

## Review Article

# Crosstalk between lncRNAs and Wnt/ $\beta$ -catenin signaling pathways in lung cancers: From cancer progression to therapeutic response

Ting Wu<sup>a</sup>, YiRan Dong<sup>a</sup>, XinZhi Yang<sup>a</sup>, Liang Mo<sup>b,\*\*</sup>, Yong You<sup>a,\*</sup><sup>a</sup> Research Laboratory of Translational Medicine/Laboratory of Protein Structure and Function, Hengyang Medical School, University of South China, Hengyang, 421001, China<sup>b</sup> Department of Thoracic Surgery, The First Affiliated Hospital, Hengyang Medical School, University of South China, Hengyang, 421001, China

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## ABSTRACT

Lung cancer (LC) is considered to have the highest mortality rate around the world. Because there are no early diagnostic signs or efficient clinical alternatives, distal metastasis and increasing numbers of recurrences are a challenge in the clinical management of LC. Long non-coding RNAs (lncRNAs) have recently been recognized as a critical regulator involved in the progression and treatment response to LC. The Wnt/ $\beta$ -catenin pathway has been shown to influence LC occurrence and progress. Therefore, discovering connections between Wnt signaling pathway and lncRNAs may offer new therapeutic targets for improving LC treatment and management. In this review, the purpose of this article is to present possible therapeutic approaches by reviewing particular relationships, key processes, and molecules associated to the beginning and development of LC.

## 1. Introduction

Lung cancer (LC), a significant worldwide health issue, is responsible for around 18% of cancer-related fatalities [1]. Because of its complicated and obscure biological processes that result in unregulated cell growth and metastasis, it leads to the primary cause of cancer-related deaths. LC is commonly categorized into two primary types: small cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC), SCLC accounts for 15%, and NSCLC accounts for 15% of all primary lung cancer cases [2,3]. Lung adenocarcinoma (LUAD), lung squamous cell carcinoma, and large cell carcinoma are the three main pathophysiological subtypes of NSCLC [4]. The prevalence of occurrences involving primary lung cancer has grown in the past few decades. In 2020, lung cancer is the second most commonly diagnosed cancer and the leading cause of cancer death [1]. Active and passive smoking, chronic exposure to carcinogens, ambient air pollution and unidentified risk factors are the most common risk factors for LC [5,6]. As clinical research is rapidly advancing, there are many various therapeutic options accessible for LC include surgical and non-surgical treatments. The non-surgical treatment includes molecularly focused treatment, immunotherapy, chemotherapy, and interventional therapy. Despite the development of

innovative and multimodal treatments, the overall prognosis of individuals with LC remains insufficient [7]. Numerous researches have proposed that the low longevity rate of LC patients may be related to the high variability in tumors and lack of an early diagnosis. Thus, to improve LC patient diagnosis and therapy, it is imperative to investigate the biological properties of LC and identify novel molecular targets.

It was determined that the Wnt signaling pathway is a highly conserved pathway which is essential for determining cell fate and embryonic patterning in all multicellular organisms [8]. This signaling pathway is primarily divided into two distinct types: the canonical signaling pathway, which depends on  $\beta$ -catenin, and the non-canonical signaling pathway, which does not. The latter is further subdivided into the Wnt/calcium and planar cell polarity (PCP) pathways, both of which influence cancer growth and dissemination [9]. The canonical signaling pathway is initiated by Wnt molecules such as Wnt1 and Wnt3a, engaging with a frizzled receptor (Fz) and lipoprotein receptor-related protein (LRP)5/LRP6. Then, Fz binds into and produces a cytoplasmic protein called Disheveled (DVL) in mammals, which causes a concentration of  $\beta$ -catenin in the cytoplasm, its movement into the nucleus, and the transcription of the target gene. The non-canonical pathway is far less researched than the canonical pathway. There are both canonical

\* Corresponding author. Research Laboratory of Translational Medicine/Laboratory of Protein Structure and Function, Hengyang Medical School, University of South China, Hengyang, China.

\*\* Corresponding author. Department of Thoracic Surgery, The First Affiliated Hospital, Hengyang Medical School, University of South China, Hengyang, China.  
E-mail addresses: [moliang@163.com](mailto:moliang@163.com) (L. Mo), [2006001977@usc.edu.cn](mailto:2006001977@usc.edu.cn) (Y. You).

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and non-canonical routes in this evolutionarily conserved signaling system.

According to study, as much as 80 % of the human genetic code maybe converted into non-coding RNAs (ncRNAs) [10]. Among them, lncRNAs are the most prevalent and functionally diverse class [11]. Long non-coding RNAs (lncRNAs) is a transcript with one over 200 nucleotides in length that is not transcribed to proteins [12]. In the last decade, mounting data show that lncRNAs have been proven to remain multiple regulatory functions, such as altering cytoplasmic mRNA stability and translation, interfering with signaling pathways, regulating chromatin function, controlling membrane-free nuclease formation and action [13]. Specifically, numerous kinds of lncRNAs can function as endogenous RNAs (ceRNAs) that compete with sponge microRNAs (miRNAs) to lessen the regulatory impact of miRNAs on target mRNAs. The dysregulation of lncRNAs and the associated ceRNA network are being mentioned to take part in the genesis and progress of various malignant cancer, including LC. For instance, lncRNA SFTA1P was reported to be abnormally expressed in LC, and to inhibit the growth of xenografts and metastasis of LUAD cells by sponging miR-4766–5p via modulating the large tumor suppressor kinase 1 (LATS1)/ Yes-associated protein (YAP) signaling pathway [14,15]. lncRNA PCAT1 was overexpressed in NSCLC tissues, and exerted an oncogenic role and immunosuppression by activating sex-determining region Y-related high-mobility group box 2 (SOX2) to repressing the cyclic GMP-AMP synthase (cGAS)/ stimulator of interferon genes (STING) signaling mediated T-cell activation [16]. Many lncRNAs regulate downstream genes or proteins to influence important pathways in LC biological activities. Although we have made a number of advances in the study of the correlation between lncRNA and the Wnt/ $\beta$ -catenin pathway in many malignancies, the underlying processes of LC pathogenesis and progression are not yet fully understood. Therefore, further studies on the effects of lncRNA interaction with the Wnt/ $\beta$ -actin pathway are necessary. This article emphasizes the sequence of events such as lncRNA involving the Wnt/ $\beta$ -catenin pathway in LC impacting the evolution of lung carcinogenesis. It is hoped that these findings may provide unique and perhaps novel concepts for targeted therapy in LC patients.

