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HMGA2 regulation by miRNAs in cancer: Affecting cancer hallmarks and therapy response

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Abbreviations: AP1, activator protein 1; APC, adenomatous polyposis coli; ALDH1, aldehyde dehydrogenase 1; AI, artificial intelligence; ATR, ataxia telangiectasia and Rad3-related protein; ABCB1, ATP-binding cassette sub-family B member 1; ATG5, Autophagy Related 5; BZW1, Basic leucine zipper and W2 domain-containing protein 1; Bcl-2, B-cell lymphoma 2; BCLAF1, Bcl-2-associated transcription factor1; BRCA1, Breast cancer gene 1; CPT1A, Carnitine palmitoyltransferase 1 A; Chk1, Checkpoint kinase 1; CircRNA, Circular RNA; ceRNA, Competing endogenous RNA; CBP, Cyclic adenosine monophosphate Response Element Binding protein Binding Protein; DCTD, Deoxycytidine monophosphate deaminase; DNMT3B, DNA methyltransferases 3 B; E2F1, E2F Transcription Factor 1; EGF-L7, Epidermal growth factor-like protein 7; ESCC, Esophageal squamous cell carcinoma; ER- α 36, Estrogen receptor alpha-36; EIF4A2, Eukaryotic initiation factor 4A-II; eIF5A2, Eukaryotic translation initiation factor 5A-2; ERK, Extracellular signal-regulated kinases; FEN1, Flap endonuclease 1; FAK, Focal adhesion kinase; Foxi1, Forkhead box I1; FOXL2, Forkhead box protein L2; GBM, Glioblastoma multiforme; GSK-3 β , Glycogen synthase kinase-3 β ; HNSCC, Head and neck squamous cell carcinoma; HN1, Hematological and neurological expressed 1; HBXIP, Hepatitis B virus X-interacting protein; HCC, Hepatocellular carcinoma; HNF4G, Hepatocyte nuclear factor 4-gamma; HNRNPK, Heterogeneous nuclear ribonucleoprotein K; HOXA9, Homeobox A9; HIF1A, Hypoxia-inducible factor 1-alpha; IKK ϵ , Inhibitor Of Nuclear Factor Kappa B Kinase Subunit Epsilon; KLHL21, Kelch-like protein 21; KRT17, Keratin 17; LAMC2, Laminin subunit gamma-2; LATS1, Large tumor suppressor kinase 1; LSCC, Laryngeal squamous cell carcinoma; LTBP-1, Latent Transforming Growth Factor Beta Binding Protein 1; LncRNA, Long non-coding RNA; mTOR, Mammalian target of rapamycin; MMP2, Matrix metalloproteinase 2; MITF, Melanocyte Inducing Transcription Factor; MET, Mesenchymal-epithelial transition factor; MTA1, Metastasis-associated protein 1; MiRNA, MicroRNA; MAPK, Mitogen-activated protein kinases; SMAD2, Mothers against decapentaplegic homolog 2; MDR-1, Multidrug resistance gene 1; MDM2, Murine double minute 2; NF1, Neurofibromatosis type 1; NETO2, Neuropilin and tolloid-like protein 2; NcrRNA, Non-coding RNA; NF- κ B1, Nuclear factor kappa-light-chain-enhancer of activated B cells 1; NR3C1, Nuclear receptor subfamily 3, group C, member 1; OSCC, Oral squamous cell carcinoma; OLR1, Oxidized Low Density Lipoprotein Receptor 1; P-gp, P-glycoprotein; PTC, Papillary thyroid carcinoma; PDAC, Pancreatic ductal adenocarcinoma; POSTN, Periostin; PTEN, Phosphatase and Tensin Homolog deleted on Chromosome 10; PI3K, Phosphoinositide 3-kinase; PAICS, Phosphoribosylaminoimidazole carboxylase/phosphoribosylaminoimidazole succinocarboxamide synthetase; PDGFRA, Platelet Derived Growth Factor Receptor Alpha; PCL, Poly (ϵ -caprolactone); PEG, Polyethylene glycol; PEI, Polyethyleneimine; PLGA, Poly(lactic-co-glycolic acid); PD-L1, Programmed death-ligand 1; PP4R1, Protein phosphatase 4 regulatory subunit 1; RBP1, Retinol-binding protein 1; RKIP, Raf kinase inhibitory protein; ROCK1, Rho-associated protein kinase; SERPINE1, Serpin Family E Member 1; STAT3, Signal transducer and activator of transcription 3; SP1, Specificity protein 1; SOX2, SRY-box 2; SOX4, SRY-related HMG box transcription factor 4; TET1, Ten-eleven translocation methylcytosine dioxygenase 1; TXNIP, Thioredoxin interacting protein; THBS2, Thrombospondin-2; TCF3, Transcription factor 3; TGF- β R1, Transforming growth factor beta receptor I; Tgfr3, Transforming growth factor beta receptor type 3; TAM, Tumor associated macrophage; TME, Tumor micro-environment; TP53INP1, Tumor protein p53-inducible nuclear protein 1; U2AF2, U2 auxiliary factor 2; VEGFR2, Vascular endothelial growth factor receptor 2; YAP, Yes-associated protein 1; ZEB, Zinc finger E-box-binding homeobox; Snail, Zinc finger protein SNAI1.

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ABSTRACT

High mobility group A 2 (HMGA2) is a protein that modulates the structure of chromatin in the nucleus. Importantly, aberrant expression of HMGA2 occurs during carcinogenesis, and this protein is an upstream mediator of cancer hallmarks including evasion of apoptosis, proliferation, invasion, metastasis, and therapy resistance. HMGA2 targets critical signaling pathways such as Wnt/ β -catenin and mTOR in cancer cells. Therefore, suppression of HMGA2 function notably decreases cancer progression and improves outcome in patients. As HMGA2 is mainly oncogenic, targeting expression by non-coding RNAs (ncRNAs) is crucial to take into consideration since it affects HMGA2 function. MicroRNAs (miRNAs) belong to ncRNAs and are master regulators of vital cell processes, which affect all aspects of cancer hallmarks. Long ncRNAs (lncRNAs) and circular RNAs (circRNAs), other members of ncRNAs, are upstream mediators of miRNAs. The current review intends to discuss the importance of the miRNA/HMGA2 axis in modulation of various types of cancer, and mentions lncRNAs and circRNAs, which regulate this axis as upstream mediators. Finally, we discuss the effect of miRNAs and HMGA2 interactions on the response of cancer cells to therapy. Regarding the critical role of HMGA2 in regulation of critical signaling pathways in cancer cells, and considering the confirmed interaction between HMGA2 and one of the master regulators of cancer, miRNAs, targeting miRNA/HMGA2 axis in cancer therapy is promising and this could be the subject of future clinical trial experiments.

1. Introduction

The high mobility group (HMG) proteins, identified in 1973, are non-histone components of chromatin, which are placed in only 3% of histone content weight [1–3]. HMG proteins including HMGA, HMGB, and HMGN are involved in modulating chromatin structure and participating in DNA recombination. Importantly, HMG proteins are highly regulated and affected by developmental and environmental factors. Also, aberrant expression of HMGs is shown to change the phenotype of the cell to increase the development of disorders [4–6]. Moreover, chromosomal translocation-induced HMGA gene rearrangement has been detected in benign tumors of mesenchymal origin. Besides, HMGA protein overexpression is a recurrent characteristic of human malignant cancers and is associated with poor prognosis and reduced survival rate in patients. Importantly, several mechanisms are involved in the oncogenic activity of HMGA which includes targeting E2F Transcription Factor 1 (E2F1) and Activator protein 1 (AP1), triggering cyclin A expression, suppression of apoptosis induction by p53, disrupting DNA repair, increasing the expression of inflammatory-related proteins, and targeting factors involved in EMT. It is worth mentioning that HMGA2 is overexpressed during embryogenesis and in cancers, while HMGA2 is hardly detected in normal cells of adults [7]. Regarding this point, targeting HMGA2 for cancer therapy could be a potential strategy in combating cancer.

