

MicroRNAs and the PTEN/PI3K/Akt pathway in gastric cancer (Review)

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Abstract. Gastric carcinogenesis arises from complicated interactions among host, environmental and bacterial factors, which cause genetic and epigenetic dysregulation of oncogenic and tumor-suppressive genes. MicroRNAs (miRNAs), a class of small non-coding RNAs that post-transcriptionally regulate ~30% human genes, may serve as oncogenes or tumor-suppressors in malignancies, including gastric cancer (GC). Although miRNA dysregulation commonly exists in GC, exact roles miRNAs serve in the pathogenesis and promotion of this tumor remain undetermined. Recently, results of previous studies regarding mechanisms underlying miRNAs generally converged on pathways critical in cellular processes, including cell proliferation, apoptosis and invasion, among which phosphatase and tensin homolog (PTEN)/phosphatidylinositol 3-kinase (PI3K)/protein kinase B (Akt) signaling is a fundamental one, with frequent oncogenic alterations in GC. Therefore, in the present review, the disorder and function of miRNAs and PTEN/PI3K/Akt signaling in GC are discussed. Additionally, how miRNAs transduce their effects by regulating this pathway, particularly in GC stem cells and the tumor microenvironment, and two novel hypotheses significant in carcinogenesis, tumor progression and recurrence, are discussed. Furthermore, the roles of miRNAs and the PTEN/PI3K/Akt pathway in target therapies against this lethal disease are outlined.

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1. Introduction

Gastric cancer (GC) is the fourth most common cancer and the second leading cause of cancer-associated mortality worldwide (1). The incidence and mortality rates of GC are the highest in East Asia, primarily in China (1-3). Gastric carcinogenesis is a complex process, which involves crosstalk among host, environmental and bacterial factors, leading to different molecular alterations at the genetic and epigenetic level; *Helicobacter pylori* is a well-recognized high-risk factor (4,5). Gastrectomy is the primary strategy for patients with early-stage GC. However, the absence of specific symptoms in the early-stage leads to the majority of patients with GC diagnosed in the unresectable stage, and systemic chemotherapy is the primary option for these patients (6). Chemotherapy resistance frequently emerges as a cause of treatment failure (6). At present, the outcome for patients with advanced GC remains poor, with 5-20% 5-year survival and a median overall survival of 10 months (3). Therefore, examining novel biomarkers for early diagnosis and other feasible treatments based on a better understanding of mechanisms underlying GC pathogenesis, in addition to chemoresistance, is urgently required.

MicroRNAs (miRNAs) represent a large group of conserved small non-coding RNAs (ncRNAs) with a length of 17-25 nucleotides, which bind to the 3'-untranslated region (UTR) of mRNAs of their target genes, silencing expression by cleaving the mRNA molecules or inhibiting their translation (1,5). In this manner, ~30% human genes are modulated by miRNAs; the majority are directly or indirectly implicated in signaling pathways fundamental in cellular activities, including proliferation, differentiation, apoptosis and migration (7,8). As a result, miRNAs are crucial regulators in the initiation and progression of various diseases, particularly cancer. In GC, dysregulated oncogenic or tumor-suppressive miRNAs promote malignant phenotypes, including tumor growth, metastasis, angiogenesis and drug-resistance, by regulating downstream targets and associated pathways (4,9,10).

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The phosphatase and tensin homolog (PTEN)/phosphatidylinositol 3-kinase (PI3K)/protein kinase B (Akt) signaling pathway represents a crucial one (11,12). PTEN, a dual protein and lipid phosphatase, primarily dephosphorylates phosphatidylinositol-3,4,5-trisphosphate (PIP3), which is the product of PI3K and is able to recruit Akt to the membrane, where it is phosphorylated and stimulated by other kinases dependent on PIP3 (13). Activated Akt may regulate multiple biological processes, including cell survival, metabolism, cell proliferation and growth, by affecting its downstream substrates (13-15). Genetic and epigenetic alterations occurring in a number of components of this pathway lead to its constitutive activation in human cancer, including GC (11,16). Furthermore, the PTEN/PI3K/Akt pathway may be regulated by miRNAs in GC, suggesting that this signaling serves an essential role in mediating oncogenic effects of dysregulated miRNAs during the onset and development of this disease (6,8). In the present review, the dysregulation and function of miRNAs, in addition to genetic alterations and the roles of the PTEN/PI3K/Akt pathway in GC are summarized. Furthermore, how this signaling serves as an important mediator of miRNAs is discussed. Based on their involvement in the mechanism underlying gastric carcinogenesis and progression, the clinical applications of miRNAs and its signaling as biomarkers or therapeutic targets in GC management are additionally discussed.

2. miRNAs in GC

Dysregulation and function of miRNAs in GC. Accumulating evidence has documented the overexpression or downregulation of specific miRNAs in GC. Due to the extensive regulatory function of miRNAs in gene expression, the dysregulated miRNAs may result in oncogenic activities regarding approximately all aspects of tumorigenesis and progression, including cell proliferation, apoptosis, invasion and migration (1,4). Generally, oncogenic miRNAs contribute to tumor development with their aberrantly high expression in GC, whereas, the silenced or lost expression of tumor-suppressive miRNAs may additionally exert positive effects during oncogenesis (1,4). Carcinogenic effects of miRNAs have been acknowledged to be the result of their disordered post-transcriptional regulation of oncogenic and tumor suppressive genes via complementary base-pairing (1,4). The aberrant expression level of miRNAs, implicated oncogenic effects and associated target genes in GC are summarized in Table I.

Tsukamoto *et al* (17) detected miRNA expression in 22 surgically resected GC tissues and identified that 39 miRNAs exhibited different expression levels between tumor and normal tissues, among which six miRNAs were downregulated; whereas, the other 33 miRNAs were upregulated in GC. miR-28 was demonstrated to be upregulated in 31 GC tissues compared with the matched adjacent non-tumor tissues ($P < 0.05$), and the higher expression of miR-28 has been additionally observed in a series of GC cell lines compared with the normal control (5). miR-28 contributed to GC cell proliferation and invasion by targeting and downregulating tumor suppressor PTEN (5). Caudal-related homeobox 1 (CDX1), an intestinal-specific transcription factor important in gastric intestinal metaplasia, could significantly repress GC cell

growth by inducing cell cycle arrest and apoptosis (10). CDX1 was targeted by oncogenic miR-296-5p, which was detected to be overexpressed in GC tissues and abolished the suppressive effects induced by CDX1 (10). Different from the elevated expression level of oncogenic miRNAs in GC, the expressions of tumor-suppressor miRNAs, including miR-137, miR-34a, miR-15a and miR-16-1, which exert negative regulations on cell proliferation, epithelial-mesenchymal transition (EMT), migration, invasion, colony formation *in vitro*, in addition to tumorigenicity and metastasis *in vivo*, have been documented to be evidently decreased in the tumor tissues and cell lines compared with normal controls (18-21). The targets responsible for their effects including Akt2, platelet-derived growth factor receptor (PDGFR) and twist family bHLH transcription factor 1 (18-21). The synergistic regulation of multiple genes, including phosphoinositide-3-kinase regulatory subunit 2 (PI3KR2), CRK proto-oncogene, adaptor protein, vascular cellular adhesion protein 1 and serine/threonine-protein kinase PLK2, affects the miR-126 diverse antitumor effect of restraining tumor cell growth, migration and invasion, and inducing cell cycle arrest in G₀/G₁ phase, apoptosis *in vitro*, in addition to inhibiting tumorigenicity, angiogenesis and metastasis *in vivo*; however, during gastric oncogenesis, the expression of miR-126 was significantly decreased (22-24). Otsubo *et al* (25) observed that miR-126 was aberrantly upregulated in a number of GC cell lines and tumor tissues, and miR-126 overexpression contributed to growth and colony formation of GC cells by modulating its tumor-suppressive target sex-determining region Y-box 2.

Possible clinical application of miRNAs in GC

miRNAs as promising biomarkers for GC. As mentioned, the significantly different expression of miRNAs may be detected between tumor and normal gastric mucosa tissues. When detecting samples from patients with GC with different clinicopathological characteristics and prognosis, the expression level of specific miRNAs may additionally be distinct. The expression of miR-10b and miR-21 was markedly higher in lymphoma node metastasis-positive tumor tissues compared with lymphoma node metastasis-free tumor tissues (26,27). The low expression of tumor suppressor miR-1 and miR-146a was associated with vascular invasion, lymph node involvement and distant metastasis, in addition to the poor prognosis of patients with GC. Furthermore, the relative level of miR-146a expression was an independent predictive factor for overall survival (28,29). Therefore, miRNA expression levels in tumor tissues may be used to diagnose patients with GC, in addition to distinguishing patients with different prognosis and developing treatment strategies.

