



Research updates on the clinical implication of long noncoding RNA in digestive system cancers and chemoresistance

Xinzhi Miao^{1,3,6} · Fang Wang^{2,3,6} · Tianyun Wang^{2,6} · Siti Razila Abdul Razak⁴ · Muhammad Amir Yunus⁵ · Ida Shazrina Ismail³

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Abstract

Long noncoding RNAs (lncRNAs) are implicated in various biological processes, such as cell proliferation, differentiation, apoptosis, migration, and invasion. They are also key players in various biological pathways. lncRNA was considered as ‘translational noise’ before 1980s. It has been reported that lncRNAs are aberrantly expressed in different cancers, either as oncogene or tumor suppressor gene. Therefore, more and more lncRNAs are recognized as potential diagnostic biomarkers and/or therapeutic targets. As competitive endogenous RNA, lncRNAs can interact with microRNA to alter the expression of target genes, which may have extensive clinical implications in cancers, including diagnosis, treatment, prognosis, and chemoresistance. This review comprehensively summarizes the functions and clinical relevance of lncRNAs in digestive system cancers, especially as a potential tool to overcome chemoresistance.

Keywords Long noncoding RNA · Diagnostic biomarker · Colorectal cancer · Gastric cancer · Pancreatic cancer · Chemoresistance

Introduction

Noncoding RNA is a type of RNA that is transcribed, but not translated into protein, such as transfer RNA, ribosomal RNA, and microRNA. It has been demonstrated that non-coding RNAs can act as key regulators of gene expression

in diverse cellular systems, biological processes, and various pathways (Yu et al. 2019b; Ferre et al. 2016; Barangi et al. 2019; Lin and Yang 2018). Long noncoding RNA (lncRNA) is defined as the transcripts exceeding 200 nucleotides that are not translated into protein. In the late 1980s and early 1990s, lncRNA H19 and Xist were first found in mouse

✉ Tianyun Wang
wty@xxmu.edu.cn

✉ Ida Shazrina Ismail
idashazrina@usm.my

Xinzhi Miao
miaoxinzhi@hotmail.com

Fang Wang
529324705@qq.com

Siti Razila Abdul Razak
sitirazila@usm.my

Muhammad Amir Yunus
amiryunus@usm.my

³ Regenerative Medicine Cluster, Advanced Medical and Dental Institute, Universiti Sains Malaysia, 13200 Kepala Batas, Penang, Malaysia

⁴ Oncological and Radiological Sciences Cluster, Advanced Medical and Dental Institute, Universiti Sains Malaysia, 13200 Kepala Batas, Penang, Malaysia

⁵ Infectomics Cluster, Advanced Medical and Dental Institute, Universiti Sains Malaysia, 13200 Kepala Batas, Penang, Malaysia

⁶ International Joint Research Laboratory for Recombinant Pharmaceutical Protein Expression System of Henan, Xinxiang Medical University, Xinxiang 453003, Henan Province, China

¹ The School of Medical Humanities, Xinxiang Medical University, Xinxiang 453003, Henan Province, China

² Department of Biochemistry and Molecular Biology, Xinxiang Medical University, Xinxiang 453003, Henan Province, China

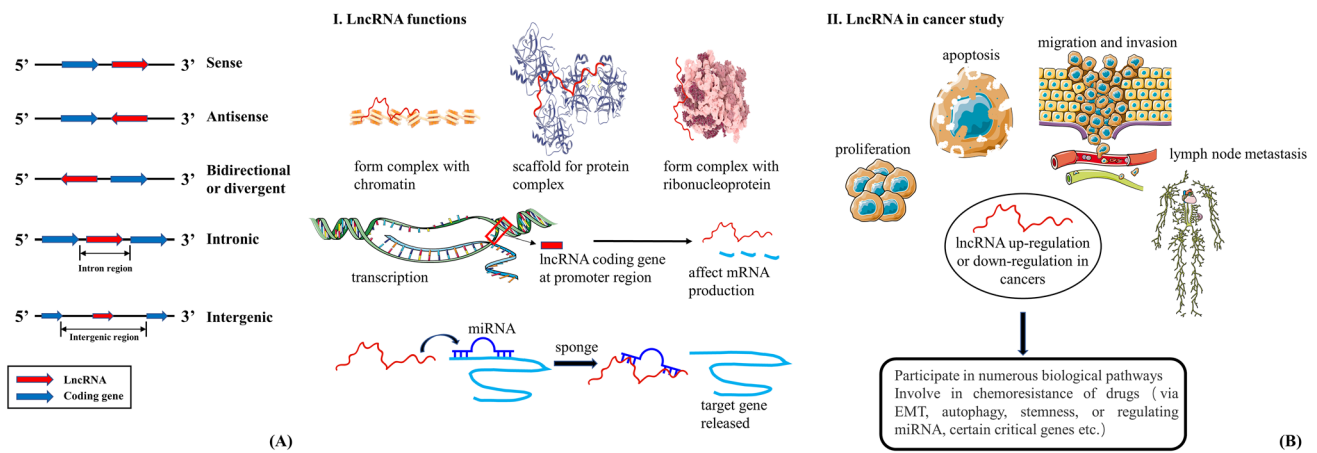


Fig. 1 **A** The type of lncRNAs. Sense, antisense, bidirectional or divergent lncRNA respectively, represent the transcription direction of lncRNA and its neighboring protein-coding genes, either in the same, or opposite, or at different directions. Intronic and intergenic lncRNA represent whether a lncRNA is transcribed from the intron region of the gene or from the intergenic region. **B** The roles and functions of lncRNA. **I** LncRNA can mediate gene expression in different ways: lncRNA can form complex with chromatin, different proteins or ribonucleoprotein, lncRNA can acts as cis-acting element

to interfere with the transcription of downstream mRNA production, target gene will be released from miRNA when lncRNA sponge to miRNA. **II** LncRNAs are involved in many biological processes which are investigated in cancer study such as cell proliferation, apoptosis, migration, invasion, and lymph node metastasis. Aberrant expression of lncRNAs is usually found in cancers, and it has been proved to play an important role in various pathways as well as in chemoresistance study