Non-coding RNAs (ncRNAs) are derived from the non-protein coding part of the genome and a vast number of studies has revealed their critical function in cell processes such as gene expression. ncRNAs are classified based on length: less than 200 nt as microRNAs (miRNAs), and more than 200 nt in length as long non-coding RNAs (lncRNAs) [8–10]. Importantly, ncRNAs are believed to affect all cancer hallmarks and critical signaling pathways in cancer progression which make these molecules eligible for targeting in cancer therapy [11]. Dysregulation of

miRNAs has been shown to be associated with malignancies. Also, different characteristics of cancer cells including proliferation, apoptosis, metabolic reprogramming, angiogenesis, metastasis, and therapy resistance have been demonstrated to occur following the alteration in miRNAs expression pattern. miRNAs mainly have onco-suppressor or oncogenic functions. However, some of them possess both functions. miRNAs which mediate malignant properties exert their role by suppressing tumor inhibitor genes or upregulating the expression level of oncogenes. In contrast, tumor suppressor miRNAs inhibit cancer progression via attenuation of oncogenes (Table 1). Thus, miRNAs are powerful targets for cancer therapy and use of onco-miRNA inhibitors or synthetic miRNA mimics are two therapeutic approaches. In addition, delivery of miRNAs to the targeted tissue is of importance. Several delivery systems and vectors are developed, including inorganic, polymer-based, and lipid-based vectors, exosomes, and extracellular vesicles [12–14]. More importantly, miRNAs are potential biomarkers for cancer diagnosis and prognosis [15,16], and various clinical trials are in progress to use miRNAs as biomarker tools.

Regarding the critical role of ncRNAs in regulating cancer progression, this review aims to discuss the regulatory role of miRNA on HMGA2 for modulating cancer progression. Moreover, lncRNAs and circular RNAs (circRNAs) as upstream mediators of miRNAs/HMGA2 axis are mentioned in this review. The published articles selected for this review were searched over online web databases and the search was mostly limited to the papers published after 2018.

2. HMGA2 protein

HMGs are non-histone, chromatin-associated proteins, which exert critical functions on DNA processes such as replication, transcription, recombination, and DNA repair. For regulating transcription and maintaining the chromatin structure, HMG proteins bind to the minor

Table 1

The regulatory role of miRNAs in various types of cancer.

Function	Expression level	miRNA	Cancer Type	Signaling network	Ref
Tumor suppressor	Downregulation	miRNA-124-3p	Gastric cancer	HRCT1/ERBB2- MAPK	[17]
		miRNA-944	Tongue cancer	MMP-10/AXL-	[18]
		miRNA-335 and – 145	Breast cancer	PD-L1	[19]
		miRNA-598	Non-small-cell lung cancer (NSCLC)	THBS2	[20]
		miRNA-10a-5p	Clear cell renal cell carcinoma (CCRC)	SERPINE1	[21]
		miRNA-766-3p	Colorectal cancer (CRC)	HNF4G/PI3K/AKT	[22]
		miRNA-4731-5p	Breast cancer	PAICS/FAK	[23]
		miRNA-375	Prostate cancer	PTPN4/STAT3	[24]
		miRNA-660	Breast cancer	KLHL21/IKK β /NF- κ B/p65	[25]
		miRNA-182	Prostate cancer	MITF	[26]
Tumor promoting	Upregulation	miRNA-23b-3p	Salivary adenoid cystic carcinoma	PTEN	[27]
		miRNA-20a	NSCLC	PD-L1	[28]

grooves of DNA. Regarding their non-specificity toward DNA sequences, HMGs supply an excellent mechanism for DNA-protein interaction [29–31]. Three subfamilies exist for the high mobility group of proteins which include HMGA, HMGB, and HMGN, and each one has its “unique protein signature and a functional sequence motif; ‘AT-hook’ for HMGA, ‘HMG-box’ for HMGB, and ‘Nucleosomal binding domain’ for HMGN” [32].

The mammalian high mobility group protein AT-hook (HMGA) consists of “four members including HMGA1a, HMGA1b, and HMGA1c which are encoded by the *HMGA1* gene, and HMGA2 which is encoded by *HMGA2* gene”. In addition to the AR-hook domain, which helps to bind short AT enriched sites on DNA, HMGAs also have a C-terminal tail. Interestingly, HMGA1 and HMGA2 have structural and functional similarities, but there are some genes which are targeted only by one of them, resulting in different functions of these two proteins in cancer [4, 32]. In addition to the DNA, HMGA2 could also interact with proteins. For instance, HMGA2 promotes pituitary tumorigenesis by promoting E2F1 activity (Fig. 1) [33,34].

3. Regulatory role of miRNA/HMGA2 axis in gastrointestinal tract cancers

3.1. Gastric cancer

Accumulating data revealed the critical role of HMGA2 in regulation of progression of gastrointestinal cancers. In gastric cancer, it was found that HMGA2 promotes gastric cancer cell motility, growth, EMT, sphere formation, and stem cell induction by augmenting stem cell markers including CD44, Aldehyde dehydrogenase 1 (ALDH1), SRY-box 2 (SOX2), and Oct4, and also EMT-related factors including Snail and β -catenin [35]. EMT is a dynamic and complicated process characterized by losing cell-cell and cell-extracellular adhesion and also gaining

mesenchymal properties. Moreover, EMT is a cancer hallmark and is involved in cancer metastasis and invasion processes, as well in drug resistance. EMT is mediated by EMT-related transcription factors including Zinc finger E-box-binding homeobox (ZEB), Zinc finger protein SNAI1 (Snail), TWIST, and Slug [36–38]. It was also found that Twist1, another EMT-related factor, could be regulated by HMGA2 in increasing EMT in gastric cancer [39]. In addition, HMGA2 accelerates transactivation of Forkhead box protein L2 (FOXL2) via E2F1, and FOXL2 downstream target ITGA2 for increasing EMT and metastasis to lymph nodes and distant tissues in gastric cancer [40]. The interaction between miRNAs and HMGA2 for modulating gastric cancer progression has been studied. For instance, miRNA-503 is an onco-suppressor miRNA whose inhibitory role on gastric cancer progression has been confirmed in distinct studies [41,42]. Also, miRNA-503 negatively regulates HMGA2 for its inhibitory function in gastric cancer cells. It was revealed that low expression level of miRNA-503 is associated with poor overall survival, lymph node metastasis, and high tumor size, while its upregulation resulted in inhibition of tumor cell growth, proliferation, colony formation, and invasion [43]. It was shown that miRNA-495 regulates multiple epigenetic modifiers to suppress gastric cancer tumorigenesis [44]. In addition, this miRNA triggers apoptosis and inhibits proliferation and migration in gastric cancer cells via upregulation of caspase 3/9 and Bax, and suppressing Cyclin D1 and PI3K/Akt/Mammalian target of rapamycin (mTOR) signaling pathway [45]. It bears noting that PI3K/Akt/mTOR is one of the most important signaling pathways in tumorigenesis and has a regulatory role in all of the cancer hallmarks [46,47]. More importantly, invasion and migration of gastric cancer could be suppressed by miRNA-495 through targeting HMGA2 [48]. Another miRNA with inhibitory effect on gastric cancer is miRNA-491. The results of a study have revealed that miRNA-491 attenuates gastric cancer cell proliferation, invasion and migration by targeting JMJD2B [49]. However, suppression of this miRNA by