## 2. The Wnt/ $\beta$ -catenin pathways related to LC

Several Wnt ligands have high levels in LC, such as Wnt1, Wnt2b, Wnt3a and Wnt5a. Reports indicated that up-regulated Wnt1 ligand can lead to resistance to immune checkpoint inhibitors (ICIs) and promote the advanced stages of LC treated with ICIs [17]. The Wnt2b gene was repressed under the influence of DDX56 down-regulating the mature miR-378a-3p, which was connected to early recurrence in squamous cell lung carcinoma [18]. Furthermore, the interaction of golgi-phosphoprotein 3 (GOLPH3) and cytoskeleton-associated protein 4 (CKAP4) enhanced the secretion of Wnt3a by binding Wnt3a in exosomes, which subsequently driven the Wnt/ $\beta$ -catenin pathway and induced distal metastasis in NSCLC [19]. Also, it was revealed that Wnt5a expression could affect the response of NSCLC cell lines to radiotherapy. The combination of Wnt5a knockdown and irradiation led to decrease translocation of  $\beta$ -catenin from the cytoplasm to the nucleus, which had a connection to the neoplastic features of NSCLC, such as tumor proliferation and apoptosis [20].  $\beta$ -catenin proteins played important roles in tumor formation, and inhibiting LC pathogenesis and delaying LC progression [21]. Further, eIF3a promoted the transcriptional activation of  $\beta$ -catenin and mediates its nuclear accumulation to form a complex with T cell factor 4 (TCF4) contributed to the maintenance of NSCLC stem cell-like characteristics [22]. In addition, it was reported that glycogen synthetic kinase-3 $\beta$  (GSK3 $\beta$ ) plays a correlated with dose role in gefitinib resistance, and serine-arginine protein kinase 1 (SRPK1) increases glycogen synthetic kinase-3 (GSK3) phosphorylation at Ser9 to trigger the Wnt pathway [23]. The Wnt signaling has many downstream targeted genes, including axis inhibition protein 2 (AXIN2), c-Myc and cyclinD1. C-Myc, a traditional

transcription mediators of PD-L1, was overexpressed in multiple types of human carcinomas, including SCLC [24]. According to one study, more than half of Asian patients had AXIN2 promoter methylation, which enhanced nuclear accumulation of  $\beta$ -catenin and was associated with poor survival [25]. In brief, Wnt signaling is emphasized as a viable target for LC precision medicine since it has a role in the development, progression, and medication resistance of LC.

## 3. Interactions between lncRNAs and Wnt signaling pathway in LC

New evidence suggested that a variety of substances may act as regulators or remarkably influence gene expression, regulating the Wnt/ $\beta$ -catenin pathway by altering the expression of a number of lncRNAs [26]. It was established that  $\beta$ -catenin proteins were important regulators that set off the Wnt/ $\beta$ -catenin cascade. The role of the lncRNA/Wnt/ $\beta$ -catenin axis in the etiology of malignant tumors has recently been successfully studied. We draw the conclusion that LC is influenced by the major lncRNA/Wnt/ $\beta$ -catenin axis (Table 1 and Fig. 1).

### 3.1. lncRNA CBR3-AS1

The lncRNA CBR3-AS1, having a transcriptional length of 749 nt, was first discovered to be substantially expressed in prostate cancer [27]. A prior investigation verified the facilitative role of CBR3-AS1 members in various tumor types. In recent studies, CBR3-AS1 expression was shown to be increased in NSCLC. It has proved linked to a poor long-term outcome in patients. In vitro cellular experiments, CBR3-AS1 suppression drove a significant reduction in proliferation, migration, and invasiveness, but an increase in apoptosis [28,29]. CBR3-AS1 was previously revealed to modify the expression of  $\beta$ -catenin proteins in A549 cells. Further CBR3-AS1 could triggered Wnt/ $\beta$ -catenin signaling cascade by inducing nuclear location of  $\beta$ -catenin in LUAD. CBR3-AS1 was knocked down, resulting lowered the activation of Wnt/ $\beta$ -catenin signaling and suggested that decreasing CBR3-AS1 may alter the concentration of  $\beta$ -catenin in the cytoplasm or nucleus. This mechanism encouraged the Wnt signaling pathway to become active, enhancing the expression of Wnt target genes such c-Myc, cyclinD1, LGR5, and MMP-7 as well as modifying cell proliferation, migration and invasion [30].

### 3.2. lncRNA CASC15

lncRNA CASC15 was originally regarded as a key tumor suppressor in carcinoma but was later discovered to play an oncogenic role in many other cancers, such as breast cancer [31], laryngeal squamous cell carcinoma [32], osteosarcoma [33], thyroid carcinoma [34], esophageal squamous cell carcinoma [35] and nasopharyngeal carcinoma [36]. Overexpression of CASC15 was observed in LC tissues, which indicates that CASC15 maybe a potential biomarker [37,38]. CASC15 overexpression has a connection with LC cell neoplasm and could determine longevity time of individuals with advanced-stage disorders [37]. Inhibition of CASC15 significantly weakened the migration and growth ability of A549 and H1299 cells. This is consistent with the findings of laryngeal squamous cell carcinoma in CASC15. According to a paper, inhibiting CASC15 had a negative impact on how lung cancer developed in vivo [39]. In LC, CAS-C15 promotes NSCLC cell proliferation and migration by increasing SOX4 and thereby maintaining the  $\beta$ -catenin protein. Accordingly, several research groups have recently discovered that CASC15 may promote carcinogenesis by activating the Wnt/ $\beta$ -catenin signaling pathway in melanoma and colon cancer, indicating that the CASC15/ $\beta$ -catenin axis exhibited a vital role in the initiation and advancement of cancer [40,41].

