Editorial

Non-coding RNAs in lung cancer

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One of the main causes of worldwide cancer contributed death is lung cancer with two main types, non-small cell lung cancer (NSCLC) and small cell lung cancer (SCLC) (1). lncRNAs are non-coding transcripts, above 200 nt, and play important regulatory roles in many types of cancer including lung cancer progression and development. lncRNAs are known to play roles as oncogenes or tumor suppressors like microRNAs (miRNAs) (2).

Recent work evidenced, lncRNAs (long non-coding RNAs) take part in cancer initiation and progression and showed high degree of deregulation in tumors. New technologies facilitated the novel marker identification with the aid of bioinformatics. In human cancer studies, RNA-seq (RNA sequencing) has shown to played significant roles for identifying potentially new disease markers and illuminated unknown perspectives of tumor molecular biology including novel lncRNA species (3).

In a study by Su *et al.*, as a lncRNA *MIR22HG* with analysis over nine hundred tissues (lung cancer and normal lung tissues) was highly deregulated and its down-regulation was connected with poor survival (4). They showed that lung cancer therapeutic targeting may be illuminated with *MIR22HG*, potentially a new marker in diagnosis and prognosis, to understand cancer-related lncRNAs and their molecular machinery.

MIR22HG is among the most down-regulated lncRNAs in lung cancer when compared to healthy lung tissues and its tumor suppressor role is a key to *MIR22HG* network containing the oncogenes such as YBX1, MET, and p21. Su *et al.* carried out a comprehensive analysis to reveal divergently expressed lncRNAs from three cohorts of RNA-seq data in lung adenocarcinomas (LUAD). *MIR22HG*, a differentially expressed lncRNA in high levels, was found to be reduced at top levels in LUAD. They revealed that the down-regulation of *MIR22HG* may play a role as a tumor suppressor in lung cancer and could step forward as a novel diagnostic marker.

They also used the MiTranscriptome database (3) to determine whether *MIR22HG* expression is involved in other cancer types by utilizing RNA-seq expression data. Results suggested that *MIR22HG* expression profile is commonly lower in many cancer types and may also give precautionary signal in metastatic tumors. Furthermore, their results demonstrated that an increase in cell growth by *MIR22HG* knockdown may related to p21 anti-apoptosis mechanisms to a certain degree and stimulate proliferation of cells in lung cancer (4).

A variety of genes are showed to feature two distinct roles in cancer participating as tumor suppressors or oncogenes including SIRT1, TGFb1, p38a, Myc, E2F1, AMPK, p21, Notch pathway, and Wnt pathway (5). Increased cell growth as a means of *MIR22HG* knockdown may somehow affected p21 anti-apoptosis and boost proliferation of cells in lung cancer indicating that oncogenic feature of p21 in lncRNA-based regulation should extend novel therapeutic aspects (4).

In conclusion, lncRNAs are played roles in molecular

Table 1 Some well-characterized lung cancer associated lncRNAs

No.	Name	References
1.	MIR22HG	(4)
2.	HOTAIR	(6)
3.	CCAT2	(7)
4.	MVIH	(8)
5.	LCAL1	(9)
6.	LUADT1	(10)
7.	AFAP1-AS1	(11)
8.	ANRIL	(12)
9.	UCA1	(13)
10.	MALAT1	(14)
11.	EPEL	(15)
12.	AGAP2-AS1	(16)
13.	ATB	(17)
14.	TCF7	(18)
15.	SBF2-AS1	(19)
16.	FOXD2-AS1	(20)
17.	HOXA11-AS	(21)
18.	PCAT-1	(22)
19.	BCAR4	(23)
20.	CCAT2	(24)
21.	00511	(25)
22.	XIST	(26)
23.	NEAT1	(27)
24.	ZFAS1	(28)
25.	SNHG1	(29)
26.	RGMB-AS1	(30)
27.	TUSC7	(31)
28.	CASC2	(32)
29.	GAS5	(33)
30.	TUG1	(34)
31.	AK126698	(35)
32.	GAS5-AS1	(36)

cancer mechanism as tumor suppressors or oncogenes like *MIR22HG* (*Table 1*). With their tumor suppressor or oncogene actions, lncRNAs may play key roles, but very few of lncRNAs have been characterized to the backbone (37). Su *et al.* demonstrated that *MIR22HG* has a tumor suppressor potential which operate YBX1 by binding and stabilizing so that regulating multiple signals on cell survival and/or death such as cell proliferation, senescence, and apoptosis via targeting oncogenes p21 and MET. *MIR22HG* is potentially a new diagnostic and/or prognostic biomarker and appear to be a therapeutic target for lung cancer treatment. To illuminate the new potential therapeutic strategies, cancer-associated lncRNAs should be further investigated with p21, SIRT1, TGFb1, p38a, Notch pathway, Wnt pathway, E2F1, AMPK, and Myc using RNA-seq, bioinformatics, and related-databases (such as MiTranscriptome) (3). Furthermore, other non-coding RNAs, e.g., miRNAs, and some keystone proteins, such as YB-1, may be included in the research to perform more precise strategies.

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Footnote

Conflicts of Interest: The authors have no conflicts of interest to declare.

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