Additionally, circulating miRNAs, which were contained in secretive exosomes, may be detected in body fluids, including sera, plasma, urine and gastric juice (1). Due to their characteristics, including high stability, close association with disease statuses and ease of measurement, circulating miRNAs have been investigated in multiple diseases, particularly cancer, regarding their promising functionality as novel non-invasive biomarkers (1). Liu *et al* (30) reported that serum exosome miR-451 of patients with GC was significantly increased compared with healthy controls. Furthermore, the high expression level of exosome miR-451 was associated

Table I. Dysregulated expression and target genes of miRs in gastric cancer.

Author, year	miRs	Studied samples	Expression levels	Target genes	Implicated processes	(Refs.)
Zhou <i>et al</i> , 2018	miR-200c	Cell lines	↓	ZEB1, ZEB2	EMT, drug-resistance, invasion, and migration	(3)
Petrocca <i>et al</i> , 2008	miR-106b miR-93	Tissues and cell lines	↑	E2F1, CDKN1A (p21)	Cell cycle	(7)
Petrocca <i>et al</i> , 2008	miR-25	Tissues and cell lines	↑	Bim	Cell apoptosis	(7)
Zhang <i>et al</i> , 2018	miR-532-5p	Tissues and cell lines	↓	NCF2	Metastasis and angiogenesis	(9)
Li <i>et al</i> , 2014	miR-296-5p	Tissues and cell lines	↑	CDX1	Tumor cell growth	(10)
Wang <i>et al</i> , 2017; Kang <i>et al</i> , 2015	miR-15a miR-16-1	Tissues and cell lines	↓	Twist1, YAP1	Cell proliferation, EMT, migration, invasion, colony formation <i>in vitro</i> , tumorigenicity <i>in vivo</i>	(19,20)
Liu <i>et al</i> , 2014; Feng <i>et al</i> , 2010; Chen <i>et al</i> , 2014; Otsubo <i>et al</i> , 2011	miR-126	Tissues and cell lines	↑/↓	PI3KR2, VEGFA, Crk, SOX2	Cell growth and colony formation, apoptosis migration and invasion, cell cycle, angiogenesis	(22-25)
Kogo <i>et al</i> , 2011	miR-146a	Tissues	↓	EGFR, IRAK1	Cell migration and invasion	(29)
Zhou <i>et al</i> , 2015	miR-141	Tissues and cell lines	↓	ZEB1	Cell proliferation, apoptosis and invasion	(33)
Han <i>et al</i> , 2015	miR-29c	Tissues	↓	ITGB1	Cell proliferation, adhesion, invasion and tumor growth	(34)
Yan <i>et al</i> , 2016	miR-126	Tissues and cell lines	↓	PI3KR2, VEGFA	drug-resistance	(75)
Nishida <i>et al</i> , 2011	miR-125a-5p	Tissues and cell lines	-	HER2	Cell proliferation	(79)
Huang <i>et al</i> , 2016	miR-508-3p	Cell lines	↓	MMP-9, NFKB1, RELA	Cell proliferation, growth, invasion	(96)
Zhou <i>et al</i> , 2014	miR-141	Tissues	STAT4	STAT4	Cell invasion	(97)
He <i>et al</i> , 2016	miR-29a	Tissues	↓	ITGB1	Cell invasion and metastasis	(98)
Huang <i>et al</i> , 2015	miR-338-3p	Tissues and cell lines	↓	ZEB2	EMT	(99)
Liu <i>et al</i> , 2014	miR-423-5p	Tissues and cell lines	↑	TFF1	Cell proliferation, colony formation, invasion	(100)

Table I. Continued.

Author, year	miRs	Studied samples	Expression levels	Target genes	Implicated processes	(Refs.)
Zhang <i>et al</i> , 2017	miR-424	Tissues	↑	LATS1	Cell proliferation, invasion and colony formation	(101)
Han <i>et al</i> , 2015	Let-7b	Tissues and cell lines	↓	ING1	Invasion and metastasis	(102)

Bim, Bcl-2-like protein 11; CDKN1A, cyclin dependent kinase inhibitor 1A; CDX1, caudal-related homeobox 1; Crk, CRK proto-oncogene, adaptor protein; E2F1, E2 transcription factor 1; EGFR, epidermal growth factor receptor; HER2, human epidermal growth factor receptor 2; ING1, inhibitor of growth factor family, member 1; IRAK, interleukin-1 receptor-associated kinase 1; ITGB1, integrin β 1; LATS1, large tumor suppressor kinase 1; miRs, microRNAs; MMP-9, matrix metalloproteinase-9; NCF2, neutrophil cytosol factor 2; NF- κ B, nuclear factor κ B subunit 1; NGS, next generation sequencing; PI3KR2, phosphoinositide-3-kinase regulatory subunit 2; RELA, RELA proto-oncogene, NF- κ B subunit; SOX2, SRY-box 2; STAT4, signal transducer and activator of transcription 4; SP1, specificity protein 1; TFF1, trefoil factor 1; Twist1, twist family bHLH transcription factor 1; VEGFA, vascular endothelial growth factor A; YAP1, Yes-associated protein 1; ZBTB10, zinc finger and BTB domain containing 10; ZEB1, zinc finger E-box binding homeobox 1; ZEB2, zinc finger E-box binding homeobox 2.

with poor differentiation, in addition to high proliferation and metastasis potential of GC, and may further predict poor outcomes of patients with GC post-surgery (30). Zhu *et al* (31) identified an miRNA signature with the capacity to diagnose early-stage GC accurately, which consisted of five miRNAs (miR-16, miR-25, miR-92a, miR-451 and miR-486-5p) overexpressed in the plasma of patients with GC.

miRNAs as potential therapeutic targets for GC. As the dysregulated miRNAs may contribute to the pathogenesis of GC, restoring the level of downregulated tumor-suppressive miRNAs and/or upregulated oncogenic miRNAs, they may represent a potential treatment strategy against the tumor. Consistently, when transfecting GC cells with an miR-590-5p inhibitor, significantly decreased proliferative and invasive abilities, in addition to increased sensitivity to cisplatin (DDP) and paclitaxel (PTX) were observed (32). Whereas, ectopic expression of miR-141 in tumor cells may lead to ~40% inhibition of proliferation and prominent reduction in invasion (33). In addition to the *in vitro* studies, miRNAs have been tested for their treatment efficacy *in vivo*. Han *et al* (34) identified that in a xenograft nude mouse model, tumor growth in mice implanted with miR-29c overexpressing GC cells was significantly slower compared with mice treated with untreated parental cells ($P < 0.0001$), and injecting miR-29c mimics intratumorally additionally resulted in a marked inhibition of tumor growth. According to the results of the bioluminescence imaging and analysis, and the number of lung metastasis in mice, miR-137 was demonstrated to exert anti-metastatic effects *in vivo* (21).

3. PTEN/PI3K/Akt pathway in GC

Components of the PTEN/PI3K/Akt pathway. PTEN is a dual lipid and protein phosphatase and a common tumor suppressor. Since its identification, the mutational and epigenetic silencing of PTEN have been documented in various cancer types, owing to its extensive function in critical cellular processes, which may be generally divided into two categories, cell growth/survival and cell migration/adhesion, regulated through its lipid and protein phosphatase activities, respectively (12,13). The primary substrate of PTEN is PIP3, the product of PI3Ks, a lipid kinase family with the typical ability to phosphorylate the 3'-OH group in inositol phospholipids on the cell membrane (35). PI3Ks generally consist of three classes (class I, class II and class III) (35). Class I PI3Ks, heterodimeric proteins comprising a catalytic subunit and a regulator subunit, may be further subdivided into subclass IA and subclass IB, which may be activated by tyrosine kinase receptors (RTKs) and guanosine-binding protein coupled receptors (GPCR), respectively (11). Among the three classes, only class I PI3Ks were identified to be implicated in human cancer (35) and is the one primarily referred to in the present review.