**Table 1**  
LncRNAs directly target Wnt/ $\beta$ -catenin signaling pathway in LC.

LncRNA	Oncogene/suppressor	Targeted miRNA	Regulation of Wnt/ $\beta$ -catenin	Biological functions	References
CBR3-AS1	Oncogene	Not available	Activation	Promote the proliferation, migration and invasion of LUAD cells	[30]
CASC15	Oncogene	Not available	Activation	Promote the proliferation and migration of NSCLC cells	[37]
MALAT1	Oncogene	miR-1297	Activation	Suppress the apoptosis and cisplatin(DDP) sensitivity of LUAD cells	[42]
DANCR	Oncogene	miR-216a	Activation	Promote the proliferation, stemness, invasion of NSCLC cells	[43]
LINC00514	Oncogene	Not available	Activation	Promote the proliferation, migration, invasion and epithelial-mesenchymal transition (EMT) of NSCLC cells	[44]
PKMYT1AR	Oncogene	MiR-485-5p	Activation	Promote the proliferation, migration, cell stemness and Xenograft tumor formation of NSCLC cells	[45]
PCAT6	Oncogene	MiR-326	Activation	Promote the proliferation and invasion but suppress the apoptosis of LC cells	[46]
NEAT 1	Oncogene	Not available	Activation	Promote the proliferation, invasion and migration but suppress apoptosis and anlotinib sensitivity of NSCLC cells	[47,48]
ITGB1-DT	Oncogene	Not available	Activation	Promote the proliferation, migration, invasion and Xenograft tumor formation of LUAD cells	[49]
SNHG11	Oncogene	MiR-4436a	Activation	Promote the proliferation and migration of LC cells	[50]
ASB16-AS1	Oncogene	Not available	Activation	Promote the proliferation and inhibit apoptosis of NSCLC cells	[51]
SNHG20	Oncogene	MiR-197	Activation	Promotes the proliferation and inhibits the apoptosis of NSCLC cells	[52]
ACO26356.1	Oncogene	Not available	Activation	Promote the stemness, proliferation and Xenograft tumor formation but increased apoptosis and cisplatin sensitivity of LUAD cells	[53]
LINC00669	Oncogene	Not available	Activation	Promote the proliferation, migration, invasion and Xenograft tumor formation but apoptosis of LUAD cells	[54]
DSCAM-AS1	Oncogene	MiR-577	Activation	Promote the proliferation, migration, invasion, and Xenograft tumor formation but suppress apoptosis of LUAD cells	[55]
UPLA1	Oncogene	Not available	Activation	Promote the proliferation, migration, invasion and Xenograft tumor formation of LUAD cells	[56]
JPX	Oncogene	MiR-33a-5p	Activation	Promote the proliferation, invasion, EMT and Xenograft tumor formation of LC cells	[57]
RPPH1	Oncogene	MiR-326	Activation	Promote the invasion, EMT and resistance to cisplatin/cis-diamminedichloridoplatinum (CDDP) of NSCLC cells	[58]
AOC4P	Suppressor	Not available	Inhibition	Suppress viability and invasion and induce apoptosis of NSCLC cells	[59]
LINC00476	Suppressor	Not available	Inhibition	Suppress the proliferation, migration, invasion and Xenograft tumor formation of NSCLC cells	[60]
DBH-AS1	Suppressor	MiR-155	Inhibition	Suppress the proliferation of NSCLC cells	[61]

### 3.3. LncRNA MALAT1

LncRNA MALAT1 as an oncogene with a high degree of conservation controls radiosensitivity and chemosensitivity in cancer cells, and fosters cancer progression [62,63]. Due to its association with tumor progression in NSCLC, MALAT1 was considered to be a prognostic cytokine that was first identified to be the survival marker [64]. For instance, increased MALAT1 expression in cisplatin (DDP) resistant A549/DDP cells encourages the activity of multiple drug resistance 1 (MDR1) by triggering signal transducer and activator of transcription protein 3 (STAT3) signaling, which decreases sensitivity to DDP and significantly worsens prognosis [65]. In A549/DDP cells, up-regulated expression of MALAT1 was linked to drug resistance through  $\beta$ -catenin/MDR1 signaling. MALAT1 boosted drug resistance in A549/DDP cells via regulating  $\beta$ -catenin/MDR1 signaling via the miR-1297/p300 axis [42]. Also miR-1297 had comparable effects in numerous experiments by regulating different signaling pathways. One study observed that miR-1297 could trigger the PTEN/AKT signaling pathway and Wnt/ $\beta$ -catenin signaling pathway to promote the proliferation of LC cells [66,67]. P300 is a transcriptional co-factor of  $\beta$ -catenin. It has been revealed that the P300/ $\beta$ -catenin complex is essential to activate  $\beta$ -catenin in transduction processes [68]. If p300 and  $\beta$ -catenin form a complex, this might improve the stability and nuclear distribution of p300 as well as enhancing  $\beta$ -catenin/LEF1 mediated transcriptional activity [69]. More research into Wnt/ $\beta$ -catenin signaling in LC is required since more molecular pathways have not yet been discovered.

### 3.4. LncRNA DANCR

LncRNA differentiation-antagonizing non-protein-coding RNA (DANCR) was initially discovered as a suppressor of epidermal ancestral differentiation [70]. In NSCLC, DANCR has been identified as a promoter of tumorigenesis by inhibiting several tumor suppressor miRNAs [43,71,72]. Wnt pathway activating genes are commonly upregulated in