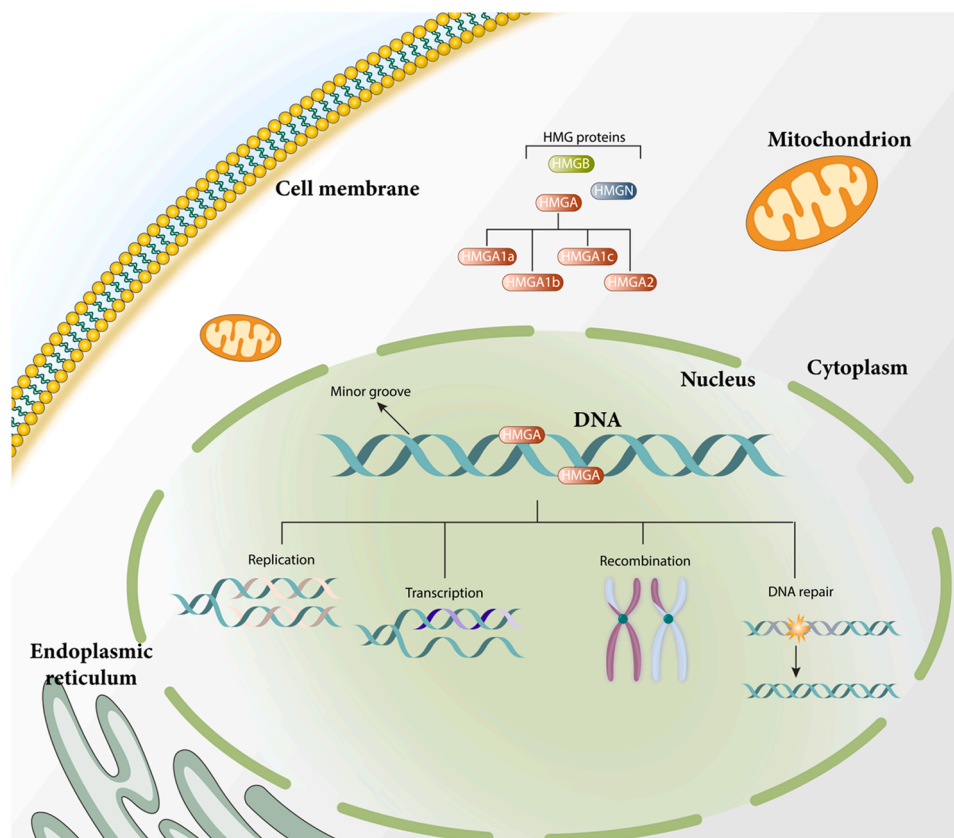


Fig. 1. HMG proteins classification and HMGA functions in cells. HMGA proteins regulate DNA processes including replication, transcription, recombination, and repair by binding to its minor grooves. HMG: High mobility group.

oncogenic factors is in favor of gastric cancer progression. For instance, lncRNA SNHG8 suppresses miRNA-491 to upregulate Platelet Derived Growth Factor Receptor Alpha (PDGFRA) in increasing gastric cancer cell proliferation and invasion [50]. Another study has shown that Forkhead box I1 (Foxi1) binds to the promoter region of miRNA-491-5p to mediate its activation. Then, miRNA-491-5p suppresses the Wnt3a/ β -catenin signaling pathway to suppress gastric cancer progression [51]. Wnt/ β -catenin signaling exerts critical roles in normal and cancer cells such as regulating homeostasis, development, cell fate, and cancer hallmarks. Wnt/ β -catenin high activation in cancers makes it a common target for cancer therapy. However, regarding its important functions in homeostasis, its suppression during cancer therapy is associated with side effects. Interestingly, some cancer-specific Wnt signaling regulators are developed to overcome this issue. Wnt signaling comprises various factors, which regulate its activation or turn off. Briefly, the destruction complex of adenomatous polyposis coli (APC), glycogen synthase kinase-3 β (GSK-3 β), Axin, and protein phosphatase 2A mediates β -catenin degradation through its phosphorylation and ubiquitination. Upon binding of Wnt ligands to their receptors, the destruction complex is interrupted and then, the level of β -catenin increases in the cytoplasm. After translocation into the nucleus, β -catenin changes the expression level of its downstream targets [52–55]. In addition, it was demonstrated that knock down of miRNA-491 leads to gastric cancer progression. In contrast, miRNA-491 overexpression suppresses cancer proliferation and migration through silencing HMGA2 [56].

MiRNA-490-3p was found to reduce gastric cancer cell proliferation while increasing apoptosis by directly targeting Akt1 [57]. In gastric cancer, circFAM73A upregulation promotes stem cell-like properties of gastric cancer cells to facilitate cell proliferation through regulation of

miRNA-490-3p/HMGA2 axis and targeting Heterogeneous nuclear ribonucleoprotein K (HNRNP) for increasing β -catenin stability. In addition, activity of E2F1 and HNRNP promotes circFAM73A expression [58]. Circ_0000267 is an oncogenic circRNA with high expression level in hepatocellular carcinoma (HCC) [59]. Also in gastric cancer, circ_0000267 facilitates tumor proliferation, EMT, invasion and metastasis. Circ_0000267 adsorbs miRNA-503-5p to increase HMGA2 expression [60]. Oncogenic function of lncRNA FEZF1-AS1 is revealed in different cancers [61]. For instance, in colorectal cancer lncRNA FEZF1-AS1 promotes tumor proliferation and metastasis [62,63]. Furthermore, Wnt signaling has been shown to be a downstream target of lncRNA FEZF1-AS1 in increasing EMT in NSCLC [64]. Moreover, breast cancer stemness and oncogenesis is regulated by lncRNA FEZF1-AS1 which targets miRNA-30a/Nanog axis [65]. Targeting miRNA-30a by lncRNA FEZF1-AS1 for increasing cancer progression has been also revealed in colorectal cancer [66]. Also, in gastric cancer, lncRNA FEZF1-AS1 targets Wnt signaling to augment tumorigenesis [67]. Interestingly, a study has revealed that lncRNA FEZF1-AS1 which plays oncogenic role in gastric cancer acts as a sponge for miRNA-363-3p to increase HMGA2, thereby promoting gastric cancer stem cell proliferation, invasion, and migration [68]. Similar to lncRNA FEZF1-AS1, various studies have confirmed the oncogenic role of lncRNA OIP5-AS1 in cancers [69–72]. LncRNA OIP5-AS1 promotes gastric cancer cell proliferation while inhibiting apoptosis by increasing HMGA2 function. Furthermore, OIP5-AS1 acts as a sponge for miRNA-367-3p to promote expression of HMGA2 and its downstream targets including PI3K/AKT and Wnt/ β -catenin pathways [73]. Additionally, it was elucidated that the expression level of lncRNA ROR and HMGA2 in gastric cancer is increased, while miRNA-519d-3p is down-regulated. ROR overexpression leads to promoted cell proliferation,