(Brannan et al. 1990; Brockdorff et al. 1991). Since then, lncRNA has attracted significant attention and becomes one of the hot topics of research interest. lncRNAs can be divided into several subclasses (Fig. 1A) according to their genomic position related to the neighboring genetic code gene: sense, antisense, bidirectional or divergent, intronic and intergenic lncRNA (Herrera-Solorio et al. 2017). Sense, antisense, bidirectional, or divergent lncRNA, respectively, represent the transcription direction of lncRNA and its neighboring protein-coding genes, either in the same, or opposite, or at different directions. Conversely, intronic and intergenic lncRNA represent whether a lncRNA is transcribed from the intron region of the gene or from the intergenic region. lncRNAs are generally, but not exclusively, spliced and transcribed by RNA polymerase II and were considered as ‘translational noise’ previously (Quinn and Chang 2016). However, increasing evidence has proven that lncRNAs perform many functions, such as mediating chromatin remodeling, acting as scaffold linking different proteins interaction and regulate transcription regulation (Chen and Carmichael 2010). At the transcriptional level, the production of mRNA can be affected by lncRNAs. Some lncRNAs gene are located at the promoter region, upstream of the coding gene, and can be transcribed into corresponding lncRNAs, which then acts as a cis-acting element to interfere with the transcription of downstream genes; thereby, affecting the production of mRNA (Martens et al. 2004). Previous studies have also found that lncRNA can form a complex with ribonucleoprotein to regulate gene expression

(Ponting et al. 2009). At post-transcriptional level, lncRNA can form complex with pre-mRNA, therefore, regulate the gene expression at post-transcription stage (Beltran et al. 2008). Also, lncRNA can bind to miRNA and indirectly affect the downstream process.

lncRNAs are involved in many biological processes, including cell proliferation, migration, and invasion (Liu et al. 2017), differentiation (Chen et al. 2017c), metastasis (Chen et al. 2017d), inflammation (Du et al. 2017b), angiogenesis (Li et al. 2017d), and metabolism (Fan et al. 2017), and so can regulate the pathophysiological processes in cancer and other human diseases. Aberrant expression of lncRNAs is usually found in cancers, which is associated with tumorigenesis by promoting malignant biological behaviors of tumor cells, such as proliferation, invasion, and metastasis (Xiao et al. 2017a; Weidle et al. 2017). Cancer-related lncRNAs can be oncogene or tumor suppressor gene depending on their dysregulated expression and corresponding function.

The number of lncRNA-related studies is increasing rapidly and new lncRNAs are identified continuously, but their functions have not been completely characterized. In this mini-review, we briefly summarize the lncRNAs implicated in digestive system cancers and their clinical relevance, with a particular focus on the multiple roles of lncRNAs in genetic alteration, molecular mechanisms and signaling pathways involved in tumor progression, metastasis, and chemoresistance.

lncRNAs in cancers

Numerous reports have showed aberrant expression, various functions as well as chemoresistance of lncRNAs in different cancers (the functions and roles of lncRNAs are displayed in Fig. 1B). Some lncRNAs are up-regulated, as oncogenes, while others are down-regulated, as tumor suppressors.

Some lncRNAs are involved in many biological processes such as cell proliferation, migration, invasion, apoptosis, lymph node metastasis, and pathological differentiation (Liu et al. 2018f), although the specific mechanisms remain unclear so far. Some lncRNAs are functional in different pathways such as Wnt/ β -catenin signaling pathway (Zhou et al. 2019a), p53 pathway, and AKT/mTOR signaling pathway (Yu et al. 2017b). In addition, there are lncRNAs that are involved in more than one pathway such as lncRNA MEG3, NF- κ B pathway, p53 signaling pathway, and PI3K/Akt pathway (Zhang et al. 2017a, 2018g; Zhu et al. 2019b). miRNA is a type of noncoding RNA with 19–25 nucleotides. miRNA is involved in many aspects of biological regulation, including regulation of cell cycle, differentiation, development, metabolism, and body aging. miRNA also serves as a potential tumor molecular marker. A change in miRNA expression is related to the progression of the tumor (Lee and Dutta 2009). lncRNAs may act as a regulator by targeting miRNA, functioning as a ‘sponge’ or competing endogenous RNA (ceRNA). Thus, it can diminish the regulatory effect of miRNAs on target mRNA. For instance, 3'-untranslated region of lncRNA FOXD2-AS1 could directly bind to miR-150-5p in breast cancer (Jiang et al. 2019a); NR2F2-AS1 functions as ceRNA that directly binds to miR-320b to regulate downstream target gene and promote tumorigenesis in nonsmall cell lung cancer (Zhang et al. 2018e); and lncRNA UCA1 regulates colorectal cancer through modulating miR-28-5p, where UCA1 binds to miR-28-5p, then targets HOXB3 to mediate cell proliferation and migration of colorectal cancer cells (Cui et al. 2019). These lncRNAs can be potential therapeutic targets because they play pivotal functions via miRNA to modulate the malignancy and tumorigenesis of diverse cancers.

lncRNAs in digestive system cancers

Colorectal cancer (CRC) and gastric cancer are among the most common malignant cancers associated with high morbidity and mortality. With the increasing cases of colorectal cancer, the development of diagnostic indicators for early diagnosis and treatment has become a common concern of many scientific and clinical researchers. It is currently known that the carcinoembryonic antigen level is a good tumor marker and can be used as a reference or an indicator

in judging the disease development, treatment efficacy, as well as in monitoring and prognostic evaluation. However, the lack of high specificity and sensitivity is making it unsuitable and ineffective as an early diagnosis tool of colorectal cancer (Wang et al. 2014).