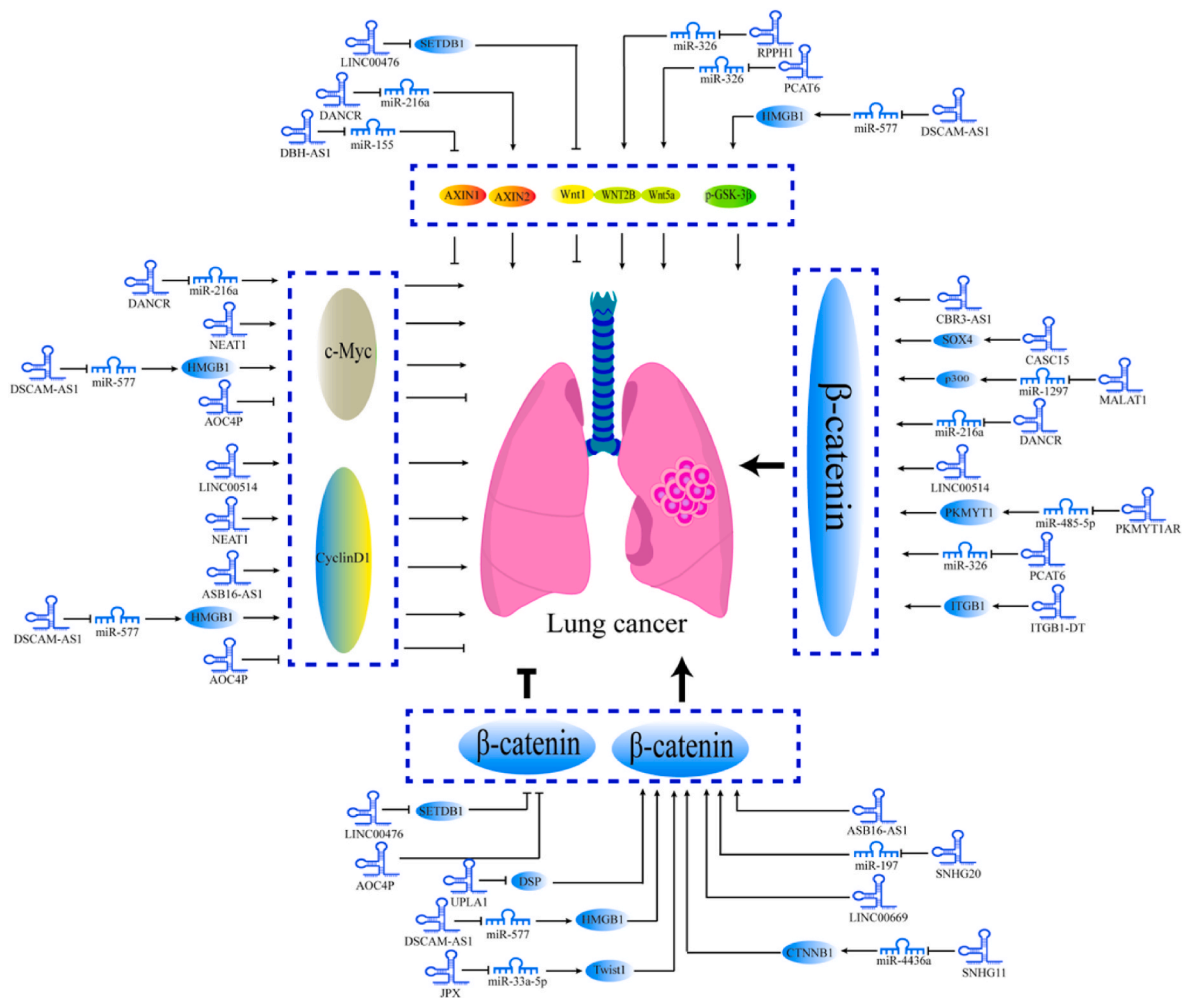
NSCLC tumorigenesis and metastasis whereas negative regulators are down-regulated [73,74]. DANCR expression was dramatically enhanced in diverse groups of NSCLC cell lines, except for H1944 cells. DANCR knockdown led to stem-like properties being reduced, long term clonogenic potential being inhibited, and impedance in cell migration, which are all classic Wnt/ $\beta$ -catenin inactivation features. In addition, DANCR knockdown reduced  $\beta$ -catenin protein expression and Wnt target genes Axin2 and c-Myc both mRNA and protein expression. Upregulation of miR-21-6a was reported to cell growth, invasion, and metastasis but induce apoptosis [75,76]. DANCR is high expressed in NSCLC tumors and cell lines. Silencing DANCR expression in NSCLC cells could inhibit long-term growth, migration and stemness by triggering Wnt/ $\beta$ -catenin signaling through miR-216a suppression [43].

### 3.5. LINC00514

LINC00514 has been shown to be overexpressed in cervical squamous cell carcinoma, gastric cancer, breast cancer and pancreatic cancer [77–80]. Zhu et al. [44] indicated that LINC00514 was significantly upregulated in NSCLC and related to poorer prognosis. They observed that silencing LINC00514 decreased the epithelial mesenchymal transition (EMT)-related proteins (E-Cadherin) and Wnt/ $\beta$ -catenin signaling related proteins ( $\beta$ -catenin, cyclinD), while enhancing N-Cadherin expression. Moreover, they revealed that LINC00514 facilitated cell proliferation, migration, and invasion by triggering the Wnt/ $\beta$ -catenin cascade.

### 3.6. LncRNA PKMYT1AR

The expression of lncRNA protein kinase, membrane associated tyrosine/threonine 1 associated lncRNA (PKMYT1AR) was up-regulated in NSCLC compared with cancer stem cells and peripheral blood serum [45]. Based on the research, PKMYT1AR serves as a sponge for miR-485-5p. MiR-485-5p may target the protein kinase, membrane



**Fig. 1.** LncRNAs related to the Wnt/ $\beta$ -catenin pathway in lung cancer.

associated tyrosine/threonine 1 (PKMYT1), a negative regulator of the typical cell cycle change by phosphorylating Tyr14/Tyr15, which suppressed the cyclin-dependent kinase 1 (CDK1)-cyclinB combination [81]. Therefore, it was a vital target in the activating Wnt/ $\beta$ -catenin pathway and thereby suppress PKMYT1 protein levels. PKMYT1AR could promote the NSCLC cell proliferation, migration and xenograft tumor formation abilities by diminishing miR-485-5p function, increasing PKMYT1 protein expression and activating Wnt/ $\beta$ -catenin pathway.

