks of IncRNAs, miRNAs, other ncRNAs and protein-coding genes based on chromatin immunoprecipitation-sequencing (seq) data. By integrating experimental and predicted ncRNA-disease associations from manual literature curation and other resources under one common framework, the MNDR v2.0
A database (http://www.rna-society.org/mndr/index.html) was developed by Harbin Medical University (Harbin, China) for ncRNAs and related diseases.

Table I. Related databases for the study of interactions between miRNAs and lncRNAs.

| Author, year  | Database                  | Website                                      | Applicable ncRNA (Refs.) |
|--------------|---------------------------|----------------------------------------------|---------------------------|
| Erdmann et al, 2000 | Non-codingRNA database | http://biobases.ibch.poznan.pl/ncRNA         | lncRNA/miRNA (40)         |
| Mituyama et al, 2009 | fRNAdb                  | http://www.ncRNA.org/frnadb                  | lncRNA/miRNA (41)         |
| Dinger et al, 2009 | NERD                     | http://jsm-research.imb.uq.edu.au/NERD        | lncRNA (42)               |
| Amaral et al, 2011 | IncRNAdb                 | http://www.mrencadb.org/                     | lncRNA (43)               |
| Yang et al, 2013  | ChipBase v2.0            | http://rna.sysu.edu.cn/chipbase/              | lncRNA/miRNA (44)         |
| Volders et al, 2013 | LNCipedia                | http://www.lncipedia.org                     | lncRNA (45)               |
| Paraskevopoulos et al, 2013 | DIANA-LncBase        | http://www.microrna.gr/LncBase                | lncRNA/miRNA (46)         |
| Cook et al, 2011  | RBPDB                     | http://rbpdb.ccb.rutoronto.ca/               | lncRNA/miRNA (47)         |
| Li et al, 2014    | IncRNABase/starBase v2.0 | http://starbase.sysu.edu.cn/                 | lncRNA (48)               |
| Hsu et al, 2006   | miRNAMap                 | http://mirnamap.mbc.nctu.edu.tw              | miRNA (49)                |
| Cui et al, 2018   | MNDR v2.0                | http://www.rna-society.org/mndr/index.html   | lncRNA/miRNA (50)         |

miRNA, microRNA; lncRNA, long non-coding RNA; ncRNA, non-coding RNA.

Figure 3. Three common types of negative feedback loops composed of miRNAs and lncRNAs. (1) lincRNA, miRNA and a protein constitute a single-negative feedback loop. (2) lncRNA, two miRNAs and a protein constitute a double-negative feedback loop. (3) lncRNA, two miRNAs and multiple proteins constitute a double-negative feedback loop. miRNA, microRNA; lincRNA, long non-coding RNA.

Research technology for lncRNAs and miRNAs. As lncRNAs/miRNAs have various functions through numerous types of mechanisms, the establishment and application of
molecular biology research methods has a very important role in investigating lncRNA/miRNA functions (Table II). At present, there are several well-developed research methods for qualitative and quantitative analysis of ncRNAs. Microarray, RNA-seq, northern blotting, reverse transcription-quantitative polymerase chain reaction (RT-qPCR) and Fluorescence in situ hybridization (FISH) have been used for such analyses of ncRNAs (51). Indeed, Ørom et al (52) observed the expression of 3,019 types of lncRNAs in a variety of human cell lines through reverse transcription-quantitative polymerase chain reaction (RT-qPCR) and Fluorescence in situ hybridization (FISH) have been used for such analyses of ncRNAs (51). Indeed, Ørom et al (52) observed the expression of 3,019 types of lncRNAs in a variety of human cell lines through reverse transcription-quantitative polymerase chain reaction (RT-qPCR) and Fluorescence in situ hybridization (FISH) have been used for such analyses of ncRNAs (51). 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| Author, year          | Technology                      | Function                                                                 | Significance                                                                                       | Applicable ncRNA | (Refs.) |
|----------------------|---------------------------------|--------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------|------------------|---------|
| Yan et al., 2012     | Microarray                      | Qualitative and quantitative research on ncRNAs                        | Detection spectrum analysis of IncRNAs in a variety of cell lines                                | IncRNA/miRNA     | (51)    |
| Yan et al., 2012     | RNA-seq                         | Qualitative and quantitative research on ncRNAs                        | Analysis of the sequence and expression level of target ncRNAs in cells                          | IncRNA/miRNA     | (51)    |
| Yan et al., 2012     | Northern blotting; RT-qPCR       | Quantitative study of target ncRNA                                      | Analysis of the expression level of ncRNAs in cells or tissues                                 | IncRNA/miRNA     | (51)    |
| Yan et al., 2012     | FISH                            | Quantitative study on the location of target ncRNA                    | Analysis of the location and expression level of ncRNAs in cells or tissues                    | IncRNA/miRNA     | (51)    |
| Chakraborty et al., 2012; Alberts et al., 2002; Keene et al., 2006 | c-KLAN; subcellular fractionation RIP-Chip | Study on the location of target ncRNA and study on the composition of complex compound with ncRNA | Clarification on the site of action of ncRNAs                                                   | IncRNA/miRNA     | (56,57) |
| Bellucci et al., 2011| catRAPID                        | Predictions of RNA and fast interactions and domains                  | Provides positive guidance for finding ncRNA targets, and it can be used to detect the interaction between RNA and DNA/protein | IncRNA/miRNA     | (63)    |
| Lagarde et al., 2017 | CLS                             | Accelerating IncRNA annotations                                        | To articulate the genome features of IncRNAs, including promoter and gene structure, and protein coding potential | IncRNA           | (64)    |
| Olivarius et al., 2009 | RACE                           | Rapidly amplifying the 5' and 3' ends of cDNA from low abundance transcripts based on PCR | To obtain the full-length IncRNA sequence for research                                             | IncRNA           | (65)    |
| Yan et al., 2012; Koshkin et al., 1998; Zhang et al., 2014 | RNAi/CRISPR/LNA | Interfering with the expression of ncRNA in varying degrees | Study of the function of ncRNAs by cell phenotype                                               | IncRNA/miRNA     | (51,58,59) |
| Tanizawa et al., 2012; Splinter et al., 2012; Dostie and Dekker, 2007; Belton et al., 2012 | 3C/4C/5C/Hi-c technology | Study on the changes in the interaction between the three dimensional structural changes between genomic regions | Used for IncRNA-mediated chromatin interaction                                                     | IncRNA           | (65-68) |