A study has shown that after a 5-year follow-up, around 70% patients with gastric cancer (GC) died from this disease globally (Verdecchia et al. 2007). Smoking, alcohol drinking, eating habits, and *Helicobacter pylori* infection are significant risks of GC. The interaction between host-related factors and environmental factors is a key factor in the high mortality rate of GC. The patients were often diagnosed as GC in late stages, when the metastasis has occurred, and the prognosis is quite poor while the palliative chemotherapy is the main treatment method (Digkila and Wagner 2016). Pancreatic cancer (PC) is not common, but aggressive at high growth rate, often diagnosed at late stages. Owing to the poor early diagnosis, most patients have already lost the surgery opportunities when diagnosed. Although the median survival period after diagnosis is around 2–8 months, the 5-year survival rate is only 5% which is largely contributed to the poor prognosis of the disease. The etiology of pancreatic cancer is unclear so far, and its occurrence and development are an extremely complex process. Epidemiological investigation results have shown that the occurrence and development of pancreatic cancer are related to a variety of risk factors. Long-term smoking, high-fat diet, and chronic pancreatitis or concomitant diabetes are nongenetic factors in the onset of pancreatic cancer (Rebello et al. 2017).

In the recent years, more studies have shown that lncRNA participates in the regulation of tumors at both molecular and cellular levels, rendering their potential as important indicators for the diagnosis, treatment, and prognosis of digestive system cancer (Lv and Huang 2019; Deng et al. 2020; Gao et al. 2020). In addition, miRNAs have been proven to be involved in tumorigenesis and development, angiogenesis, metastasis, invasion, and apoptosis by inhibiting/promoting the expression of oncogene. The ceRNA regulatory network composed of lncRNA–miRNA–mRNA network has been revealed in digestive system cancer study (Gong et al. 2018; Lv and Huang 2019; Chen et al. 2017b). lncRNAs can bind to miRNAs as ceRNA, suppress the expression of miRNA, and negatively regulate the downstream target gene. Thus, by interfering the lncRNA expression, the proliferation, and invasion of cancer cells can be inhibited, and cancer progression can be prevented. Some lncRNAs are shared by different digestive system cancers, but function via different mechanisms. For example, lncRNA CRNDE acts as a regulator by targeting miR-217, miR-136, miR-181a-5p (Han et al. 2017) in CRC, miR-384 in PC (Wang et al. 2017a), and miR-145 in GC (Hu et al. 2017). Several new lncRNAs are found only in a single cancer and implicated in some basic biological processes. Table 1 summarizes the functions and

Table 1 Summary of different lncRNAs and their clinical relevance in digestive system cancers

lncRNA designation	Cancer type	lncRNA role	Biological processes and/or pathways involved	Clinical relevance	References
<i>Digestive system (C = colorectal cancer; G = gastric cancer; P = pancreatic cancer; O = oncogene; T = tumor suppressor)</i>					
BCYRN1	Colorectal, Gastric	O	Cell proliferation, apoptosis, tumor size, pathological stages, regulate expression of epithelial cell adhesion molecules	Biomarker	Gu et al. (2018a), Ren et al. (2018a)
CRNDE	Colorectal, Gastric, Pancreatic	O	Regulate DUSP5 and CDKN1A ^C expression; targeting miR-217 ^C , miR-136 ^C , miR-181a-5p ^C , miR-384 ^P , miR-145 ^G ; PI3K/AKT signal pathways ^G , Wnt/ β -catenin signaling pathway ^C , Ras/MAPK signaling pathways ^C	Metastasis, chemoresistance	Ding et al. (2017), Han et al. (2017), Du et al. (2017a), Yu et al. (2017a), Wang et al. (2017a), Jiang et al. (2017a), Hu et al. (2017), Gao et al. (2017a)
GASS	Colorectal, Gastric, Pancreatic	T	Targeting miR-182-5p ^C , miR-222 ^G , miR-23a ^G , miR-106a-5p ^G , miR-32-5p ^P , miR-181c-5p ^P , miR-221 ^{C,P} ; Wnt/ β -catenin signaling pathway ^C , PTEN/Akt/Mtor pathway ^G	Prognosis, metastasis, chemoresistance	Song et al. (2019), Li et al. (2017h), Liu et al. (2016, 2018b, 2018d), Dong et al. (2019b), Gao et al. (2017c, 2018), Cheng et al. (2018)
CYTOR	Colorectal, Gastric	O	regulate Bcl-2 ^G ; Targeting miR-3679-5p ^C , miR-139-5p ^{C,G} , miR-193a-3p ^G , miR-193b-3p ^G , miR-206 ^C , miR-376c-3p ^C ; Wnt/ β -Catenin Signaling pathway ^{C,G}	Metastasis, chemoresistance	Li et al. (2019a), Yue et al. (2018), Shang et al. (2019), Mao et al. (2019), Chen et al. (2018b), Huang et al. (2018b), Bian et al. (2017), Sun et al. (2018a), Shan et al. (2017), Zhang et al. (2016b)
NEAT1	Colorectal, Gastric, Pancreatic	O	Targeting miR-495-3p ^C , miR-196a-5p ^C , miR-34a ^C , miR-17 ^C , miR-335-5p ^G , miR-506 ^G , miR-302a-3p ^P , miR-506-3p ^P , miR-335-5p ^P ; Wnt/ β -catenin signaling pathway ^C	Prognosis	He et al. (2019b), Wang et al. (2018a, 2018c), Tan et al. (2019), Luo et al. (2019b, 2019a), Huang et al. (2017), Cao et al. (2016), Zhong et al. (2018)
UCA1	Colorectal, Gastric	O	Targeting miR-28-5p ^C , miR-18a ^C , miR-182 ^C , miR-203 ^G , miR-495-3p ^G , miR-7-5p ^G , miR-590-3p ^G , miR-107 ^P , miR-96 ^P ; PI3K-Akt-Mtor signaling pathway ^G , Hippo pathway ^P	Prognosis, metastasis, chemoresistance	Cui et al. (2019), Gong et al. (2018, 2019), Sun et al. (2019), Yang et al. (2018b), Gu et al. (2018b), Li et al. (2017a), Horita et al. (2019), Zhang et al. (2018b), Zhou et al. (2018a)
SNHG6	Colorectal, Gastric	O	Targeting miR-181a-5p ^C , miR-26a/b ^C , miR-214 ^C , miR-760 ^C , miR-101-3p ^G ; TGF- β /Smad signaling pathway, PI3K/AKT/Mtor pathway ^C , JNK pathway ^G	Prognosis, metastasis	Yu et al. (2019a), Wang et al. (2019d), Meng et al. (2019), Zhang et al. (2019a), Xu et al. (2019), Zhu et al. (2018c), Yan et al. (2017), Li et al. (2018a)
XIST	Colorectal, Gastric, Pancreatic	O	Regulates the EGF receptor ^P ; Targeting miR-486-5p ^C , miR-30a-5p ^C , miR-124 ^C , miR-137 ^C , miR-486-5 ^C , miR-185 ^G , miR-497 ^C , miR-141-3p ^P , miR-429 ^P , miR-34a-5p ^P , miR-133a ^P	Metastasis, treatment target, chemoresistance	Chen et al. (2017a), Liu et al. (2019a, 2019b, 2018e), Zhang et al. (2018c, 2019c), Zhu et al. (2018a), Ma et al. (2017), Sun and Zhang (2019), Shen et al. (2019), Zou et al. (2019), Sun et al. (2018b), Wei et al. (2017)