Akt, additionally termed PKB, is a serine-threonine kinase downstream of PTEN/PI3K signaling. Akt includes three isoforms transcribed from different genes, Akt1/PKB α , Akt2/PKB β and Akt3/PKB γ (14). Each member comprises three conserved domains; a pleckstrin homology (PH) domain in the N-terminal, a central kinase domain and a hydrophobic

C-terminal tail (14). In the first and the third domain, a regulatory site exists, which is necessary for the PI3K-dependent activation of Akt (Thr308 and Ser473 in Akt1) (36).

Activation process of the PTEN/PI3K/Akt pathway. The stimulation of GPCRs or RTKs [including IGFR, PDGFR, epidermal growth factor receptor (EGFR) and c-Met] by various stimuli, including growth factors, hormones and extracellular matrix (ECM) components, initiates the activation of the PI3K/Akt pathway (14). The interaction of the Src homology 2 (SH2) domains in the regulatory subunit of PI3K with the intracellular section of the activated cell-surface receptors or their adaptor proteins leads to the allosteric activation of the PI3K catalytic subunit (37,38). Alternatively, the activated Ras may stimulate PI3K by binding to a Ras binding domain (RBD) located at p110 catalytic subunits (39). Subsequently, activated PI3K associates and phosphorylates lipids, which in turn phosphorylates phosphatidylinositol-4,5-bisphosphate (PIP2) at the inner side of the plasma membrane into phosphatidylinositol-3,4,5-trisphosphate (PIP3), a significant second messenger in cells (14). The production of PIP3 results in the recruitment of proteins containing a PH domain to cellular membranes, including Akt and its activating kinase 3-phosphoinositide-dependent protein kinase 1 (PDK1), which are critical for transducing the activity of PI3K (40). It is generally acknowledged that the conformational alterations of Akt, which refers to the exposure of its two primary regulatory residues, may occur following the interaction of the PH domain with PIP3. The PH domain is additionally accountable for the heterodimerization of Akt and PDK1, which results in activation of Akt through the phosphorylation of PDK1 at Thr308 of Akt (14). However, apart from the phosphorylation of this residue, full activation of Akt still requires phosphorylation of the other regulatory site in the carboxyl-terminal hydrophobic motif, Ser473, which is fulfilled by mammalian target of rapamycin (mTOR) complex 2, additionally termed PDK2 (11,41). Subsequently, activated Akt will be translocated into the nucleus to phosphorylate its downstream substrates involved in multiple cellular processes, including apoptosis, cell cycle progression, metastasis and metabolism (14,42).

Among multiple substrates, PTEN primarily targets and dephosphorylates lipid PIP3 at the D3 position of the inositol ring, and thus serves as the primary negative regulator of PI3K/AKT signaling by reducing PIP3 production and inhibiting subsequent recruitment along with activation of Akt (14). In the same manner, other phosphatases may additionally block the activation of PI3K/Akt signaling, including SH2-containing inositol 5-phosphatase and inositol polyphosphate 4-phosphatase type II (37). Carboxyl-terminal modulator protein, a protein partner which binds to the C terminus of Akt1 at the plasma membrane, is able to block the phosphorylation on Ser473 and Thr308, thus reducing the activation of Akt (43).

Genetic alterations of the PTEN/PI3K/Akt pathway in GC. Genetic alterations of different codes of PTEN/PI3K/Akt signaling may be frequently detected in GC (Table II), which contribute to the overactivation of this signaling (11). However, as genetic analysis is a reliable experiment strategy for validating specific genes involved in pathologic processes, these

documented genetic alterations may reflect the involvement of the PTEN/PI3K/Akt pathway in gastric carcinogenesis and progression.

Loss of the tumor suppressor PTEN, was considered a common mechanism for the activation of Akt signaling and inversely, the constitutive activation of Akt was demonstrated to be largely responsible for PTEN-mediated carcinogenesis (14,44). The mutational inactivation of PTEN may be identified in numerous carcinomas, including GC (45). Wen *et al* (46) identified mutations of PTEN in 27 of 144 patients with GC, and the mutation rate was higher in advanced tumor, node and metastasis (TNM) stages in addition to poorly differentiated ones, which may account for the downregulated PTEN expression and the activation of PI3K/Akt signaling detected in tumor tissues. Epigenetically silencing PTEN by methylating 5' CpG islands in the promoter possibly accounts for the its downregulated expression in GC (16). Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit α (PIK3CA), the gene encoding PI3K catalytic subunit p110 α , has been documented to be one of the most frequently mutated genes in human cancer (42). Samuels *et al* (47) identified activating mutations of PIK3CA in numerous cancer types, among which the mutation rate in GC was 25% (3 in 12 cases), and >75% of the mutations occurred in two small clusters located in the helical and kinase domains, causing the significant upregulation of lipid kinase activity and the resultant stimulation of downstream Akt signaling. In addition to mutations, the genomic amplification of PIK3CA was additionally an important mechanism underlying the oncogenic activation of the PI3K/Akt pathway in malignant diseases (14). Shi *et al* (48) determined that PIK3CA amplification in 88 of 131 tested samples (67%) was closely correlated with the elevated activation of the PI3K pathway, in addition to a poor outcome for patients with GC. Furthermore, in the same previous study, the PIK3CA amplification rate was significantly higher compared with the mutation rate [8/113 (7.1%)] (48). The genetic alteration, including mutation and amplification, may additionally occur to Akt in GC, although the documented incidence is low.

Function of the PTEN/PI3K/Akt pathway in GC. PI3K signaling is vital in regulating multiple fundamental cellular activities, including cell proliferation, apoptosis and metastasis (49). With frequent alterations identified in GC, the PTEN/PI3K/Akt pathway is significantly involved in gastric carcinogenesis and progression (11,50).

The disturbed balance between cell growth and apoptosis leads to tumorigenesis, is a result from the disorder of complex regulation networks, comprising of pivotal proteins and signaling cascades. The PTEN/PI3K/Akt pathway is critical due to its fundamental role in the decision of cell death and survival (14,42). Pro-survival effects of Akt signaling have been identified in previous studies using antitumor factors. Zhao *et al* (51) identified that overexpression of a tumor suppressor gene, inhibitor of growth 3, in GC cells was able to reduce cell proliferation and arrest the cell cycle at G₂/M phase, in addition to induce cell apoptosis, and the impairment of PI3K/Akt signaling was the involved mechanism. Geridonin and paclitaxel was able to serve synergistically to suppress Akt signaling by inhibiting Akt phosphorylation at Thr308

Table II. Genetic alterations of the PTEN/PI3K/Akt pathway in GC.

Author, year	Altered sites	Detection methods	Samples	Primary results	(Refs.)
Soung <i>et al.</i> , 2006	Akt	PCR-SSCP, direct sequencing	Tumor specimens	Akt2 mutation was identified in 3 out of the 294 tumor samples. Mutations were identified in 2 of 79 lung carcinomas (2.5%) and 1 of 51 GC (2.0%) cases. The GC mutation was in intron 10. There was no mutation in Akt1 or Akt3 in these cancer tissues.	(42)
Li <i>et al.</i> , 2005	PIK3CA	Direct sequencing	Tumor specimens	Mutations in PIK3CA were identified in 4 of 94 GAC samples. In total, two cases had the mutation A3140G (H1047R) in exon 20, and the other two cases had mutations G1624A (E542K) and G1633A (E545K) in exon 9.	(44)
Wen <i>et al.</i> , 2010	PTEN	Direct sequencing	Tumor specimens	Mutations in PTEN were detected in 27 of 144 GC specimens, consisting of 15 cases (55.6%) of missense mutation, nine nonsense mutations (33.3%), two cases of 1-bp deletion (7.4%) and a mutation within intron 6 (3.7%).	(46)
Samuels <i>et al.</i> , 2004	PIK3CA	Direct sequencing	Tumor specimens	PIK3CA mutation was detected in 3 of 12 GC cases (25%) and >75% of the mutation occurred in two small clusters located in the helical and kinase domains.	(47)
Shi <i>et al.</i> , 2012	PIK3CA	Direct sequencing, RT-qPCR	Tumor specimens	PIK3CA mutations and amplification (gene copy number ≥ 4) were detected in 8/113 (7.1%) and 88/131 (67%) GC specimens, respectively.	(48)
Wang <i>et al.</i> , 2003	PTEN	PCR-SSCP, direct sequencing	Tumor specimens	Mutations in PTEN occurred in 17 of 60 (28.3%) advanced GC specimens, consisting of eight missense mutations (47.1%), five silent mutations (29.4%), two nonsense mutations (11.8%), a 12-bp deletion (5.9%) and a mutation within the splice donor site of intron 6 (5.9%).	(103)
Velho <i>et al.</i> , 2005	PIK3CA	PCR-SSCP, PCR	Tumor specimens	Mutations in exons 9 and 20 of PIK3CA were identified in 5/47 (10.6%) of GC. The mutation rate was significantly different between microsatellite instable GC [19.2% (5/26)] and microsatellite stable GC [0% (0/21)].	(104)
Staal, 1987	Akt	Southern blotting	Tumor specimens	In 225 human tumors, a 20-fold amplification of Akt1 was identified in one of the five GAC cases.	(105)