### 3.7. LncRNA PCAT6

LncRNA PCAT6 is a sort of lncRNAs which has been discovered to have involved in different types of cancer, including LC. PCAT6 was highly expressed in lung cancer samples and cells induced by sevoflurane, and overexpression of PCAT6 reversed the suppression of sevoflurane on viability, proliferation, invasion and enhancement on apoptosis of LC cells. Depletion of PCAT6 was shown to significantly increase miR-326 levels in LC cells. Overexpression of miR-326 inhibits production of Wnt5a which acts as a positive activator of the Wnt/ $\beta$ -catenin pathway [46].

### 3.8. LncRNA NEAT1

Anlotinib an orally administered multi-targeting tyrosine kinase inhibitor (TKI) which is used in the patients with advanced refractory NSCLC [82]. LncRNA NEAT1 has been shown to exert an oncogenic role in NSCLC [83]. Gu et al. [48] [] [] [] observed that NEAT1 considerably

induce the anlotinib resistance by hindering the tumor cell proliferation, migration, and invasion. NEAT1 was involved in the sponging of miR-760 and miR-361-5p. MiR-760 and miR-361-5p could considerably suppress Wnt/ $\beta$ -catenin signaling cascade. Therefore, anlotinib resistance is maintained by NEAT1, which regulates the Wnt/ $\beta$ -catenin pathway.

### 3.9. LncRNA ITGB1-DT

LncRNA ITGB1-DT has been associated with the progression of multiple malignant solid tumors, such as breast cancer, colon cancer, stomach adenocarcinoma and NSCLC [84–87]. ITGB1-DT is significantly elevated in LC, operates as an oncogene in LC, and is the independent risk factors for poor prognosis, and had diagnostic value for NSCLC patients. It has been seen that interfering with the ITGB1-DT expression can decrease the proliferation, migration, and invasion of LC cells, and drug-resistant A549/DDP by influencing the MAPK/ERK signaling pathway [88]. Besides, Chang et al. [88] uncovered that ITGB1-DT may induce epigenetic enhancement of ITGB1 expression, which is reverse transcribed from the ITGB1-DT gene. ITGB1, also known as integrin  $\beta$ 1, was found to exert oncogenic roles in various cancers by regulating AKT/Wnt/ $\beta$ -catenin pathway [89,90]. Thus, by modulating ITGB1, ITGB1-DT activated the Wnt/ $\beta$ -catenin/MYC axis and formed a positive feedback loop, allowing ITGB1-DT silencing as a new potential therapeutic target for LUAD [49].

### 3.10. *LncRNA SNHG11 (lncRNA NCRNA00101)*

According to earlier research, lncRNA SNHG11 functions as an oncogene, preventing the growth of numerous tumors including gastric cancer, colorectal cancer, hepatocellular cancer and NSCLC.

[91–94]. SNHG11 was shown to be highly expressed and correlated with poor patient prognosis, TNM stage and tumor size in LC. Silencing SNHG11 reduced the cancer cells proliferation, invasion, and metastasis *in vitro*, while inhibiting tumor growth *in vivo* [50].

The ceRNAs are RNA transcripts that interact with one another by depressing other mRNAs that share the same miRNA response regions and reducing the production of targeted miRNAs [95]. SNHG11 could act as a sponge for miR-4436. Overexpression of miR-4436 reduces the production of catenin beta 1 (CTNNB1) protein, which positively regulates the Wnt/ $\beta$ -catenin signaling cascade. As a consequence, SNHG11 might thereby increase CTNNB1 protein by blocking miR-4436, which activates the Wnt/ $\beta$ -catenin axis in LC [50].

### 3.11. *LncRNA ASB16-AS1*

The lncRNA ASB16 antisense RNA 1 (ASB16-AS1), located on chromosome 17, has been identified as an oncogene that promotes the development and incidence of several types of cancer [96,97]. The expression of ASB16-AS1 was found to be high expression in NSCLC. Tan et al. [51] that ASB16-AS1 could promote proliferation but inhibits apoptosis of LC cells *in vitro*. Further evidence suggests that ASB16-AS1 overexpression caused the levels of  $\beta$ -catenin and cyclinD1 to reduce considerably but p21 to increase by triggering the Wnt/ $\beta$ -catenin signaling cascade.

### 3.12. *LncRNA SNHG2*

The research has revealed that lncRNA SNHG20 expression was higher in NSCLC cell lines and tissues than the non-tumor cells and tissues [98]. SNHG20 might be functioning as a sponge for miR-197 and inhibit its downstream activity. Wang et al. [52] found out that SNHG20 could promote proliferation but inhibit apoptosis by bounding to miR-197 in a targeted manner. In addition, miR-197 downregulation led to the remarkably down-regulation in TCF and LEF1, while significantly enhancement in nuclear translocation of  $\beta$ -catenin after transfection experiments. As a result, the SNHG-20/miR-197/Wnt/ $\beta$ -catenin axis may have therapeutic potential for NSCLC through influencing the Wnt/ $\beta$ -catenin signaling cascade.

### 3.13. *LncRNA AOC4P*

LncRNA amine oxidase, copper containing 4, pseudogene (AOC4P) is a novel lncRNA which has received much attention. Before that, AOC4P is found to be a novel tumor suppressor in ovarian cancer and hepatocellular carcinoma (HCC) [99,100]. Low expression of AOC4P is positively linked to poor prognostic outcomes in HCC. Li et al. [59] discovered that overexpressing AOC4P inhibited the NSCLC cells proliferation, invasion and tumor growth, while induced apoptosis both *in vitro* and *in vivo*. The Wnt/ $\beta$ -catenin is widely recognized as a significant oncogenic pathway in cancer progression [101]. AOC4P overexpression could hinder the Wnt/ $\beta$ -catenin signaling cascade, leading to decreased  $\beta$ -catenin, cyclinD1, and c-Myc tumor suppressors as Wnt/ $\beta$ -catenin pathway target genes [59]. These findings showed that AOC4P suppressed tumor growth in NSCLC. In conclusion, these lncRNAs are reported to have a substantial connection with prognosis, and it is necessary to further investigate the mechanism by which lncRNAs influence the Wnt/ $\beta$ -catenin pathway. Fortunately, the cited study offers encouraging suggestions for LC diagnostic or therapeutic tactics.