Table 1 (continued)

lncRNA designation	Cancer type	lncRNA role	Biological processes and/or pathways involved	Clinical relevance	References
PVT1	Colorectal, Gastric	O	Targeting miR-214-3p ^C , miR-266 ^C , miR-152 ^G , miR-20a-5p ^P , miR-1207 ^P ; regulate STAT3/VEGFA signaling axis ^G , TGF- β /Smad pathway ^P	Biomarker	Shang et al. (2019), Zhang et al. (2018d, 2018f), Zhao et al. (2018), Li et al. (2017f), You et al. (2018), Huang et al. (2018a)
PANDAR	Colorectal, Gastric, Pancreatic	O	Cell growth, migration, invasion, local invasion, lymph node metastasis, TNM stage, cell cycle, and EMT pathway	Prognosis, metastasis	Rivandi et al. (2019), Li et al. (2017g), Lu et al. (2017), Liu et al. (2018c), Jiang et al. (2017b), Ma et al. (2016), Wang et al. (2019a)
FOXD2-AS1	Colorectal, Gastric	O	Pathological differentiation, TNM stage, lymph nodes metastasis, invasion depth, silence EphB2 through EZH2 and LSD1 ^G , targeting microRNA-185-5p ^C ; EMT and Notch signaling pathway ^C	Prognosis	Yang et al. (2017a, 2019b), Zhu et al. (2018b), Xu et al. (2018)
ANCR	Colorectal	T	Cell invasion and migration	Biomarker	Yang et al. (2017b)
CPS1-IT1	Colorectal	T	Cell proliferation, invasion and metastasis, EMT	Metastasis	Zhang et al. (2017b)
TP53TG1	Pancreatic	O	Targeting miR-96	Biomarker	Zhang et al. (2019e)
CHRF	Colorectal	T	TWIST1/EMT signaling pathway	Metastasis	Tao et al. (2017)
ARAPI-AS1	Colorectal	O	Wnt/ β -Catenin signaling Pathway	Biomarker	Ye et al. (2019a)
OLC8	Gastric	O	Interact with IL-11	Biomarker	Zhou et al. (2019b)
UJCLM	Colorectal	O	Targeting miR-215	Metastasis	Chen et al. (2017b)

clinical relevance of a wide range of lncRNAs in terms of digestive system cancer type.

lncRNA and tumor chemoresistance in digestive system cancers

Even though chemotherapy is currently an effective treatment in cancer, chemoresistance is still one of the major barriers that leads to cancer relapse and eventually treatment failure (Zheng 2017). One of the underlying mechanisms of chemotherapy is to induce apoptosis, however, cancer cells may improve survival via autophagy and so show poor sensitivity to chemotherapy (Yang and Klionsky 2010). Some biological processes, such as epithelial–mesenchymal transition (EMT) process could confer drug resistance (Mitra et al. 2015). Prominent activation of some signaling pathways (e.g., Erk/MAPK and p38/MAPK pathways) has been reported in case of chemoresistance (Chung et al. 2012). Interestingly, the regulation of lncRNA can induce drug resistance by interfering with the drug efflux system, drug metabolism, DNA repair, cell cycle, EMT, and others. Table 2 summarizes the involvement and critical roles played by lncRNA in chemoresistance to several commonly used chemotherapy drugs in the treatment of digestive system cancers.