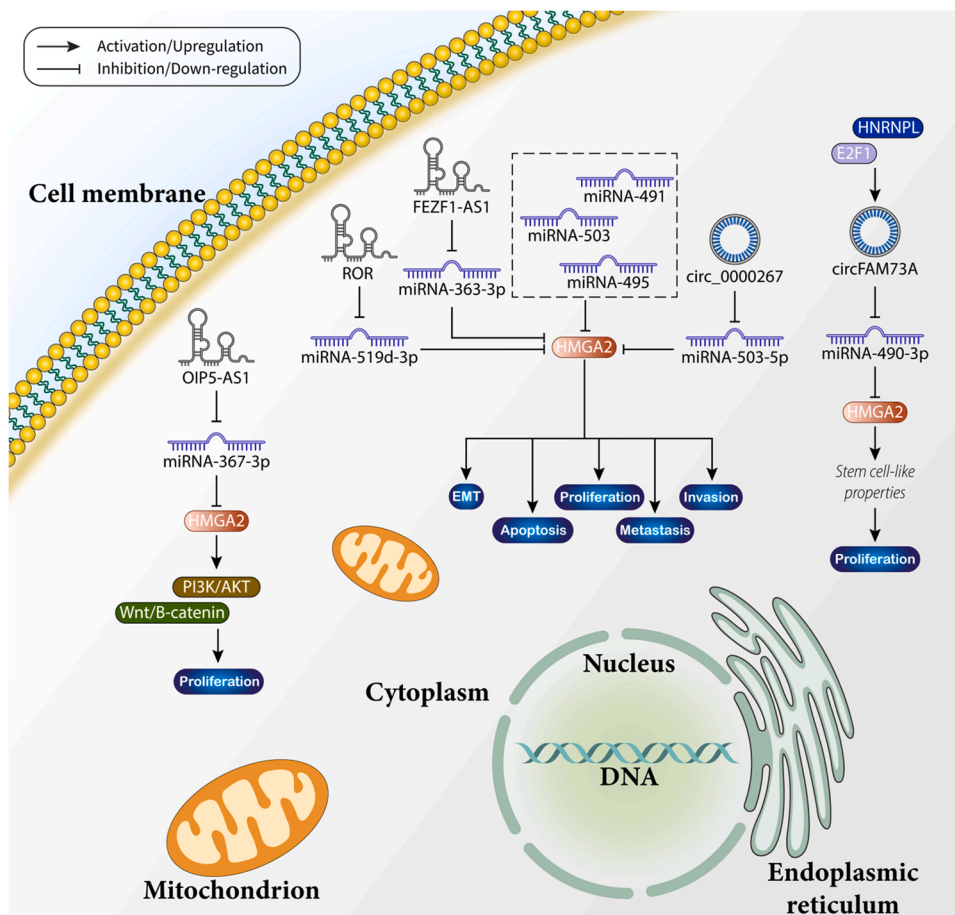


Fig. 2. The miRNA/HMGA2 axis in gastric cancer. MiRNAs with tumor suppressor function in gastric cancer could exert their inhibitory function on cancer progression via inhibiting HMGA2. Tumor promoting lncRNAs and circRNAs augment HMGA2 expression via suppressing these miRNAs to induce cell proliferation, EMT, invasion, and metastasis, and reduce apoptosis in cancer cells through inhibition of miRNAs and upregulation of HMGA2. HMGA2: High mobility group protein AT-hook 2, EMT: Epithelial-to-mesenchymal transition, HNRNP: Heterogeneous nuclear ribonucleoprotein K, E2F1: Transcription Factor 1, PI3K: Phosphoinositide 3-kinase.

EMT, invasion, and migration. To exert its functions, ROR upregulates HMGA2 via inhibiting miRNA-519d-3p [74]. As lncRNA ROR oncogenic role in different types of tumors including gastric cancer is also proved [75–78], targeting this lncRNA in cancer therapy could be beneficial (Fig. 2).

3.2. Pancreatic cancer

Intriguingly, the critical role of HMGA2 in pancreatic cancer has been studied before. In this study, it was elucidated that HMGA2 is a marker of a subpopulation of pancreatic ductal adenocarcinoma (PDAC) with high metastatic capacity. Furthermore, HMGA2 overexpression was associated with cancer cell growth and metastasis in vivo [79]. A newly discovered lncRNA named HMGA2-AS1 associated with HMGA2 gene regulates the expression of its own sense gene to mediate tumorigenesis in pancreatic cancer [80]. A lectin-like scavenger receptor named Oxidized Low Density Lipoprotein Receptor 1 (OLR1) upregulates c-Myc expression to increase HMGA2 transcription, thereby augmenting pancreatic cancer cell metastasis. In addition, activation of the OLR1/c-Myc/HMGA2 axis was shown to be associated with worse prognosis compared with patients with a low level of activation of this pathway [81]. In addition, it was found that HMGA2 overexpression in pancreatic cancer is accompanied by increased expression of Snail, ZEB1, N-cadherin and vimentin, while decreased E-cadherin. Moreover, suppression of HMGA2 resulted in inhibited invasion and metastasis [82]. Besides, HMGA2 promotes oncogenesis in pancreatic cancer cells by targeting ANLN [83]. Intriguingly, in vitro and in vivo, miRNA-590 has been shown to suppress cell proliferation and triggers cell apoptosis in PDAC cells via negatively regulating HMGA2 [84]. In addition, miRNA-497 suppresses PDAC cell proliferative and invasive capacity through directly targeting HMGA2 [85]. MiRNA-497 also

regulates pancreatic cancer proliferation, migration, and invasion by targeting NF-κB1 [86]. Accumulating evidence has proved anti-tumor activity of miRNA-497 [87–90]. As an example, the critical role of miRNA-497 in inhibiting tumor angiogenesis via targeting Vascular endothelial growth factor receptor 2 (VEGFR2) has been confirmed in a study [91]. In addition, miRNA-497 has been elucidated to be a downstream target of has-circ-0136666 in colorectal cancer. Knocking down of miRNA-497 by these circRNAs leads to activation of PD-L1 and further Treg-mediated immune escape of tumor cells [92]. It was also revealed that miRNA-101 targets Transforming growth factor beta receptor I (TGF-βR1) to suppress oral squamous cell carcinoma (OSCC) [93]. In addition, lncRNA SNHG1 sponges miRNA-101-3p to promote Rho-associated protein kinase (ROCK1) expression in increasing cancer cells proliferation, invasion, and migration [94]. Furthermore, other studies have indicated the importance of miRNA-101 function as an onco-suppressor in cancer [95–97]. In the case of miRNA/HMGA2 interaction, miRNA-101 decreases EMT in pancreatic cancer via negatively affecting HMGA2 [98].

ZFAS1 is a tumor promoting lncRNA whose overexpression in pancreatic cancer results in growth and metastasis of cancer cells. For this purpose, lncRNA ZFAS1 promotes HMGA2 expression via decoying miRNA-497-5p [99]. LncRNA ZFAS1 sponges miRNA-3924 to increase RHOA/ROCK2 and correspondingly augment pancreatic adenocarcinoma metastasis [100]. In addition, stabilization of HMGR mRNA mediated by lncRNA ZFAS1 through binding to U2 auxiliary factor 2 (U2AF2) resulted in pancreatic carcinoma progression [101]. Also, lncRNA CXCR4 inhibits let-7a to promote HMGA2 expression and enhance tumorigenesis and metastasis in pancreatic cancer cells, in vitro and in vivo [102]. Moreover, H19, a well-known oncogenic lncRNA [103–105], suppresses let-7 to increase HMGA2-mediated EMT and metastasis in pancreatic cancer (Fig. 3) [106].

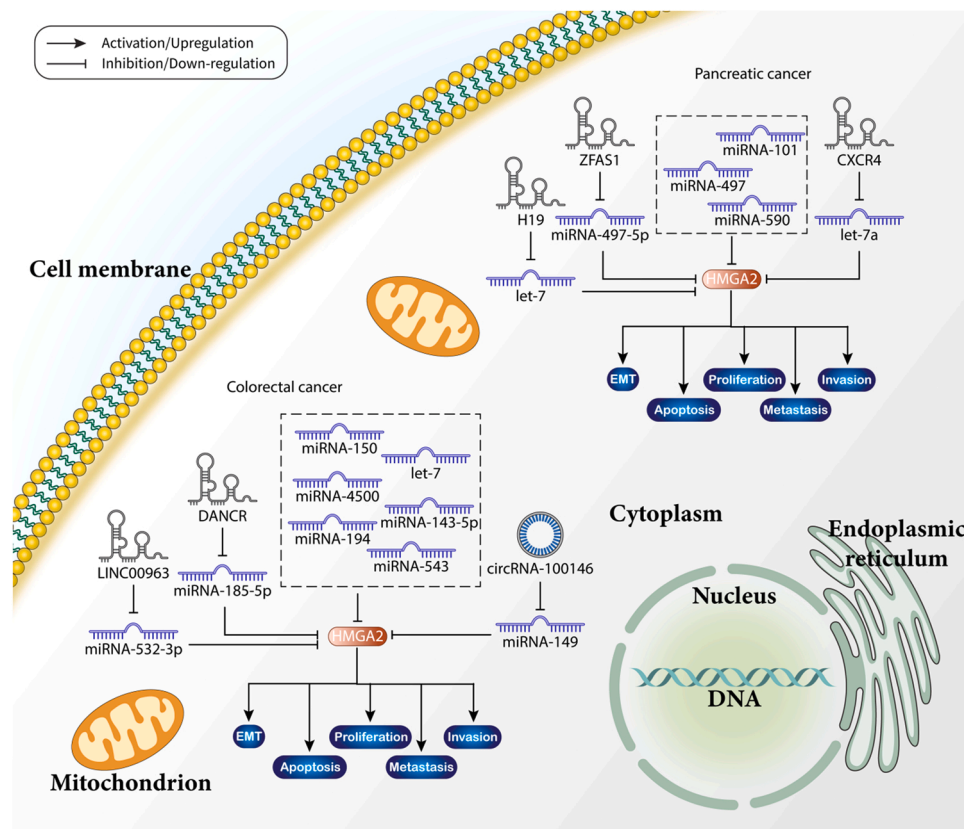


Fig. 3. The miRNA/HMGA2 axis in pancreatic and colorectal cancers. MiRNAs that possess tumor suppressor function in pancreatic and colorectal cancer could exert their function via inhibiting HMGA2. Oncogenic lncRNAs and circRNAs induce cell proliferation, EMT, invasion, and metastasis, and reduce apoptosis in cancer cells through inhibition of miRNAs and upregulation of HMGA2. HMGA2: High mobility group protein AT-hook 2, EMT: Epithelial-to-mesenchymal transition.