Akt, protein kinase B; CRC, colorectal cancer; GAC, gastric adenocarcinoma; GC, gastric cancer; PCR-SSCP, polymerase chain reaction-single-strand conformation polymorphism; PI3K, phosphatidylinositol 3-kinase; PTEN, phosphatase and tensin homolog; RT-qPCR, reverse transcription-quantitative polymerase chain reaction.

and Ser473, in addition to elevating the PTEN expression level, which led to the accumulation of p53 and pro-apoptotic apoptosis regulator Bcl-2 (Bcl-2) family members, together with downregulation of anti-apoptotic members (52). These molecular alterations accounted for the enhanced apoptosis and repressed growth *in vitro* and *in vivo* induced by this combination therapy against GC (52).

Apart from contributing to the initiation of GC, the aberrantly activated PI3K signaling was additionally able to contribute to the progression of GC into highly malignant types characterized by metastasis and resistance to chemotherapy. Metastasis is a high potential risk and the predominant cause of recurrence and mortality among patients with GC, and a number of cell biological activities are controlled in this multistep process, including adhesion, migration, invasion and angiogenesis (1). Lectin-like oxidized low-density lipoprotein receptor-1 was overexpressed in GC cells and increased the migratory and invasive ability by enhancing EMT, and activating the PI3K/Akt/glycogen synthase kinase 3 β (GSK3 β) pathway (53). Vascular endothelial growth factor-A (VEGF-A) was suggested to promote angiogenesis by activating the downstream Akt/mTOR cascade in GC (24). Phosphatase of regenerating liver-3 (PRL-3), a protein tyrosine phosphatase, silenced PTEN by reducing its expression and enhancing its phosphorylation, leading to the activation of PI3K/Akt signaling and upregulation of matrix metalloproteinase (MMP)-2/MMP-9, through which PRL-3 contributed to the lethal peritoneal metastasis of GC (49). Chen *et al* (54) documented the enrichment and activation of PI3K/Akt/mTOR signaling along with decreased PTEN expression in GC cells resistant to PTX, a microtubule stabilizer widely used in the front-line chemotherapy for patients with advanced GC. The low response to other antitumor agents, including DDP and 5-fluorouracil (5-FU), may additionally be attributed to the stimulated PI3K signaling (6,11,32).

Anticancer drugs targeting the PTEN/PI3K/Akt pathway. As a most frequently dysregulated pathway in cancer, the PTEN/PI3K/Akt pathway has attracted increasing attention for its potential in target therapies for a number of malignancies. In this context, >40 inhibitors against different points of this pathway, primarily PI3Ks, Akt and mTOR, reached various stages of clinical trials; the mTOR inhibitors, temsirolimus and everolimus, in addition to the PI3K inhibitors, idelalisib and copanlisib, have been approved by the Food and Drug Administration for clinical anticancer treatment (38). Consistently, these therapies have additionally been investigated for GC in numerous previous studies regarding treatment effects of inhibiting tumor growth, metastasis and modifying chemo-sensitivity, including LY294002, a commonly used PI3K inhibitor, and the Akt inhibitor MK-2206 (6,49,55). A number of effective and safe inhibitors, including BKM120 targeting PI3K and everolimus against mTOR, were enrolled in the clinical studies of different phases among patients with GC (11). Antibodies or inhibitors against the RTKs or the ligands have additionally been examined as potential target therapies for GC. Trastuzumab, a humanized monoclonal antibody against human epidermal growth factor receptor 2 (HER2), is the first molecular target drug in GC and may be combined with

chemotherapy as a standard treatment for cases with HER2 overexpression/amplification, which affect 11-20% patients with GC (3). Furthermore, it was observed that the combined use of trastuzumab and LY294002 may exhibit a synergistic repression on downstream Akt signaling in GC cells (56). Ramucirumab and apatinib, inhibitors of vascular endothelial growth factor receptor-2 (VEGFR-2), have additionally been approved as anti-angiogenic therapies for advanced GC (57).

4. Regulation of miRNAs on the PTEN/PI3K/Akt pathway in GC

miRNAs regulate PI3K/Akt signaling. The activated PI3K signaling contributed to the initiation and development of GC through involvement in different cellular activities. Multiple evidence has demonstrated that miRNAs were highly implicated in the regulation of the PI3K/Akt pathway by targeting this pathway (Table III; Fig. 1), which partially identified the mechanisms underlying the oncogene or tumor-suppressor role of miRNAs in GC.

During gastric carcinogenesis, the oncogenic effects caused by the overexpressed oncogenic miRNAs or down-regulated tumor-suppressive miRNAs may be attributed to the aberrantly activated PI3K/Akt signaling. It was observed that miR-196b promoted GC tumor growth through its promotion in the cell cycle and cell proliferation, possibly by stimulating the PI3K/Akt/mTOR pathway (58). Conversely, it was identified that the tumor suppressor miR-203, inhibited GC cell proliferation by targeting PIK3CA and consequently attenuated activation of Akt (59). Tsukamoto *et al* (17) observed that ectopic expression of miR-375 lead to a decrease in PDK1 expression and a subsequent decline in phosphorylation of Akt at Ser473 and Thr308. Furthermore, the dysregulated expression level of an anti-apoptosis substrate of Akt, E3 ubiquitin-protein ligase XIAP, along with the increased activity of specific apoptosis executioners, including Bcl-2 homologous antagonist/killer, Bcl-2-like protein 11 and tumor necrosis factor ligand superfamily member 12, was additionally documented (17). miR-137, as possible negative component of gastric tumorigenesis, suppressed GC cell survival by inducing early apoptosis through targeting Akt2 and affecting downstream Bcl2-associated agonist of cell death, a pro-apoptotic member of the Bcl-2 family, which functions by selectively dimerizing with pro-survival members, B-cell lymphoma-extra large and Bcl-2 (21). Bcl-2, another substrate of Akt, may be directly regulated by miR-449a and thus transduced its tumor-suppressive effects of inducing tumor cell apoptosis and inhibiting cell growth in gastric adenocarcinoma (60). Other proteins of the PI3K/Akt/mTOR pathway, PIK3CB, downstream tuberous sclerosis 1 (TSC1) and mTOR have been demonstrated to be negatively modulated by miR-125b-2, miR-451a and miR-101-2, respectively, which accounted for their inhibitory effects on GC growth, including blocking cell proliferation and colony formation, and inducing cell death (61). Furthermore, upstream RTKs PDGFR and hepatocyte growth factor receptor, receiving platelet-derived growth factor and hepatocyte growth factors respectively, were additionally targeted by miR-34a and mediated its suppression on GC cell proliferation via the PI3K/Akt pathway (18).

Table III. Regulation of miRs on the PTEN/PI3K/Akt pathway in GC.