Chemoresistance to 5-fluorouracil (5-Fu)

Among all the chemotherapeutic drugs, 5-Fu is the most commonly used in digestive cancers. lncRNA SLC25A25-AS1 expression was significantly decreased in both serum and tumor tissues of CRC patients. In addition, it was reported that SLC25A25-AS1 was associated with EMT process. Upregulation of SLC25A25-AS1 led to declined mesenchymal characteristics such as mesenchymal marker vimentin and snail expression. Elevated levels of Erk phosphorylation and p38 downregulation were found in cell line which suggests that SLC25A25-AS1 affects the activation of these pathways. Downregulation of SLC25A25-AS1 apparently increased chemoresistance, whereas overexpression increased the sensitivity to 5-Fu and DOX in CRC cell line (Li et al. 2016).

Another example of EMT-related lncRNA was LEIGC in GC. The overexpression of LEIGC promoted the sensitivity of GC cells to 5-Fu by inhibiting EMT (Han et al. 2014). lncRNA CRNDE was upregulated in CRC tissue sample and miR-181a-5p was identified as the inhibitory target. An increasing serial of concentrations of 5-Fu was applied to make lncRNA CRNDE knockdown or overexpression in CRC cells. The results indicated that CRNDE knockdown and miR-181a-5p overexpression increased the sensitivity of

CRC cells to 5-Fu therapy, but the sensitivity was decreased in CRNDE overexpression and miR-181a-5p knockdown group (Han et al. 2017).

Another lncRNA HOTAIR also contributes to 5-Fu resistance by inhibiting miR-218 and promoting NF- κ B signaling pathway in CRC (Yu et al. 2017b), by inhibiting miR-203a-3p and activating Wnt/ β -catenin signaling pathway (Xiao et al. 2018). The expression of miR-31 was up-regulated in 5-Fu-resistant cell line, while lncRNA ENST00000547547 could bind to miR-31 and suppress its expression, indicating that ENST00000547547 diminished the chemoresistance to 5-Fu via competitively binding to miR-31 (LI et al. 2017b).

Thymidylate synthase (TYMS) was thought to be a critical target when 5-Fu exerts its anticancer effect (Marquez-Jurado et al. 2018). The expression of lncRNA XIST was reported to be increased in 5-Fu resistant CRC cell lines and knockdown of XIST could boost the sensitivity through regulating TYMS expression (Xiao et al. 2017b). Another research showed that TYMS was the direct downstream target of lncRNA TUG1, knockdown of which could re-sensitize the cells to 5-Fu and cause CRC cell apoptosis (Wang et al. 2019c).

ABCC1 was highly linked to the emergence of chemoresistance in cancer cells (Gottesman et al. 2002). High level of lncRNA ANRIL was demonstrated in CRC tissues and cells. Knockdown of ANRIL enhanced the sensitivity to 5-Fu in HCT116 and SW480. Further study revealed that ANRIL could affect the expression of ABCC1 by regulating Let-7a (Zhang et al. 2018h).

Autophagy also played an important role in chemotherapy. SIRT1-mediated autophagy could be upregulated by lncRNA H19 via modulating miR-194-5p to confer 5-Fu resistance in CRC (Wang et al. 2018d). Another lncRNA, i.e., SNHG6, also regulates autophagy to induce 5-Fu chemoresistance by sponging miR-26a-5p both in vitro and in vivo, where the cell lines with knockdown of SNHG6 could be more sensitive to 5-Fu, which improved 5-Fu therapy in mouse tumor model (Wang et al. 2019e). Knockdown of lncRNA NEAT1 also increased 5-Fu sensitivity by targeting miR-34a and consequently attenuating autophagy (Liu et al. 2020).

There are some other lncRNAs examples related to 5-Fu resistance. SCARNA2 expression increased in CRC tissue, which induced the resistance to 5-Fu by inhibiting miR-342-3p signaling pathway (Zhang et al. 2019b). MiR-204-mediated HMGA2/PI3K signaling pathway was inhibited by lncRNA PCAT6 to enhance the 5-Fu-based therapy, which was confirmed in CRC cells (Wu et al. 2019). Linc00467/miR-133b/ferritin light chain (FTL) formed an axis in the chemoresistance to 5-Fu in CRC, where linc00467 regulates FTL expression through miR-133b to

Table 2 lncRNAs involves in chemoresistance to several commonly used drugs in digestive system cancers treatment