3.3. Colorectal cancer

It should be mentioned that the emerging role of HMGA2 in CRC development has been elucidated in various studies [107–110]. As an example, HMGA2 accelerates CRC progression through STAT3-mediated tumor-associated macrophage recruitment [111]. Another study has revealed that HMGA2 overexpression is in favor of resistance to 5-fluorouracil which is mediated by targeting Dvl2/Wnt pathway [112]. Moreover, this oncogene also develops angiogenesis in CRC by targeting both Sema3A and VEGFA [113]. In CRC, it was revealed that miRNA-1249 overexpression inhibits tumor progression and TNM stage, while increasing overall survival. MiRNA-1249 overexpression induced by p53 inhibits tumor growth, proliferation, metastasis and angiogenesis by targeting VEGFA/Akt/mTOR signaling pathway, and suppresses EMT by targeting VEGFA and HMGA2 [114]. In addition, previous studies have confirmed the important role of miRNA-543 in CRC by targeting factors such as PLAS3, large tumor suppressor kinase 1 (LATS1), and PTEN/Akt/mTOR signaling pathway [115–117]. Also, miRNA-543 inhibits CRC cell growth, proliferation, invasion and metastasis by targeting KRAS and Metastasis-associated protein 1 (MTA1), as well HMGA2 [118]. Furthermore, the oncogenic role of HMGA2 in CRC including cell survival and EMT has been elucidated to be suppressed by miRNA-194 [119]. Moreover, miRNA-4500 which negatively regulates HMGA2 expression inhibits CRC cell proliferation, cell cycle progression, invasion and migration [120]. Let-7 has been shown to be down-regulated in colon cancer while HMGA2 is increased. It was found that overexpression of let-7 results in HMGA2 suppression, thereby cancer cell proliferation, invasion and metastasis is reduced [121]. MiRNA-150 is also a tumor suppressor agent whose overexpression mediates HMGA2 downregulation and subsequent inhibition of colon cancer cells proliferation and cell cycle progression [122]. Similarly, miRNA-143–5p overexpression in CRC disrupts cancer cell proliferation, EMT, invasion, and metastasis by targeting HMGA2 [123]. Importantly, miRNA-143 has been demonstrated to have a promising role in colorectal cancer therapy [124,125].

It was also found that circRNA-100146 promotes CRC progression via inhibiting miRNA-149 and upregulating HMGA2 [126]. In addition, DANCR is an oncogenic lncRNA whose upregulation is associated with CRC cell proliferation, invasion, cell cycle progression, and metastasis, while decreasing apoptosis. DANCR overexpression is positively correlated with TNM stage and lymph node metastasis. For exerting its function, DANCR suppresses miRNA-185–5p to increase HMGA2 expression [127]. Furthermore, LINC00963 positively affects CRC proliferation, invasion, metastasis, and cell cycle progression by suppressing miRNA-532–3p and upregulation of HMGA2 expression (Fig. 3) [128].

3.4. Esophageal cancer

Like other parts of the gastrointestinal tract, esophageal cancer is also one of the tumors in which HMGA2 expression plays a key role in regulating its progression. It was elucidated that upregulation of HMGA2 by an oncogenic transcriptional co-activator named Hepatitis B virus X-interacting protein (HBXIP) is associated with advanced tumor stage and decreases overall survival in esophageal squamous cell carcinoma (ESCC). Besides, HBXIP increased the phosphorylation of p300/Cyclic adenosine monophosphate Response Element Binding protein (CBP) through Akt pathway to mediate acetylation of HMGA2 at lysine 26, thereby increasing its accumulation, DNA binding capacity and inhibiting its ubiquitination and degradation by proteasomes. Stabilization of HMGA2 ultimately resulted in cancer cell growth in vitro and in vivo [129]. Using RNA sequencing, Wada et al. have revealed that the expression levels of 47 miRNAs, miRNA-143–5p and miRNA-143–3p were decreased in ESCC, while their overexpression inhibited cell proliferation, invasion, and metastasis. It was also demonstrated that miRNA-143–5p targets six genes including *HMGA2*,

Hematological and neurological expressed 1 (HNI1), *Neuropilin and tolloid-like protein 2 (NETO2)*, *STMN1*, *Transcription factor 3 (TCF3)*, and *Mesenchymal-epithelial transition factor (MET)* [130].

In ESCC, it was found that miRNA-490–3p upregulation leads to inhibition of HMGA2 reduction and suppression of cancer cell proliferation and metastasis [131]. Moreover, miRNA-125b–5p negatively regulates *HMGA2* at mRNA and protein levels to disrupt proliferation, EMT, invasion, and metastasis in ESCC. It was found that upregulation of miRNA-125–5p not only resulted in reduced level of cell cycle related genes (*CCNA2*, *CCND1*, and *CCNE1*), but also regulates EMT markers including E-cadherin, N-cadherin, Slug, and MMPs [132]. In addition, the oncogenic function of HMGA2 on ESCC cell growth and metastasis has been demonstrated to be suppressed by miRNA-204–5p [133].

In addition, circ-0003340 enhances esophagus cancer tumorigenesis via modulating miRNA-198/HMGA2 axis and this oncogenic axis could be suppressed by dexmedetomidine [134]. Hsa_circ_0006948 directly binds to miRNA-490–3p to sponge it and increase HMGA2 expression in promoting EMT in ESCC [135]. In addition to this circRNA, lncRNAs are also involved in regulating the negative effects of miRNAs on HMGA2 in esophageal cancers. For instance, lncRNA ZEB-AS1 enhanced ESCC proliferation, invasion and metastasis by suppressing miRNA-574–3p and increasing HMGA2 (Fig. 4) [136].

3.5. Tongue cancer

Aggressiveness of tongue squamous cell carcinoma was shown to increase following the HMGA2 upregulation [137]. Moreover, induction of EMT by HMGA2 has been found to be associated with tongue squamous cell carcinoma high metastasis capacity [138]. In tongue squamous cell carcinoma (TSCC), miRNA-493 with onco-suppressor function directly binds HMGA2 to inhibit cancer tumorigenesis, cell proliferation, migration, and invasion, while increasing apoptosis [139].

lncRNA HOTTIP overexpression resulted in a reduction in expression level of miRNA-124–3p and increase in HMGA2 expression. Function of HOTTIP in TSCC ultimately increases tumor proliferation, invasion and migration [140]. Similarly, LINC00466 suppresses TSCC malignant behaviors via rising HMGA2 expression through miRNA-493 suppression [141]. It bears noting that lncRNAs could affect miRNAs through competing endogenous RNA (ceRNA) networks between them which affects cancer progression. For this purpose, lncRNAs compete with miRNAs to regulate the expression level of miRNAs' mRNA targets [142]. For instance, lncRNA H19 knocking down in TSCC impaired cancer cells invasion and metastasis. In TSCC, H19 acts as a ceRNA for let-7a to increase HMGA2, and subsequently EMT, invasion, and metastasis (Fig. 4) [143].