Author, year	miRNAs	General role	Regulatory sites	Pathway activity	Results	(Refs.)
Li <i>et al</i> , 2017	miR-28	oncomiR	PTEN	Positive	Advancing tumor cell proliferation and invasion	(5)
Yang <i>et al</i> , 2013	miR-21	oncomiR	PTEN	Positive	Conferring drug-resistance to tumor cells	(6)
Chen <i>et al</i> , 2018	miR-136	oncomiR	PTEN	Positive	Enhancing tumor cell proliferation and invasion	(12)
Tsukamoto <i>et al</i> , 2010	miR-375	anti-oncomiR	PDK 1	Negative	Inducing apoptosis	(17)
Peng <i>et al</i> , 2014	miR-34a	anti-oncomiR	PDGFR, MET	Negative	Inhibiting cancer cell migration, invasion, proliferation	(18)
Wu <i>et al</i> , 2015	miR-137	anti-oncomiR	Akt-2	Negative	Repressing cell proliferation, migration and invasion <i>in vitro</i> , and proliferation as well as metastasis <i>in vivo</i>	(21)
Liu <i>et al</i> , 2014;	miR-126	anti-oncomiR	PI3KR2, VEGFA	Negative	Blocking cell growth, clone formation and inducing apoptosis <i>in vitro</i> , suppressing tumor growth and angiogenesis <i>in vivo</i>	(22,24)
Chen <i>et al</i> , 2014						
Liu <i>et al</i> , 2012	miR-10b	oncomiR	HOXD10	Positive	Promoting tumor cell invasion	(26)
Zhang <i>et al</i> , 2012	miR-21	oncomiR	PTEN	ND	Facilitating GC cell growth, invasion and migration	(27)
Xie <i>et al</i> , 2018	miR-1	anti-oncomiR	VEGFA	ND	Inhibiting proliferation and migration of tumor cells and endothelial cells, repressing angiogenesis	(28)
Shen <i>et al</i> , 2016	miR-590-5p	oncomiR	RECK	Positive	Promoting cell proliferation, invasion and drug-resistance <i>in vitro</i> and tumor growth <i>in vivo</i>	(32)
Ma <i>et al</i> , 2014	miR-425	oncomiR	PTEN	Positive	Promoting cell survival, proliferation and drug-resistance <i>in vitro</i> and tumorigenicity <i>in vivo</i>	(45)
Pan <i>et al</i> , 2018	miR-7	anti-oncomiR	PTEN, PI3K	Negative	Repressing cell migration <i>in vitro</i> and tumor growth <i>in vivo</i> , and inducing apoptosis	(50)
Qi <i>et al</i> , 2017	miR-125	anti-oncomiR	HER2	Negative	Impairing the migration ability of tumor cells	(56)
Wu <i>et al</i> , 2018	miR-616-3p	oncomiR	PTEN	Positive	Facilitating EMT and angiogenesis	(57)
Li <i>et al</i> , 2016	miR-196b	oncomiR	ND	Positive	Positively regulating GC cell proliferation and invasion	(58)
Liang <i>et al</i> , 2015	miR-203	anti-oncomiR	PIK3CA	Negative	Suppressing tumor cell proliferation, colony formation and invasion	(59)
Wei <i>et al</i> , 2013	miR-449a	anti-oncomiR	Bcl-2	ND	Inducing GAC cell apoptosis and suppressing cell growth	(60)
Riquelme <i>et al</i> , 2016	miR-125b-2 miR-101-2, miR-451a	anti-oncomiR	PIK3CB, mTOR, TSC1 ^a	ND	Reducing cell viability, colony formation, migration and invasion, and increasing cell death	(61)
Zhang <i>et al</i> , 2015	miR-29s ^b	anti-oncomiR	Akt-2	Negative	Inhibiting invasion	(62)

Table III. Continued.

Author, year	miRNAs	General role	Regulatory sites	Pathway activity	Results	(Refs.)
Xu <i>et al.</i> , 2017	miR-379	anti-oncomiR	FAK	Negative	Repressing EMT and metastasis	(63)
Zhang <i>et al.</i> , 2010	miR-221	oncomiR	PTEN	Positive	Facilitating tumor cell growth, invasion and radio-resistance	(64)
	miR-222					
Yang <i>et al.</i> , 2013	miR-214	oncomiR	PTEN	ND	Positively regulating tumor cell proliferation, migration and invasion	(65)
Zhang <i>et al.</i> , 2017	miR-106b,	oncomiR	PTEN	ND	ND	(67)
	miR-93					
Guo <i>et al.</i> , 2014	miR-338-3p	anti-oncomiR	P-Rex2a	Negative	Inhibiting tumor cell proliferation, clonogenicity, and inducing G ₁ /S arrest, apoptosis <i>in vitro</i> and tumorigenicity <i>in vivo</i>	(68)
Ni <i>et al.</i> , 2018	miR-21	oncomiR	PTEN	Positive	Enhancing cancer stem cell properties, including cell self-renewal, cell migration, and chemoresistance	(71)
Wang <i>et al.</i> , 2016	miR-34a	anti-oncomiR	c-Myc	ND	Inhibiting cell proliferation, microsphere formation, drug-resistance, and migration potential	(72)
Yan <i>et al.</i> , 2016	miR-126	anti-oncomiR	PI3KR2, VEGFA	Negative	Modifying drug-resistance	(75)
Wang <i>et al.</i> , 2013	miR-19a/b	oncomiR	PTEN, Akt	Positive	Contributing to EMT and MDR of GC cells	(76)
Cao <i>et al.</i> , 2014	miR-34a	anti-oncomiR	ND	Negative	Mediating drug-sensitivity	(77)
Eto <i>et al.</i> , 2014	miR-21	oncomiR	PTEN	Positive	Promoting drug-resistance	(78)
Yang <i>et al.</i> , 2014	miR-106b	oncomiR	PTEN	ND	Advancing cell migration and invasion	(81)
Liu <i>et al.</i> , 2014	miR-34a	anti-oncomiR	EGFR	Negative	Repressing cell invasion	(83)
Li <i>et al.</i> , 2016	miR-23a	oncomiR	PTEN	Positive	Inducing EMT and tumor growth	(86)
Yu <i>et al.</i> , 2016	miR-148a	anti-oncomiR	CCK-BR	Negative	Repressing proliferation and migration of tumor cells <i>in vitro</i> , and tumorigenicity <i>in vivo</i>	(87)
Zhang <i>et al.</i> , 2016	miR-128b	anti-oncomiR	PDK 1	Negative	Suppressing tumor cell cycle, proliferation and invasion, and inducing apoptosis	(89)
Huang <i>et al.</i> , 2015	miR-338-3p	anti-oncomiR	MACC1	Negative	Inhibiting the migration, invasion and EMT	(99)
Cheng <i>et al.</i> , 2014	miR-137	anti-oncomiR	Cox-2	Negative	Suppressing cell proliferation, impairing cell migration and invasion as well as inducing apoptosis	(106)
Lu <i>et al.</i> , 2014	miR-19a	oncomiR	ND	Positive	Promoted cell proliferation, migration, invasion as well as EMT	(107)
Li <i>et al.</i> , 2013	miR-107	oncomiR	FOXO1	ND	Advancing proliferation and cell cycle	(108)

Table III. Continued.

Author, year	miRNAs	General role	Regulatory sites	Pathway activity	Results	(Refs.)
Xu <i>et al</i> , 2011	miR-335	anti-oncomiR	Bcl-w, SP1	Negative	Repressing invasion and metastasis <i>in vitro</i> and <i>in vivo</i>	(109)
Zhao <i>et al</i> , 2017	miR-320	anti-oncomiR	ND	Negative	Inhibiting invasion and inducing apoptosis	(110)

^amiR-101-2, miR-125b-2 and miR-451a target mTOR, PIK3CB and TSC1, respectively. ^bmiR-29s includes miR-29a, miR-29b and miR-29c. Akt, protein kinase B; Bcl-2, apoptosis regulator Bcl-2; Bcl-w, Bcl-2-like protein 2; CCK-BR, cholecystokinin B receptor; Cox-2, cyclooxygenase 2; EGFR, epidermal growth factor receptor; EMT, epithelial-mesenchymal transition; FAK, focal adhesion kinase; FOXO1, forkhead box protein O1; GAC, gastric adenocarcinoma; HER2, human epidermal growth factor receptor 2; HOXD10, homeobox D10; MACC1, metastasis-associated in colon cancer-1; MET, hepatocyte growth factor receptor; MDR, multidrug-resistance; miR, microRNA; mTOR, mammalian target of rapamycin; ND, not described; PDGFR, platelet-derived growth factor receptor; PI3K, phosphatidylinositol 3-kinase; PI3KR2, phosphoinositide-3-kinase regulatory subunit 2; P-Rex2a, phosphatidylinositol 3,4,5-trisphosphate RAC exchanger 2a; PTEN, phosphatase and tensin homolog; RECK, reversion-inducing-cysteine-rich protein with kazal motifs; SP1, specificity protein 1; TSC1, tuberous sclerosis 1; VEGFA, vascular endothelial growth factor A.