Chemotherapy drug	lncRNA	Regulation mode	Cancer type	References	
<i>Digestive system (CRC = colorectal cancer; GC = gastric cancer; PC = pancreatic cancer)</i>					
5-Fluorouracil (5-Fu)	SLC25A25-AS1	EMT	CRC	Li et al. (2016)	
	LEIGC	EMT	GC	Han et al. (2014)	
	CRNDE	Regulate miR-181a-5p	CRC	Han et al. (2017)	
	HOTAIR	Regulate miR-218 and NF- κ B signaling pathway, regulate miR-203a-3p and Wnt/ β -catenin signaling pathway	CRC	Li et al. (2017e), Xiao et al. (2018)	
	ENST00000547547	Regulate miR-31	CRC	LI et al. (2017b)	
	XIST	Regulate thymidylate synthase	CRC	Xiao et al. (2017b)	
	TUG1	Regulate thymidylate synthase	CRC	Wang et al. (2019c)	
	ANRIL	Regulate ABCC1	CRC	Zhang et al. (2018h)	
	H19	Autophagy	CRC	Wang et al. (2018d)	
	SNHG6	Autophagy	CRC	Wang et al. (2019e)	
	NEAT1	Autophagy	CRC	Liu et al. (2020)	
	SCARNA2	Regulate miR-342-3p	CRC	Zhang et al. (2019b)	
	PCAT6	Regulate miR-204 and HMGA2/PI3K signaling pathway	CRC	Dong et al. (2019a)	
	Linc00467	Regulate miR-133b	CRC	Yang et al. (2019a)	
	HAND2-AS1	Regulate miR-20a	CRC	Jiang et al. (2020)	
	LINC00152	Regulate miR-139-5p	CRC	Bian et al. (2017), Chen et al. (2018a)	
	Linc01296	Regulate miR-26a	CRC	Liu et al. (2018a)	
	FGD5-AS1	Regulate miR-153-3p	GC	Gao et al. (2020)	
	Oxaliplatin (OXA)	MEG3	Regulate miR-141	CRC	Li et al. (2017c), Wang et al. (2018b)
		MALAT1	EMT	CRC	Li et al. (2017e)
CACS15		Regulate ABCC1	CRC	Gao et al. (2019)	
KCNQ1OT1		Autophagy	CRC	Li et al. (2019b)	
LINC00152		Regulate miR-193a-3p	CRC	Yue et al. (2016)	
CCAL		Regulate β -catenin pathway	CRC	Deng et al. (2020)	
BLACAT1		Regulate ABCB1	GC	Wu et al. (2018)	
H19		Regulate stemness	CRC	Ren et al. (2018b)	
lnc273-31/34		Regulate stemness	CRC	Zhao et al. (2019)	
MACC1-AS1		Regulate stemness	GC	He et al. (2019a)	
Cisplatin (DDP)	HOTTIP	Regulate miR-218	GC	Wang et al. (2019b)	
	MALAT1	Autophagy	GC	Zhang et al. (2020a), Xi et al. (2019), YiRen et al. (2017)	
	ARHGAP5-AS1	Autophagy	GC	Zhu et al. (2019a)	
	HOXD-AS1	Regulate EZH2	GC	Ye et al. (2019b)	
	PCAT-1	Regulate EZH2, regulate miR-128	GC	Li et al. (2020a), Guo et al. (2019)	
	FOXD1-AS1	Regulate PI3K/AKT/mTOR pathway	GC	Wu et al. (2020b)	
	SNHG14	Regulate miR-186	CRC	Han et al. (2020)	
	FGF9	Regulate β -catenin signaling pathway	CRC	Zhang et al. (2020b)	
	PVT1	Regulate miR-3619-5p	CRC, GC	Ping et al. (2018), Wu et al. (2020a)	
	CASC2	Regulate miR-19a	GC	Li et al. (2018b)	
	DANCR	Regulate miR-125b-5p	CRC	Shi et al. (2020)	

Table 2 (continued)

Chemotherapy drug	lncRNA	Regulation mode	Cancer type	References
Gemcitabine	SLC7A11-AS1	Regulate stemness	PC	Yang et al. (2020)
	HOTTIP	Regulate HOXA13	PC	Li et al. (2015)
	GSTM3TV2	Regulate let-7	PC	Xiong et al. (2019)
	Linc-DYNC2H1-4	EMT	PC	Gao et al. (2017b)
	SNHG14	Autophagy	PC	Zhang et al. (2019d)
	HOST2	Unknown	PC	An and Cheng (2020)
	PVT1	Regulate miR-1207, miR-619-5p	PC	You et al. (2018), Zhou et al. (2020)
	TUG1	Regulate ERK pathway	PC	Yang et al. (2018a)
	HOTAIR	Regulate stemness	PC	Wang et al. (2017b)
	GAS5	Regulate miR-181c-5p	PC	Gao et al. (2018)
	HOTTIP	Regulate HOXA13	PC	Li et al. (2015)
	AGAP2-AS1	Regulate miR-497	CRC	Hong et al. (2020)

promote metastasis and chemoresistance in CRC (Li et al. 2019c). HAND2-AS1/miR-20a/PDCD axis was also identified to inhibit 5-Fu resistance in CRC both in vitro and in vivo (Jiang et al. 2020). Furthermore, LINC00152 was implicated in conferring 5-Fu resistance (Bian et al. 2017; Chen et al. 2018a). Linc01296 upregulation advocated tumorigenesis and chemoresistance of CRC both in vitro and in vivo (Liu et al. 2018a). Chemoresistance response to 5-Fu was suppressed in GC by downregulating lncRNA FGD5-AS1, which showed significant antitumor effect on GC proliferation both in vitro and in vivo (Gao et al. 2020).

Chemoresistance to oxaliplatin (OXA)

OXA is a platinum compound which is often used to treat CRC and GC (Dy et al. 2009). Similar obstacle as 5-Fu, large proportion of patients turned into chemoresistant and metastatic (Goldberg et al. 2004). lncRNA MEG3 was downregulated in OXA resistant CRC cell lines, while overexpression of MEG3 could partially reverse the chemoresistance to OXA in CRC. Investigation also reported that MEG3 could improve OXA-induced apoptosis in CRC cells (Li et al. 2017c). The mechanism lies in that MEG3 as a ceRNA regulated OXA sensitivity by modulating miR-141/PDCD4 axis, where MEG3 bound and suppressed miR-141 directly through binding site. As the target of miR-141, PDCD4 contained a binding site of miR-141, and MEG3 could increase PDCD4 expression by binding miR-141 as ceRNA. MEG3 overcame OXA resistance by regulating miR-141/PDCD4 axis (Wang et al. 2018b).

MALAT1 is another lncRNA associated with OXA and overexpressed in CRC patients as an oncogene, linked to poor response to OXA treatment. The 3' end region of

MALAT1 interacted with EZH2 to inhibit E-cadherin expression. Such a negative regulation of E-cadherin expression in CRC indicates that MALAT1 is involved in OXA-induced EMT process (Sha et al. 2017).