## 4. Biological functions of lncRNAs/wnt/ $\beta$ -catenin axis in LC

lncRNAs exert diverse biological functions of LC through the regulation of Wnt/ $\beta$ -catenin cascades. As it turned out, we described the processes associated with LC actions in Fig. 2, hoping for full insight into the molecular of lncRNAs in LC.

### 4.1. *Cancer cell stemness*

Cancer stem cells (CSCs), a distinct class of cancer cells, have a limitless capacity for self-renewal and differentiation, which aids in the development of treatment resistance and the start, progression, and metastasis of malignant tumors [102,103]. Existing research find that lncRNAs promote cancer stem cell maintenance in lung cancer through activating Wnt signaling pathway. Yu et al. [43] illustrated that DANCRC knockdown could attenuate malignant phenotype and stem-like characteristics in A549 and H19755 cell lines by sponging miR-216a. DANCRC increased NSCLC stemness through the activation of CSC regulators Wnt and Sox2 and the action was found inversely correlated with activating Wnt/ $\beta$ -catenin signaling through suppressing miR-216a. Moreover, m6A-mediated up-regulation of lncRNA-AC026356.1 induced cell stemness by the mediation of upstream molecule METTL14 and IGF2BP2. It suggests that there might be a METTL14/IGF2BP2/AC026356.1 loop that regulates cancer stemness via activating Wnt signaling pathway in LUAD [53].

### 4.2. *Proliferation and apoptosis*

A variety of cancer treatments, including radiation therapy and cytotoxic chemotherapeutic drugs, have as their primary objective the inhibition of cancer cell growth and proliferation, which is an efficient technique to halt the course of cancer. Wnt/ $\beta$ -catenin are essential signals that govern cell growth and proliferation. By preventing  $\beta$ -catenin from nuclear translocation and decreasing downstream transcription factor T cell factor 1 (TCF-1), LINC00669 activates Wnt/ $\beta$ -catenin to promote cell proliferation but inhibit apoptosis [54]. Also, DSCAM-AS1 knockdown inhibited cell proliferation but promoted apoptosis by sponging miR-577 and reducing HMGB1 protein expression under the control of the Wnt/ $\beta$ -catenin pathway in NSCLC [55].

### 4.3. *Migration and invasion*

Invasion and metastasis are the primary causes of shorter life expectancy for patients, as they are the basic characteristics of malignant tumors. lncRNAs that promote lung cancer cell migration and invasion are up-regulated in lung cancer tissues. For instance, LINC00514 increases the migration and invasion of NSCLC. On the one hand, LINC00514 silencing reduced TCF/LEF1 activity, demonstrating yet another way that LINC00514 knockdown inactivated Wnt signaling in NSCLC cells; on the other hand, down-regulation of LINC00514 inhibited migration and invasiveness abilities of cells and tumor xenograft growth [44]. The Wnt/ $\beta$ -catenin pathway is recognized as carcinogenic. Functionally, the lncRNA LUAD-associated transcript-1 (UPLA1) promotes cell invasion and proliferation in LUAD. Mechanistically, By binding to desmoplakin (DSP), UPLA1 increased Wnt/ $\beta$ -catenin signaling and was discovered to be negatively controlled by the transcription factor YY1 [56].

### 4.4. *Epithelial mesenchymal transition*

Epithelial cells can turn into mesenchymal cells through a process known as EMT. During this process, epithelial cells gradually shed their epithelial identity in favor of more mesenchymal characteristics, such as a spindle-like shape and a lack of intercellular adhesion. The partial or complete activation of EMT is necessary for the malignant growth of many malignant tumors in addition to its function in pathophysiological

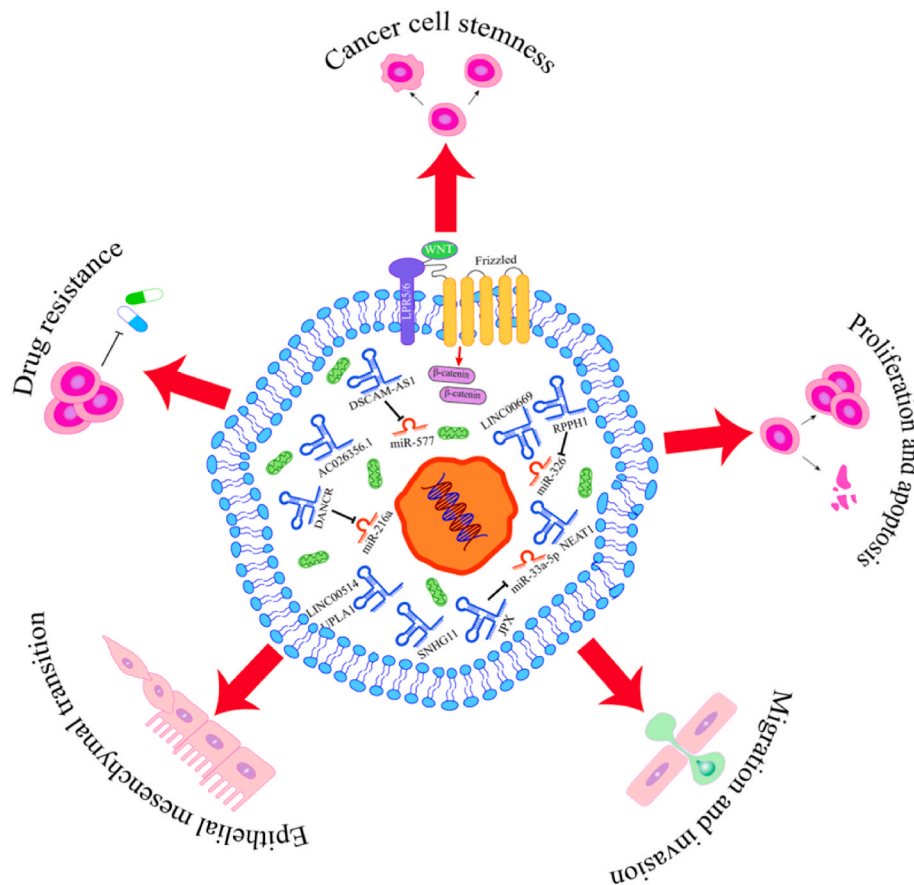


Fig. 2. The mechanism and function of lncRNAs in lung cancer progression.