miRNA, microRNA; IncRNA, long non-coding RNA; ncRNA, non-coding RNA.
| Author, year | ncRNAs | Upregulated | Downregulated | Mechanism | Outcomes | Cancer | (Refs.) |
|--------------|--------|-------------|----------------|-----------|----------|--------|--------|
| Yang *et al.*, 2019 | IncRNA00173, miRNA182-5p | miRNA182-5p | IncRNA00173 | Sponge effect | Facilitate cell proliferation, migration and apoptosis | Non-small cell lung cancer | (77) |
| Li *et al.*, 2019 | IncRNA XIST, miR-497-5p | miR-191 | IncRNA XIST | Sponge effect | Facilitate cell proliferation, migration | Hepatocellular carcinoma | (78) |
| Zhang *et al.*, 2019 | miR-191 | miR-191 | | Regulation of signaling pathway (axis) | Facilitate cell proliferation | Hepatocellular carcinoma | (79) |
| Hu *et al.*, 2016 | miRNA 21, IncRNA GAS5 | miRNA 21 | IncRNA GAS5 | Transcriptional regulation | Promote cell migration and invasion | Hepatocellular carcinoma | (80) |
| Wu *et al.*, 2015 | IncRNA uc002yu.2 | IncRNA uc002yu.2 | | Post-transcriptional regulation | Promote cell proliferation, migration and invasion | Esophageal cancer | (81) |
| Chen *et al.*, 2014; Kang *et al.*, 2015 | IncRNA ANRIL | | IncRNA ANRIL | Transcriptional regulation | Promote cell proliferation and anchorage-dependent growth; inhibits apoptosis | Esophageal cancer | (82,83) |
| Zhang *et al.*, 2017 | IncRNA CCAT1 | IncRNA CCAT1 | | Epigenetic modification | Promote cell growth, migration, tumour occurrence | Esophageal cancer | (84) |
| Mazzu *et al.*, 2019 | miRNA 193b | miRNA 193b | | Epigenetic modification | Facilitate prostate cancer progression | Prostate cancer | (85) |
| Chen *et al.*, 2019 | miRNA 31-5p, miRNA 223-3p | miRNA 31-5p. miRNA 223-3p | | Post-transcriptional regulation | Promote the occurrence of colon cancer | Colitis-associated cancer | (86) |

miRNA, microRNA; lncRNA, long non-coding RNA; ncRNA, non-coding RNA.
5. Conclusion

In conclusion, the mechanisms by which miRNAs and IncRNAs mediate the occurrence and development of cancer still need further exploration in order to provide broader prospects for cancer treatment. Currently, the miRNA-IncRNA interaction mechanisms are an important part of research and treatment for most cancer types. However, there are numerous challenges to be addressed, such as the safety of miRNAs for the treatment of tumors. Nonetheless, with additional research on ncRNAs in the field of cancer, it is considered likely that the specific mechanism of ncRNA-mediated tumorigenesis and development will be found, offering accurate entry points for the treatment of tumors. Therefore, exploring miRNA and IncRNA interactions could provide new breakthroughs for the clinical treatment of tumors.

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Availability of data and materials

Not applicable.

Authors' contributions

BS and CL wrote the manuscript draft. BS, CL, HL and LZ contributed to the preparation of the manuscript. ML, SL and GL revised the manuscript. BS, CL, ML conceived the design of the figures. All authors read and approved the final manuscript.

Ethics approval and consent to participate

Not applicable.

Patient consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

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