3.6. Hepatocellular cancer

HMGA2 has a crucial role in regulating HCC progression by affecting various cancer hallmarks. For instance, EMT is shown to be induced upon HMGA2 upregulation in HCC [144]. It was demonstrated that EMT is regulated by angiogenin via targeting HMGA2 in HCC [145]. Moreover, propofol has inhibitory effect on HCC cell growth and invasion by suppressing activation of Wnt/ β -catenin by HMGA2 [146]. As previously mentioned, miRNAs play onco-suppressor or oncogenic roles in cancer. In HCC, it was found that miRNA-363–3p suppresses carcinogenesis by inhibiting HMGA2 [147]. Also, overexpression of miRNA-760, an upstream regulator of HMGA2, is associated with reduction in HCC progression. Importantly, transcription of miRNA-760 could be suppressed by Specificity protein 1 (SP1), a way by which SP1 promotes HCC progression [148]. Anti-tumor effect of miRNA-9 in HCC is also revealed in a study, and for this purpose, miRNA-9 suppresses HMGA2 [149]. It was found that proliferation and cancer progression in HCC is suppressed by miRNA-377 through targeting HMGA2. In this study, it was uncovered that miRNA-337 inhibits HMGA2 to suppress PI3K/Akt and Wnt/ β -catenin pathways in preventing tumor

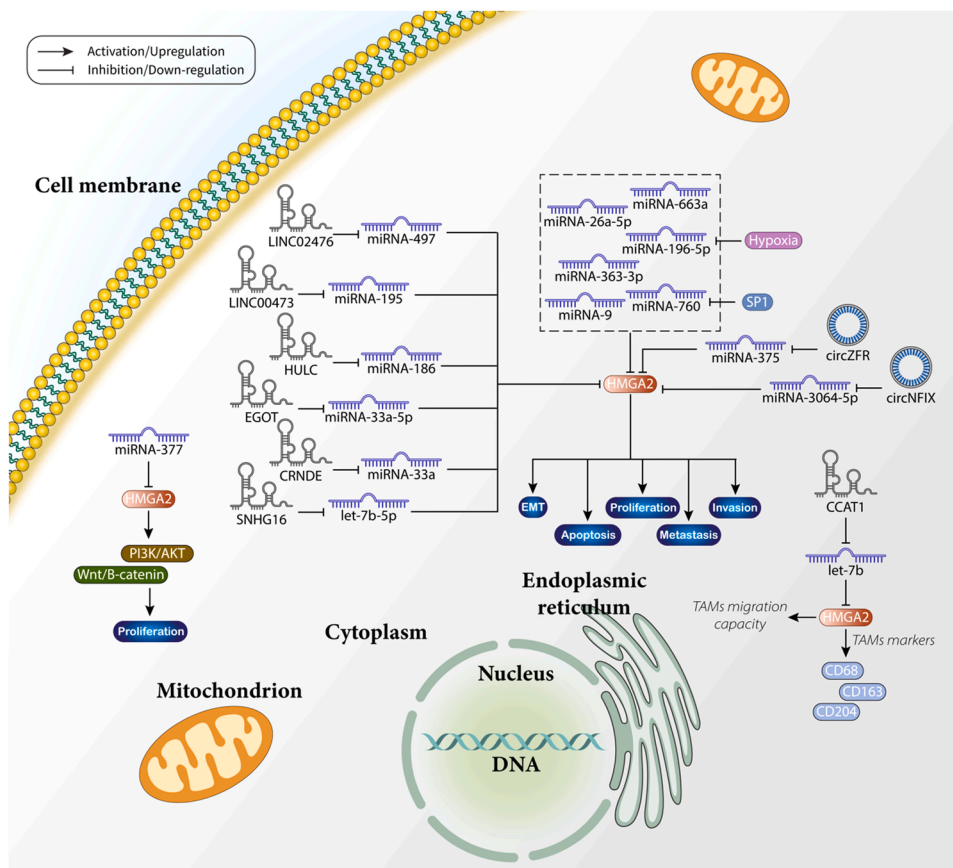


Fig. 5. The miRNA/HMGA2 axis in hepatocellular carcinoma. Onco-suppressor miRNAs negatively regulate HMGA2 in hepatocellular carcinoma. Oncogenic lncRNAs and circRNAs suppress these miRNAs to increase HMGA2 expression, thereby promoting cell proliferation, EMT, invasion, and metastasis, while decreasing apoptosis. HMGA2: High mobility group protein AT-hook 2, SP1: Specificity protein 1, EMT: Epithelial-to-mesenchymal transition, TAMs: tumor associated macrophages, PI3K: Phosphoinositide 3-kinase.

axis in thyroid cancer is low, more in-depth studies could increase the understanding of the critical function of this axis, and leading to find if targeting this pathway could be promising for thyroid cancer therapy.

5. Regulatory role of miRNA/HMGA2 axis in lung cancer

Accumulating data has proved the critical role of HMGA2 in lung cancer [171–173]. For instance, HMGA2 interaction with Protein phosphatase 4 regulatory subunit 1 (PP4R1) resulted in NSCLC metastasis through promoting EMT induced by MAPK/Extracellular signal-regulated kinases (ERK) signaling pathway [174]. Furthermore, although the evidence represents the facts that HMGA2 mainly serves as a downstream factor for ncRNA, some studies have revealed that HMGA2 could target ncRNAs for regulating cancer development. As an example, HMGA2 regulates circRNA ASPH to enhance lung adenocarcinoma cell growth [175]. Moreover, HMGA2 could act as ceRNA for miRNA let-7 to promote NSCLC cell growth, invasion, and dissemination through targeting Transforming growth factor beta receptor type 3 (Tgfr3)/TGF- β [176]. It bears noting that the interaction between let-7 and HMGA2 in lung cancer has been discussed in several studies [177, 178].

MiRNA-498, a tumor suppressor miRNA, has been confirmed to function in NSCLC as HMGA2 suppressor [179]. MiRNA-219 is another upstream mediator of HMGA2 which regulates cell growth and metastasis [180]. Similarly, miRNA-363–3p directly targets HMGA2 to suppress its oncogenic functions and subsequently inhibits NSCLC growth and invasion [181]. Moreover, in cancer stem cells of NSCLC, miRNA-150–5p acts as a suppressor to inhibit cancer stem cells-induced metastasis and recurrence via targeting Wnt/ β -catenin and HMGA2 [182]. MiRNA-154 acts in the same way of aforementioned miRNAs and targets HMGA2 for its further inhibitory function in NSCLC [183]. Also, another study has shown that lung cancer cell proliferation is suppressed

via upregulation of miRNA-495 which is an inhibitor of HMGA2 [184]. Additionally, proliferation and invasion of squamous cell carcinoma cells have been elucidated to be suppressed upon miRNA-541 upregulation which inhibits HMGA2 expression [185]. Interestingly, a study has revealed that hydrophobically modified let-7b could be internalized by NSCLC cells, in which let-7b targets HMGA2 for inhibiting cancer progression [186].

In addition, circ-100565 enhances NSCLC proliferation, invasion and migration by increasing HMGA2 through acting as a sponge for miRNA-506–3p [187]. Circ-0000514 overexpression in NSCLC cells is associated with malignancy through suppression of miRNA-330–5p and upregulation of HMGA2 [188]. In NSCLC, it was found that lncRNA VPS9D1 upregulation leads to induction of malignant phenotypes which is exerted by sponging miRNA-532–3p for increasing HMGA2 [189]. Furthermore, lncRNA ZFAS1 downregulation was elucidated to retard NSCLC cells. In contrast, its upregulation is in favor of tumor promotion via inhibiting miRNA-150–5p and increasing HMGA2 (Fig. 6) [190]. These data allowed identifying the critical role of miRNA/HMGA2 axis and its upstream mediator ncRNAs in the regulation of lung cancer progression.