processes including embryonic development and wound healing. By attaching to the appropriate ligand of the tumor cell and initiating a series of cascade events in the cell, the tumor microenvironment releases particular signals that activate the EMT program. TGF, WNTs, and NOTCH are examples of signaling pathways associated with EMT [104]. The up-regulation of LINC00514 was observed in non-small cell lung cancer lines and clinical samples, which activated Wnt pathway and triggered EMT by positively regulating the expression of Wnt [44]. Pan et al. [57] found that lncRNA JPX promoted cell proliferation, EMT and cell invasion in lung cancer by inhibiting the tumorigenesis and metastasis processes triggered through miR-33a-5p/Twist1 axis by activating Wnt/ $\beta$ -catenin signaling. It has been found that SNHG11 was high expressed in LC and played the role of tumor oncogene. SNHG11 can directly bind with  $\beta$ -catenin to activate classic Wnt pathway by facilitating the EMT process [50].

#### 4.5. Drug resistance

These lncRNAs that impede drug resistance are frequently found to exhibit high expression levels in drug resistant lung cancer cells. This finding holds significant importance in the selection and application of targeted therapeutics. RPPH1 promoted tumor development by inducing invasion and EMT in lung cancer cells. In cellular experiments, RPPH1 might improve A549 and H1299 resistance to cisplatin/cis-diamminedichloridoplatinum (CDDP) therapy by enhancing cell viability and colonial formation. Furthermore, in vitro research revealed that RPPH1 promoted NSCLC advancement via regulating miR-326 and WNT2B [58]. In addition to this, lncRNAs also influence drug resistance by regulating cell proliferation and apoptosis. The existence of cancer stemness is the main cause of drug resistance. The AC026356.1 has been observed to enhance resistant to erlotinib treatment by increasing

stemness of stem-like LC cells in the context of LC therapy. Researchers have demonstrated that m6A-mediated AC026356.1 expression was substantially up-regulated in stem cells and chemoresistant LC cells. As a result, silencing AC026356.1 markedly suppressed proliferation and migration but increased apoptosis in A549/DDP cells [53]. By suppressing proliferation but increasing apoptosis, NEAT 1 knockdown sensitizes NSCLC cells to chemotherapy. Mechanistically, NEAT 1 knockdown enhances the anti-apoptotic and cytotoxic effect of anlotinib, making NSCLC cells more sensitive to anlotinib through down-regulation of the Wnt/ $\beta$ -catenin signaling cascade [48]. Anlotinib paired with NEAT 1 knockdown therapy offers unique insights into creating a combination therapeutic strategy to chemotherapy insensitivity in LC patients. Nevertheless, the mechanism through which lncRNA acts as a positive regulator in the treatment of LC still require more in-depth analysis.

## 5. Clinical applications of lncRNAs and wnt/ $\beta$ -catenin signaling in LC

In order to find more positive and useful clinical applications for LC patients, we enlarge on the crucial roles played by lncRNAs and the Wnt/ $\beta$ -catenin cascade in LC. Accordingly, we further concentrate on the potential targets of lncRNAs and Wnt/ $\beta$ -catenin pathway as well as diagnostic biomarkers and prognostic biomarkers.

### 5.1. Effective diagnostic biomarkers

The majority of cancer biomarkers used today are proteins or peptides whose alterations in tissue or blood levels indicate the development of the tumor [105]. But the invasive and uncomfortable nature of biopsy or blood makes it difficult to use. So, it is vital to create

non-protein biomarkers that are very sensitive and non-intrusive. Due to the absence of recognizable symptoms in the early stages of LC, the majority of patients only have limited survival spans after they are detected. As a result, specialists have recently investigated more accurate LC diagnostic biomarkers [106,107]. Based on reports, increased expression of ASB16-AS1 contributed to promoting proliferation while inhibiting apoptosis in NSCLC through the Wnt/ $\beta$ -catenin signaling pathway [51]. It was previously reported that NEAT1 functioned as an oncogene in NSCLC through regulating the Wnt signaling pathway [47]. Additional investigation is needed to better understand the diagnostic functions of lncRNAs in LC.

### 5.2. Possible prognosis biomarkers

Effective prognostic biomarkers are now essential for estimating the likelihood of LC recurring in clinical practice. HIF1A-AS2, a KRAS responding lncRNA, was found to be elevated in LC and its high expression was correlated with poor patient prognosis. HIF-1A-AS2 and MYC formed a double-regulatory loop that could promote cell survival, tumor growth and metastasis [108]. Increased levels of LINC00669 was generally linked with a bad prognosis. When the expression level of LINC00669 was down, the cell proliferation was weakened while apoptosis was enhanced by inactivating Wnt/ $\beta$ -catenin pathway in NSCLC [54]. These findings offer a wide range of indicators to properly estimate the likelihood of recurrence in LC patients.

## 6. Conclusion

LC is a prevalent illness that poses a major global health risk to people. The Wnt/ $\beta$ -catenin signaling pathway is a widely acknowledged oncogenic pathway that is implicated in the beginning and progression of a broad variety of human malignancies, including LC. In several studies, lncRNAs have been shown to affect the Wnt/ $\beta$ -catenin signaling pathway in LC. In this review, we summarized the essential signaling cascade of the Wnt/ $\beta$ -catenin signaling pathway and emphasized the critical functions of lncRNAs in regulating this pathway in LC.

As previously indicated, mounting data suggests that the Wnt/ $\beta$ -catenin signaling system is crucial to the initiation and spread of human malignancies. The Wnt/ $\beta$ -catenin signaling pathway has been implicated in multiple roles, including normal embryonic development, tissue differentiation, tissue homology, and carcinogenesis [109]. By activating  $\beta$ -catenin, Wnt signaling controls several processes of cancer cells, including invasion, proliferation, flexibility and cell cycle determination [110]. This review suggests that the lncRNA-regulated Wnt/ $\beta$ -catenin pathway functions as a carcinoma promoter as well as suppressor. Therefore, for lncRNAs to be used in therapeutic settings going forward, a deeper comprehension of the intricate mechanisms behind their impact on the Wnt/ $\beta$ -catenin pathway is required.