In addition to the involvement in the formation of GC tumors, the regulation of PI3K/Akt signaling by miRNAs is involved in oncogenic activities responsible for GC progression. The miR-29 family, consisting of miR-29a, miR-29b and miR-29c, was able to restrain Akt2 expression and subsequently inactivate GSK3 β , leading to the impaired invasive ability of GC cells (62). Focal adhesion kinase (FAK) is a crucial transducer of integrin-mediated signaling to downstream pathways, including the PI3K/Akt pathway (63). The activated FAK by integrins may form a binding site for the SH2 domain of p85 subunit and phosphorylate it, which may subsequently activate the p110 catalytic subunit of PI3K (63). Xu *et al* (63) identified that miR-379 inactivated Akt signaling by suppressing FAK expression, thus leading to inhibition of cell migration, invasion and EMT process. Cullin 4B, a scaffold protein, directly binds to the S2 region of the miR-125a promoter and transcriptionally represses miR-125a, through which it promotes HER2 expression, thus stimulating downstream PI3K/Akt signaling and the migration of GC cells. In addition to EMT, the activated Akt/mTOR signaling is an underlying mechanism of the induced angiogenesis by miR-616-3p in GC (57). Conversely, the reduced activation of Akt/mTOR signaling partially mediated the suppression of miR-126 on GC tumor growth and angiogenesis (24).

miRNAs target and regulate PTEN in GC

miRNAs are involved in PTEN downregulation. As mentioned above, genetic and epigenetic alteration of PTEN may lead to its downregulation in GC. A number of overexpressed miRNAs may additionally deregulate PTEN by directly combining to the 3'-UTR of its mRNA and thus silencing PTEN at the post-transcriptional level, which is considered another form of epigenetic modification. Chun-Zhi *et al* (64) demonstrated that miR-221 and miR-222 were upregulated in GC and possessed the ability to target PTEN. Furthermore, ectopic expression of miR-221 and miR-222 in GC cells led to a decreased expression level of PTEN (64). The silenced expression of PTEN in GC may additionally be due to other miRNAs negatively regulating it, including miR-136, miR-214 and miR-28 (5,12,65). Furthermore, the downregulated PTEN expression level was associated with adverse clinical parameters, including lymph node metastasis, poor differentiation and advanced TNM stage of patients with GC (65-67). Different from directly targeting PTEN, the tumor suppressor miR-338-3p was able to indirectly upregulate the activity of PTEN without altering its expression, by suppressing phosphatidylinositol 3,4,5-trisphosphate RAC exchanger 2a, a guanine nucleotide exchange factor for the RAC guanosine triphosphatase (GTPase), which stimulated PI3K signaling by serving as a PTEN-interacting protein and antagonizing it (68).

PTEN mediates oncogenic activities of miRNAs via PI3K/Akt signaling. Due to the critical negative regulator role of PTEN in PTEN/PI3K/Akt signaling, the suppression of PTEN by oncogenic miRNAs results in increased activity of downstream PI3K signaling, and consequently contributed to the malignant phenotypes of GC, including the promoted cell proliferation and survival, impaired drug-sensitivity, and enhanced invasiveness, metastasis and angiogenesis (Table III and Fig. 1). Among these miRNAs, miR-21 is significant. Zhang *et al* (27) demonstrated that miR-21 promoted the growth, invasion and

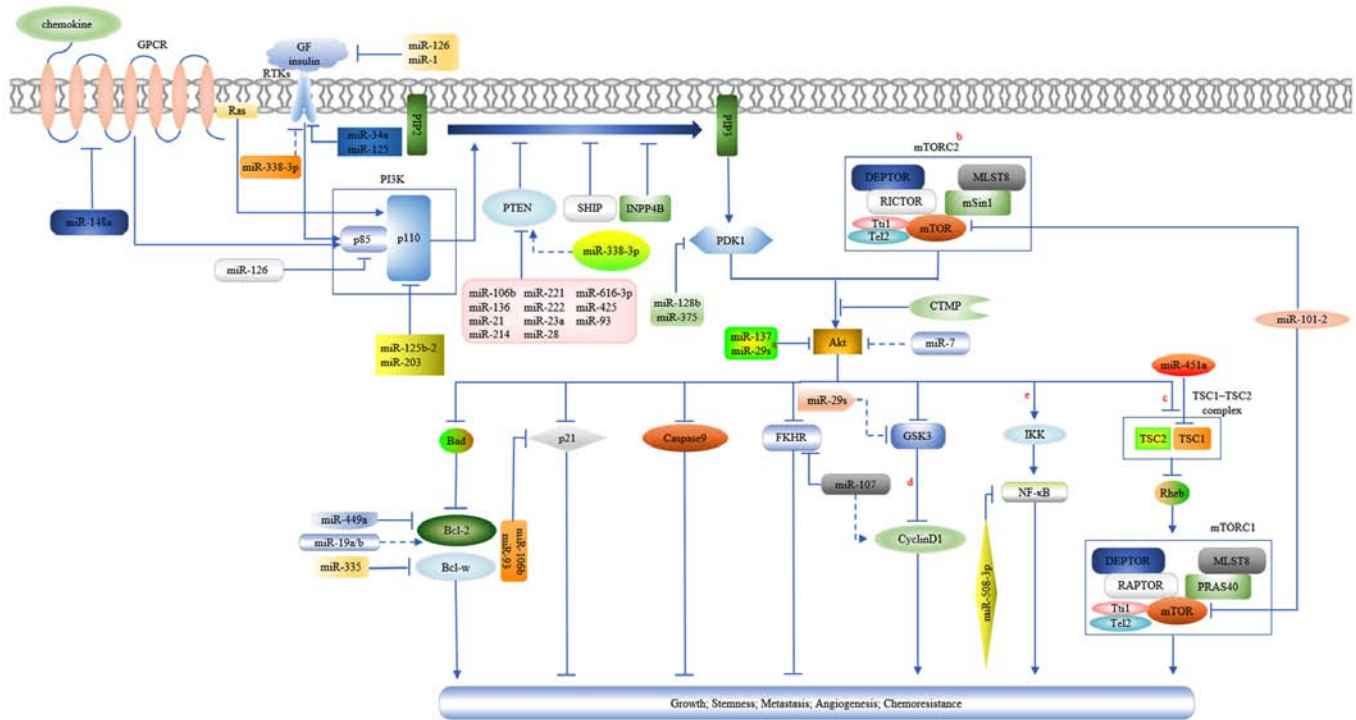


Figure 1. A diagram presenting the activation of the PTEN/PI3K/Akt signaling pathway and the regulations of miRNAs on it in GC. a, miR-29s include miR-29a, miR-29b and miR-29c. b, AKT may promote protein synthesis and cell growth by disintegrating the TSC1/TSC2 complex by phosphorylating TSC2. c, TSC1/TSC2 complex is a negative regulator of mTORC1 due to its GTPase-activating protein activity for the Rheb GTPase (a member of the Ras family), which may activate mTORC1. mTORC1 is involved in protein and lipid synthesis and anti-autophagy, thus promoting cell growth and proliferation. mTORC1 and mTORC2 possess the mTOR kinase, the scaffolding protein MLST8, the mTOR regulatory subunit DEPTOR, and the Tti1/Tel2 complex, which is critical for mTOR complex assembly and stability. The scaffolding protein RAPTOR and activity inhibitor PRAS40 are specific components belonging to mTORC1. Similarly, mTORC2 has its specific negative regulators, mSin1 and mTOR associated protein RICTOR (38,94,95). d, Inhibition of GSK3 by Akt leads to the accumulation and nuclear translocation of cytoplasmic β -catenin, which may induce the expression of cyclin D1 through its combination with transcription factors in the nucleus. The increased expression of cyclin D1 facilitates cell cycle progression. Furthermore, the decreased phosphorylation of cyclin D1 from GSK3 inhibition enhances its stabilization (14). e, Akt stimulates IKK by phosphorylation and subsequently, IKK activates NF- κ B by phosphorylating the inhibitor of κ B, which may mask the nuclear localization signals of NF- κ B and keep it sequestered in an inactive state in the cytoplasm. Activated NF- κ B may be translocated into the nucleus where it transcriptionally upregulates multiple genes, including positive cell-cycle regulators, anti-apoptotic and pro-survival factors (14,88,96). Arrowheads and perpendicular lines indicate stimulation and inhibition of downstream substrates, respectively; straight lines and dotted lines indicate direct and indirect effects on downstream substrates, respectively. Akt, protein kinase B; DEPTOR, DEP domain-containing mTOR-interacting protein; GF, growth factor; GSK3, glycogen synthase kinase 3; GTPase, guanosine triphosphate hydrolase; IKK, inhibitor of nuclear factor κ B kinase; miR, microRNA; MLST8, target of rapamycin complex subunit LST8; mSin1, mammalian stress-activated protein kinase interacting protein 1; mTOR, mammalian target of rapamycin; mTORC1, mTOR complex 1; mTORC2, mTOR complex 2; NF- κ B, nuclear factor κ B; PI3K, phosphatidylinositol 3-kinase; PRAS40, proline-rich AKT/PKB substrate 40 kDa; PTEN, phosphatase and tensin homolog; RAPTOR, regulatory-associated protein of mTOR; Rheb, guanosine triphosphate-binding protein Rheb; RICTOR, rapamycin-insensitive companion of mTOR; Tel2, telomere maintenance 2; TSC1, tuberous sclerosis protein 1; TSC2, tuberous sclerosis protein 2; Tti1, Tel2-interacting protein 1.