As mentioned in 5-Fu chemoresistance, ABCC1 is also a critical factor in OXA resistance, which was positively regulated by lncRNA CACS15 via sponging miR-145. The silencing of CACS15 was proved to overcome OXA resistance of CRC in vivo (Gao et al. 2019). It is elucidated that lncRNA KCNQ10T1 can promote the protective autophagy of CRC cells by increasing the expression of Atg4B via regulating miR-34a, so that the chemoresistance to OXA was enhanced in vitro and in vivo (Li et al. 2019b). Another lncRNA, linc00152, was mentioned above in 5-Fu chemoresistance, which also reported that functioned as ceRNA through sponging miR-193a-3p to confer OXA resistance in CRC both in vitro and in vivo (Yue et al. 2016).

lncRNA CCAL was associated with apoptosis and lower OXA chemoresistance in CRC cells, which could be a potential target to reverse the chemoresistance (Deng et al. 2020). lncRNA BLACAT1 was upregulated in OXA-resistant GC tissue and cells. Knockdown of BLACAT1 could inhibit ABCB1 expression and invasion in vitro and in vivo as well as OXA resistance with higher apoptosis (Wu et al. 2018).

Stemness is a significant factor in cancer stemness maintenance and chemoresistance. For example, lncRNA H19 not only overcame 5-Fu resistance, but also confer OXA resistance, in terms of carcinoma-associated fibroblast (CAF). OXA resistance in CRC was markedly promoted by overexpression of H19, while knocking down of H19 suppressed the tumor growth in xenograft model. The study indicated that CAF-derived exosomes increase the

expression of H19, stemness and OXA resistance of CRC cells both in vitro and in vivo (Ren et al. 2018b). Other two lncRNAs, name as lnc273–31 and lnc273–34 were reported to be upregulated by p53-R273H then enhancing CRC stem cell stemness and chemoresistance of OXA both in vitro and in vivo (Zhao et al. 2019). The combination use of 5-Fu and OXA is also common seen in treatment. The mesenchymal stem cells (MSCs) play a critical role in tumor progression and anticancer drug resistance (Houthuijzen et al. 2012). LncRNA MACC1-AS1 was overexpressed in GC, and the study revealed that MSC boosted MACC1-AS1 expression which subsequently positively regulated fatty acid oxidation-dependent stemness and 5-Fu/OXA resistance were verified both in vitro and in vivo (He et al. 2019a).

Chemoresistance to cisplatin (DDP)

DDP-based chemotherapy is the backbone of GC treatment. Yet, cisplatin resistance may lead to tumor recurrence (Amabile 2016). Body of evidence suggests that cancer-derived exosomes can advocate tumor progression and metastasis (Kahlert and Kalluri 2013), and the exosomes related to chemosensitive or resistant cells might influence the therapeutic response through transferring specific lncRNAs (Xu et al. 2016; Qu et al. 2016). In DDP-resistant GC cells, EMT and higher level of lncRNA HOTTIP were observed. Downregulation of HOTTIP could decrease cisplatin sensitivity. Exosomal HOTTIP activated HMGA1 to induce DDP-resistance in GC cells (Wang et al. 2019b).

Autophagy increased in DDP-resistant GC cells but could be suppressed by MALAT1 via binding with miR-30e to coordinate the expression of ATG5. Silencing of MALAT1 could prohibit chemo-induced autophagy, thus overcome chemoresistance in GC cell lines as well as in GC xenograft mice model (Zhang et al. 2020a). Another investigation stated that MALAT1 sequestered miR-30b from ATG5 to increase its expression and potentiated autophagy-related DDP resistance (Xi et al. 2019). When MALAT1 sequestered miR-23b-3p, then the expression of its target ATG12 increased, which contributed to autophagy-related chemoresistance to DDP and the drug-sensitivity assay were performed both in vitro and in vivo (YiRen et al. 2017). Previous studies found that MALAT1 was a promising target for DDP resistance in GC. Another lncRNA ARHGAP5-AS1 can also promote DDP resistance in GC by autophagy and adds more evidence that autophagy was a critical process in chemoresistance (Zhu et al. 2019a).

The mechanism underlying DDP resistance conferred by lncRNA HOXD-AS1 may be epigenetically silencing of PDCD4 via recruiting EZH2 in GC (Ye et al. 2019b). EZH2 also can be recruited by lncRNA PCAT-1 via epigenetically silencing of PTEN. Downregulation of PCAT-1 could promote sensitivity of DDP-resistant GC cells to DDP (Li et al.

2020a). Hence, EZH2-related lncRNA provided a novel therapeutic strategy targeting DDP chemoresistance in GC. DPP resistance is also conferred by PCAT-1 via another axis (i.e., miR-128/ZEB1). PCAT-1 acted as a sponge of miR-128 and the target was ZEB1. Knockdown of PCAT-1 could improve DDP sensitivity in GC tumors in vivo (Guo et al. 2019). The resistance of GC cells to DDP was promoted by FOXD1-AS1, so that depletion of FOXD1-AS1 reversed DDP resistance both in vitro and in vivo by targeting PI3K/AKT/mTOR pathway (Wu et al. 2020b).

DDP was also used in CRC treatment, even not commonly as 5-Fu and OXA, additional example about autophagy in chemoresistance is lncRNA SNHG14 in CRC, which stimulated CRC cell autophagy via miR-186/ATG14 axis (Han et al. 2020). There are some other lncRNAs examples related to DDP resistance. For example, silencing of lncRNA FGF9 could reverse DDP resistance via regulation of Wnt/ β -catenin signaling pathway in CRC (Zhang et al. 2020b). Silencing of PVT1 could inhibit DDP resistance in CRC cells (Ping et al. 2018) and GC cells both in vitro and in vivo (Wu et al. 2020a). The overexpression of CASC2 could overcome DDP resistance in GC by binding to miR-19a (Li et al. 2018b). LncRNA DANCR could promoted DDP resistance through miR-125b-5p/HK2 axis both in vitro and in vivo (Shi et al. 2020).