6. Regulatory role of miRNA/HMGA2 axis in breast cancer

Breast cancer cell proliferation, invasion, metastasis [191,192], tumor aggressiveness, and poor prognosis [193] were elucidated as an effect of HMGA2 overexpression in cancer cells. Moreover, Wnt10B/ β -catenin signaling is able to induce HMGA2 expression for developing proliferation in metastatic triple negative breast cancer (TNBC) cells [194]. In addition, HMGA2 targets Ten-eleven translocation methylcytosine dioxygenase 1 (TET1)/Homeobox A9 (HOXA9) signaling pathway to promote breast cancer cell growth and metastasis [195]. Also, promoting metastasis of breast cancer cells by HMGA2

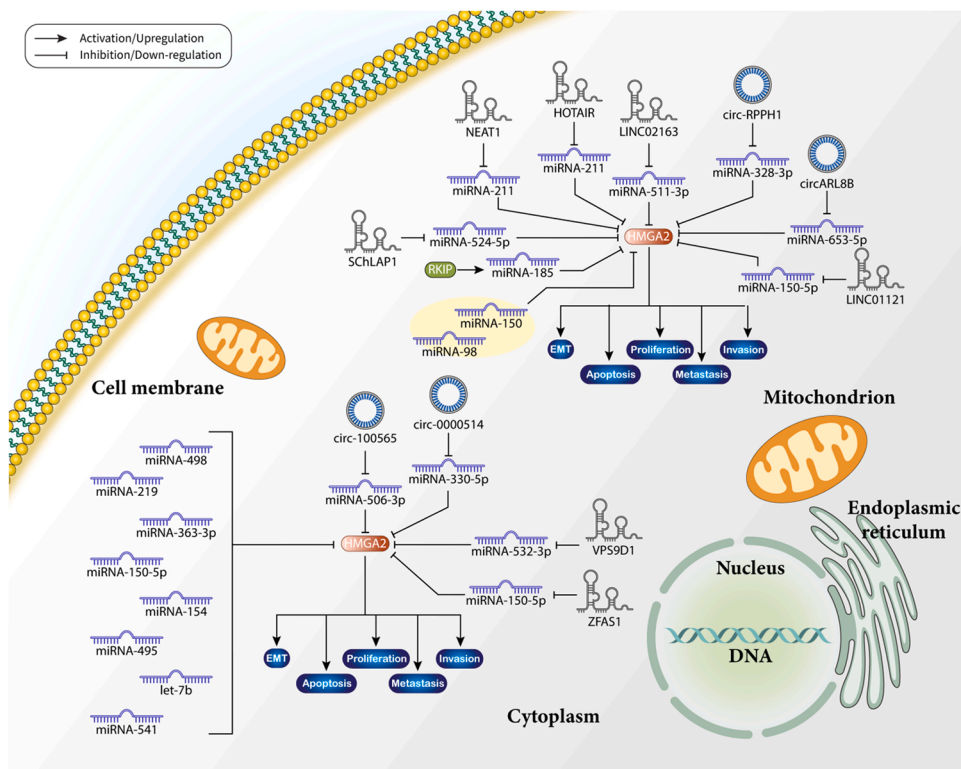


Fig. 6. The miRNA/HMGA2 axis in lung and breast cancer. Various miRNAs have been found to negatively affect HMGA2 in lung and breast cancer. Moreover, lncRNAs and circRNAs with oncogenic function could inhibit these miRNAs to augment HMGA2 expression, thereby promoting cell proliferation, EMT, invasion, and metastasis, and decreasing apoptosis. HMGA2: High mobility group protein AT-hook 2, RKIP: Raf kinase inhibitory protein, EMT: Epithelial-to-mesenchymal transition.

could be exerted by targeting Hippo- Yes-associated protein 1 (YAP) signaling pathway [196]. Intriguingly, it was elucidated that M1 macrophages induced stem cell properties in non-stem breast cancer cells via EMT process in a paracrine manner. In fact, STAT3/NF- κ B in macrophages activates Lin-28B-let-7-HMGA2 axis to promote cancer stem cell formation [197].

Accumulating evidence has revealed the critical role of tumor suppressor miRNAs in inhibiting HMGA2 oncogenic functions. For instance, miRNA-150 upregulation in TNBC could be beneficial for suppressing tumor metastasis which is exerted through negative regulation of HMGA2 [198]. Similarly, breast cancer proliferation, invasion and metastasis are all suppressed when HMGA2 expression is reduced by miRNA-98 [199]. Raf kinase inhibitory protein (RKIP) which targets Raf for regulating cell growth and differentiation, has been proven to be involved in regulating miRNAs inhibitory effect on HMGA2. It was elucidated that RKIP increases miRNA-185 to suppress HMGA2 expression, thereby inhibiting breast cancer cell growth and invasion [200].

In addition, circRNAs are one of the upstream mediators of miRNAs and in the case of miRNA/HMGA2 pathway, circRNAs also have regulatory roles. For instance, circRPPH1 overexpression is in favor of cancer progression, while its knock down retards breast cancer tumorigenesis. Circ-RPPH1 acts as a sponge for miRNA-328-3p to promote HMGA2 expression, which is followed by breast cancer cell proliferation, invasion, as well metastasis, while suppressing apoptosis [201]. Furthermore, circARL8B targets miRNA-653-5p/HMGA2 pathway to regulate breast cancer cell progression [202]. Also, LINC02163 facilitates breast cancer malignancy by suppressing miRNA-511-3p and upregulating HMGA2 [203]. In addition, LINC01121 augments breast cancer cell proliferation, invasion and metastasis by targeting miRNA-150-5p/HMGA2 axis [204]. Moreover, HOTAIR is an lncRNA with proven tumor promoting function in breast cancer [205–208]. HOTAIR upregulation accelerates cancer cell progression, and prevents apoptosis induction via suppressing miRNA-20a-5p and increasing HMGA2 expression level [209]. Also, NEAT1 is another common lncRNA with regulatory roles in breast cancer [210–212]. LncRNA NEAT1 prevents

negative regulatory function of miRNA-211 on HMGA2 to facilitate cancer cell growth and invasion in breast cancer [213]. Besides, lncRNA SchLAP1 functions in the same way and suppresses miRNA-524-5p to upregulate HMGA2 in increasing TNBC cell proliferation (Fig. 6) [214]. Although these studies have confirmed the importance of miRNAs and HMGA2 interaction in regulation of breast cancer, more in-depth studies may bring a new viewpoint on the crucial function of tumor suppressor miRNAs in the inhibition of breast cancer progression through targeting HMGA2 protein.

7. Regulatory role of miRNA/HMGA2 axis in bladder cancer

HMGA2 affects various aspects of bladder cancer cells including proliferation, invasion, EMT, as well metastasis [215,216]. The critical role of HMGA2 as a prognostic biomarker was confirmed in a study [217,218].

It was demonstrated that let-7c-5p prevents bladder cancer progression via negative regulation HMGA2 [219]. In bladder cancer, circ-0000658 is overexpressed which is in favor of cancer progression. Circ-0000658 exerts its oncogenic function in cancer cells via suppressing miRNA-498 and augmenting HMGA2 expression [220]. It was found that exosomes containing LINC00355 derived from cancer-associated fibroblasts augments bladder cancer cell proliferation and invasion through suppressing miRNA-15a-5p and enhancing HMGA2 expression [221]. As the effect of miRNA/HMGA2 and its upstream regulators on bladder cancer progression is still poorly understood, more detailed studies will reinforce their critical functions in the development of bladder cancer cells.

8. Regulatory role of miRNA/HMGA2 axis in reproductive system cancers

8.1. Ovarian cancer

It is worth noting that overexpression of HMGA2 could be considered as a promising biomarker in high-grade ovarian serous carcinoma [222,

223] and a target for ovarian cancer therapy [224]. In addition, HMGA2 regulates important cancer hallmarks such as proliferation, invasion and metastasis in ovarian cancer [225].