migration of GC cells by directly binding to the 3'-UTR of PTEN. Whereas antisense oligonucleotides against miR-21 were able to increase PTEN expression and impair downstream PI3K/Akt/mTOR signaling, leading to reverse effects on these biological behaviors of GC cells (27,69).

In addition, miR-21 was involved in the regulation of a number of Polycomb group (PcG) proteins on gastric cancer stem cells (CSCs), a small subset of cancer cells with self-renewal and tumor-initiating properties, which are critical in tumor metastasis, recurrence and chemoresistance (70). PcG family proteins, including polycomb group RING finger protein 2 (Mei-18), chromobox homolog 7 (CBX7) and enhancer of zeste homolog 2, form the multi-protein complexes, called polycomb repressive complexes, through which they epigenetically regulate homeotic genes expression by altering chromosomal structure or transcriptional repression (71). In this manner, PcG proteins exert effects in embryonic development, cell proliferation and differentiation, stem cell properties and tumorigenesis (71). Ni *et al* (71) demonstrated that in addition

to inhibiting p16, CBX7 was additionally able to upregulate miR-21 and thus enhance its downstream PTEN/Akt/p53 signaling, whereby it potentiated stem cell-like properties of GC cells, including augmented self-renewal and cell migration, enhanced chemoresistance and increased expression of stem cell markers (CD44 antigen and POU domain, class 5, transcription factor 1). B cell-specific Moloney murine leukemia virus integration site 1 (Bmi-1) is another significant PcG family member, which positively regulates stem cell-like phenotypes of GC, and similarly, it contributed to the CSCs characteristics via the miR-21/PTEN/Akt axis (72). However, Bmi-1 was additionally able to directly inhibit the expression of PTEN and thus activate Akt signaling (72). miR-34a, which negatively regulated CSCs phenotypes, was upregulated by Bmi-1. Notably, miR-34a was able to conversely inhibit Bmi-1 by binding to its promoter, and this reciprocal modulation between Bmi-1 and miR-34a constitute a negative feedback loop in maintaining the stem cell-like properties of GC

cells (72). Mel-18 was additionally reported to be involved in the regulation of gastric CSCs properties; however, inversely, it exerted negative effects by downregulating the expression of miR-21 and therefore increasing PTEN expression (73).

miRNAs regulate chemosensitivity via the PTEN/PI3K/Akt pathway. miRNAs and PTEN/PI3K/Akt signaling have been significantly implicated in the occurrence of drug-resistance in GC (11,74). Therefore, elucidating the regulation of PTEN/PI3K/Akt pathway by miRNAs involved in the decreased response to chemotherapies may help to clarify the underlying mechanisms.

There are numerous identified causes responsible for tumor chemo-resistance, including intracellular drug efflux, failure to undergo apoptosis, target gene alteration, drug or metabolite detoxification and DNA repair enhancement, among which, the increased drug efflux is a most common one, involving a family of ATP-dependent efflux pumps, termed ATP-binding cassette (ABC) transporters (6,74). Consistently, the enhanced resistance of tumor cells to DDP resulted from overexpression of the ABC transporter, and multidrug resistance-associated protein 1 was observed in GC, which was induced by the attenuated repression of PI3K/Akt pathway due to downregulated miR-126 expression (75). Wang *et al* (76) demonstrated that miR-19a/b modulated multidrug resistance by targeting PTEN, which may be partly attributed to the accelerated efflux through miR-19a/b induced upregulation of permeability glycoprotein, another primary member of the ABC transporter. The increased Bcl-2, together with the decreased apoptosis regulator BAX and caspase-3, in GC cells transfected with miR-19a/b represented reduced susceptibility to drug-induced apoptosis, which is another pivotal mechanism underlying chemoresistance as anticancer agents function by inducing tumor cells apoptosis (76). The activated PI3K pathway frequently transduces survival signals in GC (11,76). Survivin, the smallest mammalian member of the inhibitor of apoptosis gene family, inhibits apoptosis initiated by the extrinsic or intrinsic pathways, and it engages in the positive regulation of DDP-induced GC cell apoptosis by miR-34a through PI3K/Akt signaling (77). In addition to conventional chemotherapeutic drugs, suppression of apoptosis induced by overexpressed miR-21 via the PTEN/PI3K/Akt pathway may additionally account for the resistance to trastuzumab of HER2-positive GC cells (78). Consistent with the prediction that miRNAs regulate drug-resistance by interfering with specific therapeutic targets, miR-125a, which targets HER2 and inhibits its downstream Akt signaling, is able to increase the efficacy of trastuzumab when used in combination with suppressing GC cell proliferation (74,79). CSCs are considered a cause of tumor relapse following successful chemotherapy, owing to their quiescence, DNA repair capacity and ABC-transporter expression (70). miRNA has been reported to regulate resistance to epirubicin and other stem cell-like properties through PTEN/PI3K/AKT signaling in GC (71,72).

In previous studies examining the involvement of PI3K/Akt signaling in GC drug-resistance, inhibitors against this pathway have been frequently employed. Yang *et al* (6) demonstrated that LY294002 inhibited miR-21-activated PI3K/Akt signaling and consequently promoted cell survival and DDP resistance. Similarly, compared with controls, lower activity of PI3K/Akt

signaling while higher percentage of apoptosis cells were documented in DDP incubated GC cells following treatment with miR-34a mimics and wortmannin (77). These results not only suggested the association of this pathway in sensitivity to anticancer drugs modulated by miRNAs; however, additionally suggest the potential clinical usage of these small molecule inhibitors in modifying chemotherapy efficacy for patients with GC.

miRNA/PTEN axis is involved in gastric tumor microenvironment. During cancer progression, a co-evolving and supportive environment termed the tumor microenvironment is important, which consists of ECM adjacent to cancer cells and non-malignant stromal cells, including fibroblasts, endothelial cells and hematopoietic cells, primarily macrophages and lymphocytes (2). The crosstalk between cancer cells and the environment may have substantial impacts on tumor development, including tumor growth, metastasis and refractoriness to therapies, wherein the regulation of PTEN/PI3K/Akt by miRNAs may be involved (2,80). Yang *et al* (81) identified four upregulated miRNAs and seven downregulated miRNAs in gastric cancer associated fibroblasts (CAFs), the most abundant cells in the tumor microenvironment, compared with normal fibroblasts. CAFs promoted the growth and metastasis of tumor cells, and silencing miR-106b in CAFs abolished the contributive effect on cell motility due to PTEN upregulation (81). Similarly, when cultured in conditioned medium derived from miR-1-transfected GC cells, microvascular endothelial cells were prevented from migrating and forming novel vessels, which was associated with the decreased VEGF-A and endothelin 1 (28). Zheng *et al* (2) observed that miR-21 in exosomes secreted from tumor-associated macrophages (TAMs) may be ingested by GC cells, and led to impaired sensitivity to DDP via the PTEN/PI3K/Akt pathway. Under low glucose condition, the energy-responding miR-451 may be transferred from GC cells to infiltrated T cells through exosomes, thus enhancing the differentiation of T-helper 17, wherein the upregulated mTOR signaling induced by miR-451 was involved (30).