Chemoresistance to gemcitabine

Gemcitabine-based chemotherapy is the first-line treatment for PC. Just as in CRC and GC, gemcitabine resistance has been major barrier in treating PC (Ju et al. 2015). LncRNA SLC7A11-AS1 was overexpressed in PC tissues and gemcitabine-resistant cell lines. Knockdown of SLC7A11-AS1 can boost pancreatic cancer cell sensitivity to gemcitabine. This implies that SLC7A11-AS1 is a promising target for stemming gemcitabine resistance in PC (Yang et al. 2020). The knockdown of lncRNA HOTTIP could promote the chemosensitivity of PC cells to gemcitabine by modulating HOXA13 both in vitro and in vivo was reported in previous paper (Li et al. 2015).

GSTM3TV2 is a lncRNA associated with higher chemoresistance to gemcitabine in pancreatic cancer in vitro and in vivo by acting as a ceRNA to sponge let-7 and regulate the expression of its direct targets LAT2 and OLR1 (Xiong et al. 2019). Linc-DYNC2H1-4 is upregulated in gemcitabine-resistant PC cells and knockdown of Linc-DYNC2H1-4 could suppress EMT via sponging miR-145, which targeted EMT markers (Gao et al. 2017b). SNHG14 is also a potential autophagy-related target in PC. It interreacted with miR-101 to stimulate autophagy and increase gemcitabine resistance (Zhang et al. 2019d). Downregulation of lncRNA HOST2 could improve the sensitivity to gemcitabine in PC,

but the detailed mechanism of which is still unknown (An and Cheng 2020). Inhibition of lncRNA PVT1 led to higher efficacy of gemcitabine by targeting miR-1207 (You et al. 2018). The recent study indicated PVT1 could promote gemcitabine resistance of PC both in vitro and in vivo. The study demonstrated that PVT1 induced gemcitabine resistance was associated with elevated increased Wnt/ β -catenin signaling pathway and autophagic activity. MiR-619-5p was directly targeted by PVT1, and the gemcitabine resistance was reversed by miR-619-5p in PC (Zhou et al. 2020). In addition, many other lncRNAs, such as TUG1, HOTAIR, GAS5, and HOTTIP, are also implicated in regulating gemcitabine resistance in PC (Yang et al. 2018a; Wang et al. 2017b; Gao et al. 2018; Li et al. 2015).

LncRNA AGAP2-AS1 worked as a ceRNA of miR-497 which targeted on fibroblast growth factor receptor 1. Gemcitabine resistance could be diminished by silencing AGAP2-AS1, which also cause G1/M phase cell cycle arrest in CRC cells (Hong et al. 2020).

Chemoresistance to other chemotherapy

Besides the commonly used drugs mentioned above, there are other chemotherapy drugs used in digestive system cancer treatment. Doxorubicin (DOX) is an anthracycline drug used to treat many malignancies and chemoresistance is the major treatment challenge. XIST is upregulated in CRC tissues and cells while knockdown of XIST could curb DOX resistance via interacting with miR-124, thereby positively regulate SGK1 expression in DOX-resistant CRC cells. The antitumor effect of DOX was improved further both in vitro and in vivo (Zhu et al. 2018a). lncRNAs D63785 and NEAT1 were also reported to regulate DOX resistance in GC (Zhou et al. 2018b; Zhang et al. 2018a).

Oxymatrine plays a role in anti-arrhythmia, antifibrosis, anti-inflammation, and antitumor in CRC and PC (Zhang and Huang 2004; Liang and Huang 2016; Chen et al. 2013). In oxymatrine-resistant CRC cells, lncRNA MALAT1 was upregulated, while knockdown of MALAT1 could partially reverse EMT. MALAT1 is a stimulator for oxymatrine resistance in CRC, which can inform better therapy treatment of CRC patients (Xiong et al. 2018). Carboplatin chemotherapy also face the challenge of chemoresistance. The expression of lncRNA BORG could enhance the viability of CRC cells by downregulating p53 so that downregulation of BORG could be a novel clue to overcoming the chemoresistance (Li et al. 2020b).

Some lncRNAs are implicated in multiple chemoresistance, such as XIST. It can modify the resistance to 5-FU, mitomycin, DDP, and DOX by collaborating with miR-30a in CRC cells (Zhang et al. 2019c). LncRNA GIHCG is associated with chemoresistance to 5-Fu and OXA and CRC

progression (Jiang et al. 2019b). Apart from in 5-Fu chemoresistance, knockdown of CRNDE can increase sensitivity to chemotherapeutic drugs. This is also confirmed for OXA (Han et al. 2017). Similar sensitivity recovery was found in 5-Fu and OXA when ANRIL was knocked down (Zhang et al. 2018h). Overexpression of SLC25A25-AS1 not only increased the sensitivity to 5-Fu, but also to DOX in CRC cell line (Li et al. 2016). Knockdown of HULC contributed to the sensitivity of GC cells to DDP, DOX and 5-Fu (Zhang et al. 2016a). Knockdown of CASC9 significantly reduced the resistance to paclitaxel and DOX in GC cells (Shang et al. 2017).

Future perspectives

LncRNAs have attracted great attention in the past decade with increasing number of studies reporting on novel lncRNAs involved in various digestive system cancers. Due to its huge potential in modulating cancer development, it is very motivating to elucidate the lncRNAs regulatory mechanisms, especially those controlling the gene expression responsible for carcinogenesis or overcoming chemoresistance. It is also encouraging to note that several clinical trials involving lncRNAs and cancers, specifically thyroid cancer and breast cancer, have already completed their studies while others are still recruiting (<https://clinicaltrials.gov/ct2/home>). Although the results of these trials have not been published yet, their promising roles have been verified both in vitro and in vivo by numerous studies, and thus, signifies the potential of lncRNAs as therapeutic targets and/or biomarkers in cancer diagnosis and therapy.

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