It has been established that lncRNAs, a class of ncRNA transcripts, are functional components engaged in a variety of biological processes in human malignancies, including angiogenesis, metastasis, apoptosis, and cell survival. According to research, lncRNAs could regulate several important pathways connected to cancer, including the STAT3, PI3K-AKT-mTOR, and Notch pathways [111–113]. In this paper, we compiled 21 lncRNAs linked to the Wnt/ $\beta$ -catenin pathway in LC, 18 of which are up-regulated and 3 of which are down-regulated. Mechanistically, in the nucleus, lncRNAs participate in the nuclear localization or degradation of  $\beta$ -catenin to regulate the Wnt/ $\beta$ -catenin signaling pathway. In the cytoplasm, lncRNAs can act as sponges to compete for binding miRNAs or interact with proteins, including Wnt/ $\beta$ -catenin pathway components and their regulatory proteins, thereby affect their stability and activity. As described in our paper, the SNHG20 activates the Wnt/ $\beta$ -catenin pathway by sponging miR-197 and promoting the nuclear localization of  $\beta$ -catenin in NSCLC but suppresses the activity of TCF and LEF1 [52].

According to a clinical standpoint, a number of studies have pointed

out that potential therapeutic and prognostic biomarkers might be molecules connected to the lncRNA-Wnt/ $\beta$ -catenin regulatory axis such as the FOXO1/lncRNA LYPLAL1-DT/hnRNPK/ $\beta$ -catenin signaling axis in triple-negative breast cancer (TNBC) [114]. It should be acknowledged that there are still a lot of restrictions. First, it is important to assess if a lncRNA expression pattern is sufficiently stable to serve as a predictive biomarker. Establishing a consistent analytical process including sample processing, recognition techniques, and standard values is also crucial. In addition, irregular Wnt/ $\beta$ -catenin signaling pathways are often not exclusively caused by lncRNAs. The Wnt/ $\beta$ -catenin pathway and other signaling pathways also communicate with one another. Applying this treatment technique clinically is quite difficult because of the need to ensure the physiological functioning of Wnt/ $\beta$ -catenin pathway while targeting it selectively. Thus, it is necessary to do more research to see whether these compounds can be used clinically to treat LC. There are still many unidentified lncRNAs in the regulatory network of the Wnt/ $\beta$ -catenin signaling pathway, and our understanding of how lncRNAs regulate the Wnt/ $\beta$ -catenin pathway is still lacking. Research has shown that lncRNAs have no effect on the activity of the Wnt/ $\beta$ -catenin pathway by a single biochemical mechanism. To gain greater understanding of the Wnt/ $\beta$ -catenin pathway and LC development, more research into the unique genetic signals controlling this process is crucial.

In summary, our analysis outlined the intricate underlying processes and demonstrated the role of lncRNAs in the Wnt/ $\beta$ -catenin signaling pathway regulation network to offer new insights into the initiation of LC. These findings also suggest that a novel approach to identifying and treating LC might involve focusing on these lncRNAs or Wnt/ $\beta$ -catenin pathway elements.

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## CRediT authorship contribution statement

**Ting Wu:** Writing – review & editing, Writing – original draft, Validation, Conceptualization. **YiRan Dong:** Visualization, Validation. **XinZhi Yang:** Visualization, Validation. **Liang Mo:** Visualization, Validation, Supervision, Funding acquisition, Conceptualization. **Yong You:** Visualization, Validation, Supervision, Funding acquisition, Conceptualization.

## Declaration of competing interest

- (1) Guarantee that there are no duplicate publications or multiple submissions.
- (2) We guarantee that there is no conflict of interest due to financial interests or other relationships.
- (3) All authors have read the article and agreed to publish it, all authors are eligible for authorship, and all authors agree that the article represents their real research results and that they are responsible for the article.
- (4) The corresponding author of the article is responsible for contacting the first author to revise and finally review the review draft.

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## Abbreviation

LC	Lung cancer
LncRNAs	Long non-coding RNAs
SCLC	Small cell lung cancer
NSCLC	Non-small cell lung cancer
LUAD	Lung adenocarcinoma
PCP	Planar cell polarity
Fz	Frizzled receptor
LRP	Lipoprotein receptor-related protein
DVL	Disheveled in mammals
NcRNAs	Non-coding RNAs
Ce-RNAs	Endogenous RNAs
MiRNAs	MicroRNAs
LATS1	Large tumor suppressor kinase 1
YAP	Yes-associated protein
SOX2	Sex-determining region Y-related high-mobility group box 2
cGAS	Cyclic GMP-AMP synthase
STING	Stimulator of interferon genes
ICIs	Immune checkpoint inhibitors
GOLPH3	Golgi phosphoprotein 3
CKAP4	Cytoskeleton-associated protein 4
TCF4	T cell factor 4
GSK3 $\beta$	Glycogen synthase kinase-3 $\beta$
SRPK1	Serine-arginine protein kinase 1
GSK3	Glycogen synthase kinase-3
AXIN2	Axis inhibition protein 2
SOX4	Sex-determining region Y-related high-mobility group box 4
DDP	Cisplatin
MDR1	Multiple drug resistance 1
STAT3	Signal transducer and activator of transcription protein 3
DANCR	Differentiation-antagonizing non-protein-coding RNA
EMT	Epithelial mesenchymal transition
E– Cadherin	EMT-related proteins
PKMYT1AR	Protein kinase, membrane associated tyrosine/threonine 1 associated lncRNA
PKMYT1	Protein kinase, membrane associated tyrosine/threonine 1
TKI	Tyrosine kinase inhibitor
CTNNB1	Catenin beta 1
ASB16-AS1	ASB16 antisense RNA 1
AOC4P	Amine oxidase, copper containing 4, pseudogene
CSCs	Cancer stem cells
TCF- 1	T cell factor 1
DSP	Desmoplakin
UPLA1	LUAD-associated transcript-1
CDDP	Cisplatin/cis-diamminedichloridoplatinum

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