The bidirectional impact between cancer cells and tumor microenvironment may additionally be fulfilled by the secreted soluble factors, including cytokines, chemokines and growth factors in autocrine or paracrine manner (80). Ma *et al* (45) demonstrated that when exposing GC cells to pro-inflammatory cytokine interleukin-1 β , miR-425 was transcriptionally induced, and thus the PTEN expression level was decreased, leading to promoted cell survival and proliferation *in vitro* in addition to tumor growth *in vivo*. EMT of GC cells induced by TGF- β 1 may be stimulated by miR-21 through its negative regulation of PTEN and the subsequent activation of PI3K/Akt signaling (66). MMPs, a family of zinc-dependent proteases released by tumor cells and TAMs, were implicated in numerous oncogenic processes, including ECM degradation, tumor cell migration and the release of growth factors sequestered within the ECM (82). A previous study demonstrated that MMP-7 was regulated by miR-34a through EGFR/PI3K/Akt signaling during GC progression (83).

Other ncRNAs in co-regulation of the PTEN/PI3K/Akt pathway. ncRNAs, refer to a type of RNA, which do not encode proteins, primarily including miRNAs, long non-coding

RNAs (lncRNAs), in addition to pseudogenes and circular RNAs (circRNAs) (84). In the competitive endogenous RNA (ceRNA) hypothesis depicting a post-transcriptional regulation network mediated by miRNAs, any RNA molecules sharing one or more miRNA response elements, including protein-coding and ncRNAs, are able to compete for binding to miRNAs and subsequently co-regulate expression of one another (9). Due to their complexity, diversity and frequent dysregulation in cancer, ncRNAs as ceRNAs have attracted increasing attention in oncogenesis and development, regarding the novel layer of post-transcriptional regulation on miRNA-targeted mRNAs provided by them (84).

HOX transcript antisense intergenic RNA (HOTAIR), a lncRNA associated with Polycomb repressive complex 2, was demonstrated to be capable of functioning as a ceRNA of miR-126 to promote expression of miR-126 target genes VEGF-A and PI3KR2, resulting in the activation of PI3K/Akt signaling, which was underlying the DDP-resistance induced by overexpressed HOTAIR in GC (75). Pseudogenes are segments of DNA associated with real genes, which are frequently derived from accumulated mutations in a gene and thus commonly lose specific functionality compared with the complete gene (85). Phosphatase and tensin homolog, pseudogene 1, was reported to serve as a tumor suppressor of GC by inhibiting tumor growth and metastasis, whereby it upregulated the expression of its cognate gene PTEN, by sponging miR-106b and miR-93 (67,84). circRNAs are another class of non-coding RNAs, with the 3' and 5' ends of RNA molecules joined together to form a covalently closed continuous loop. Pan *et al* (50) identified that the circRNA sponge for miR-7, was able to antagonize the effects of miR-7 on the PTEN/PI3K/Akt pathway, and reverse its repression of tumor cell migration and colony formation *in vitro* and GC genesis *in vivo*.

miRNAs synergistically modulate the PI3K cascade with other pathways. The complex crosstalk and pathway convergence among different signaling pathways ensure that no pathway operates in isolation; however, miRNAs exert extensive regulation and a single miRNA may regulate multiple targets due to its imperfect complementary pairing with mRNAs. It is therefore rational to address that miRNAs may regulate PTEN/PI3K/Akt signaling with other crucial pathways co-operatively. Indeed, this has been validated in the pathologic process of GC.

The complex associations between the PI3K/Akt pathway and the Ras/Raf proto-oncogene serine/threonine-protein kinase (Raf)/mitogen-activated protein kinase (MAPK) kinase/MAPK pathway have been well documented, including the inhibition of the extracellular-regulated kinase (ERK) pathway by Akt via its direct phosphorylation of c-Raf on T259, and similarly, the phosphorylation of Akt on amino acid residue S83 of apoptosis signal-regulated kinase 1, which leads to the impaired activation of the c-Jun N-terminal kinase and p38 pathways (4,15). Ras was additionally able to function upstream of PI3K by interacting with the RBD of p110 catalytic subunit and thus activating PI3K signaling (39). In GC, Li *et al* (86) demonstrated that the activation of Akt in addition to the ERK pathways accounted for miR-23a-induced EMT. It was observed that miR-126 repressed angiogenesis by simultaneously inhibiting downstream Akt/mTOR and

ERK signaling (24). In addition to Akt and ERK signaling, the activation of the signal transducer and activator of transcription 3 (STAT3) pathway was involved in the oncogenic activities induced by miR-590-5p, including the promotion of cell proliferation, invasion, drug-resistance and tumor growth (32). Conversely, the negative regulation of Akt and STAT3 signaling by targeting the GPCR for gastrin and cholecystokinin may be the underlying mechanism for the tumor-suppressive role of miR-148a in GC (87).

In GC cells, it has been suggested that the activation of PI3K or loss of PTEN was able to protect integrin-linked kinase (ILK) from proteasome-mediated degradation (88). Enhanced ILK may subsequently activate Ras and promote the formation of the IQ motif-containing GTPase-activating protein 1-Ras complex, which stimulated the c-Raf/MEK1/2/ERK1/2/ribosomal S6 kinase/inhibitor of κ B α /nuclear factor (NF)- κ B signaling, leading to the increased cell growth, migration and decreased sensitivity of 5-FU and DDP (88). Consistently, miR-128b was reported to repress GC cell growth, invasion and promote apoptosis through Akt/NF- κ B signaling due to its negative post-transcriptional regulation of PDK1 (89). Furthermore, PI3K/Akt/NF- κ B signaling inactivation was a possible mechanism of the pro-apoptosis effect of celastrol, an antitumor plant triterpene with the ability to inhibit miR-21 expression (90). Apart from serving roles downstream of the PI3K/Akt pathway, NF- κ B was additionally able to affect the expression of PTEN and downstream Akt signaling, mediated by its transcriptional regulation of miRNAs, including miR-425 and miR-21 (45,71). Notably, the increased NF- κ B transcriptional activity may be due to the upregulated Akt activation (45,71).

5. Conclusion

In the last decade or two, the close association between miRNA dysregulation and GC has been well documented. In previous studies investigating the mechanisms by which miRNAs are involved in gastric tumorigenicity and progression, the results demonstrated that dysregulated miRNAs exerted their promotive effects by post-transcriptionally regulating oncogenes and tumor-suppressors, and thus affecting associated canonical pathways, among which PTEN/PI3K/Akt was a critical one due to its decisive role in GC tumor growth, metastasis, angiogenesis, stemness and chemoresistance.

Identifying molecular causes of GC is of great importance in pattern recognition and therapeutic strategies. The poor prognosis of patients with GC primarily results from late detection, aggressive progression, poor response to available therapies and relapse (6,8,49). Therefore, in the present review, it was discussed how miRNAs are involved in the regulation of gastric CSCs and tumor environment through PTEN/PI3K/Akt signaling, which bears resemblance to the 'seed' and 'soil' in GC pathogenesis (91), respectively. Similar investigations have additionally been summarized regarding sensitivity to conventional chemotherapies in addition to target therapies against this tumor. Based on these molecular mechanisms, the potential applications of miRNAs as novel biomarkers for diagnosis and prognosis-prediction were discussed. As drugs (including miRNA mimics and inhibitors) have been tested in preclinical and clinical trials of a number of diseases (92), the

role of miRNAs as promising therapeutic targets for GC was additionally discussed. Besides, inhibitors or monoclonal antibodies against the PTEN/PI3K/Akt pathway and its up/down stream molecules have been in different phases of clinical trial or in applications for GC. Furthermore, it has been reported that ectopic expression of miRNA in combination with a PI3K/Akt pathway inhibitor may acquire synergistic treatment efficacy (93). Therefore, further investigations into miRNAs and PTEN/PI3K/Akt signaling in addition to their interactions are necessary and rewarding for improving the clinical management and outcome of patients with GC.

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Availability of data and materials

Data sharing is not applicable to this article, as no datasets were generated or analyzed during the current study.

Authors' contributions

MH and SZ wrote the manuscript. SX and XX constructed the tables and diagrams. MH, SZ, SX, XX and XZ checked and revised the manuscript and were involved in the conception of the study. Additionally, XZ was responsible for the organization, revision and submission of this manuscript. 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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