It was demonstrated in a study that dysregulation of miRNA-30c and let-7a leads to HMGA2 overexpression in ovarian cancer, thereby tumor progression. In contrast, upregulation of these miRNAs induced a reverse effect on ovarian cancer progression through HMGA2 suppression [226]. Moreover, it was elucidated that overexpressed miRNA-493-3p leads to apoptosis induction through both intrinsic and extrinsic pathways. MiRNA-493-3p exerts its function via downregulation of mRNA and protein level of *HMGA2*, *AKT2*, *RAF1*, and *ETS1* [227]. Furthermore, miRNA-219-5p downregulation has been shown to be associated with ovarian cancer progression. However, growth and metastasis of cancer cells was diminished followed by miRNA-219-5p upregulation which resulted from HMGA2 reduction by this miRNA (Fig. 7) [228].

8.2. Cervical cancer

In a study, it was demonstrated that HMGA2 overexpression by Estrogen receptor alpha-36 (ER- α 36) leads to progression of malignancy in cervical cancer [229]. By affecting Ataxia telangiectasia and Rad3-related protein (ATR)/Checkpoint kinase 1 (Chk1) signaling pathway, HMGA2 promotes EMT and lymph node metastasis in cervical cancer [230]. HMGA2 also promotes the process of cervical intraepithelial neoplasia transition into cervical cancer [231]. Moreover, miRNA-142-3p ectopic expression was found to be accompanied by inhibition of cervical cancer cell growth, migration, and colony formation, while triggering apoptosis. MiRNA-142-3p exerts its onco-suppressor function by targeting not only *HMGA2*, but also other *HMG* genes (Fig. 7) [232].

8.3. Endometrial cancer

Similar to other cancer types, HMGA2 also plays critical roles in endometrial cancer [233]. In endometrial cancer, it was revealed that upregulation of miRNA-302a-5p and miRNA-367-3p is inversely correlated with HMGA2 expression. Overexpression of these two miRNAs is associated with inhibition of lymph node metastasis and malignant behavior of cancer cells which is exerted by suppression of HMGA2 [234]. As an example of regulation of miRNA/HMGA2 axis, circ-0109046 targets miRNA-136 can increase HMGA2 expression for promoting endometrial cancer progression [235]. In addition, lncRNA MIR210HG functions as a sponge for miRNA-337-3p and miRNA-137 to augment HMGA2 expression and promote Wnt/ β -catenin and TGF- β /Smad3 signaling pathways in increasing endometrial cancer progression (Fig. 7) [236].

8.4. Prostate cancer

In prostate cancer HMGA2 could repress apoptosis activation and promote invasion and migration of cancer cells. However, knockdown of HMGA2 has opposite effects and leads to activation of apoptotic pathways [237,238]. Activation of EMT occurred in prostate cancer upon overexpression of HMGA2 by targeting MAPK signaling pathway [239]. MiRNA-219-5p has been proven to be an onco-suppressor in prostate cancer by inhibiting HMGA2 to prevent cell growth and metastasis [240]. In prostate cancer, hsa_circ_0062019 has been shown to accelerate cell proliferation, invasion and metastasis via targeting miRNA-195-5p/HMGA2 axis [241]. LncRNA NEAT1 could serve as a sponge for miRNA-98-5p to enhance prostate cancer progression through HMGA2 (Fig. 7) [242]. Although some studies have revealed the critical role of the interaction between miRNAs and HMGA2 in regulating

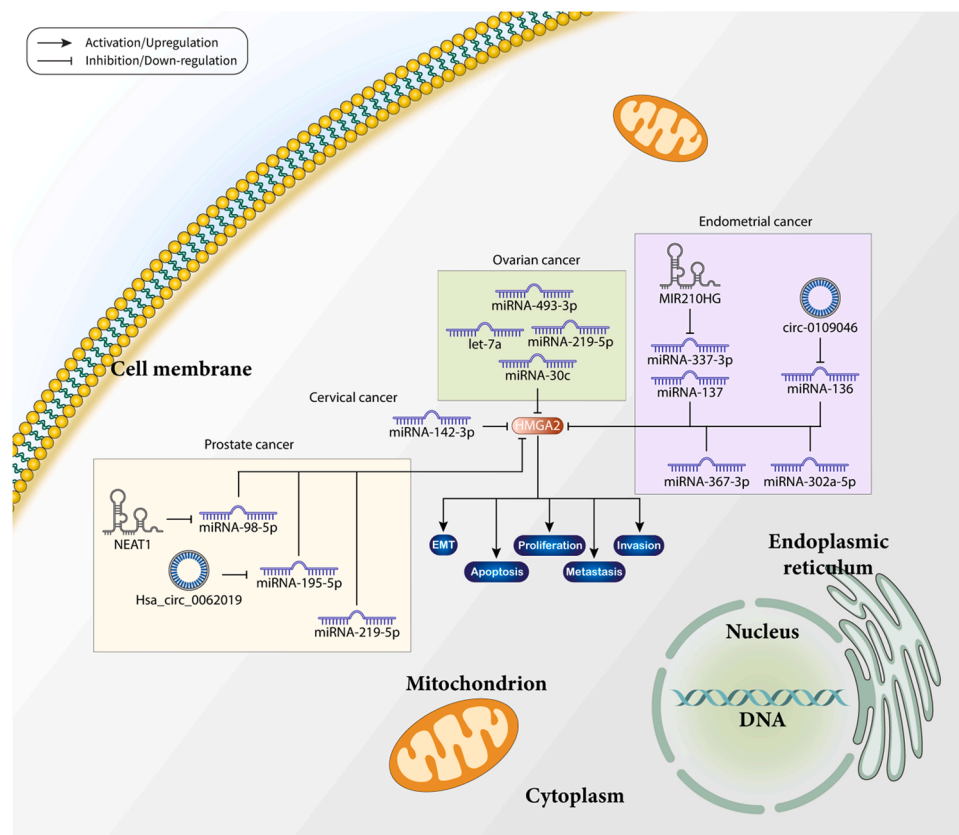


Fig. 7. The miRNA/HMGA2 axis in prostate, cervical, ovarian, and endometrial cancers. MiRNAs reversely affect the expression of HMGA2 to inhibit reproductive system cancer progression. Also, lncRNAs and circRNAs could suppress the inhibitory function of these miRNAs by downregulating their expression, thereby enhancing the tumor progression. HMGA2: High mobility group protein AT-hook, EMT: Epithelial-to-mesenchymal transition.

different hallmarks of reproductive system cancers, also further studies are needed to bring new insight in cancer therapy.

9. Regulatory role of miRNA/HMGA2 axis in brain tumors

In glioblastoma, HMGA2 overexpression is associated with invasion, stemness and tumor formation [243]. Interestingly, the association between HMGA2 polymorphism and brain tumor survival and susceptibility was studied before [244,245]. Besides, it was shown that invasiveness and self-renewal of glioma-initiating cells is increased following the HMGA2 overexpression [246]. HMGA2 was found to augment invasion of glioma cells through activating *MMP2* gene transcription via triggering the chromatin conformational remodeling of the *MMP2* gene promoter [247].

MiRNAs are important molecules with critical function in brain tumors [248,249]. Accumulating data have revealed the importance of miRNA/HMGA2 axis in regulation of brain tumors' progression. For instance, miRNA-370-3p attenuates glioblastoma stem-like cell malignancy and cell growth, invasion, as well metastasis through targeting HMGA2, lncRNA NEAT1, and Hypoxia-inducible factor 1-alpha (HIF1A) [250]. Various studies have revealed the regulatory role of miRNA-370 in glioblastoma. MiRNA-370-3p targets MGMT expression to increase glioblastoma multiforme (GBM) cells sensitivity to temozolomide [251]. Furthermore, miRNA-370-3p directly targets β -catenin to induce cell cycle arrest and suppress cell proliferation in glioma [252]. Despite the importance of miRNA-370-3p in glioblastoma, there wasn't any significant relation between miRNA-370-3p expression and prognosis value for survival. Also, it was demonstrated that temozolomide therapy accompanied by miRNA-370-3p overexpression has better therapeutic effect than temozolomide alone [253]. Similarly, it was demonstrated that glioma cell proliferation and migration are suppressed by miRNA-490-3p due to its inhibitory function on HMGA2 [254]. Moreover, miRNA-340 overexpression was found to suppress glioblastoma multiforme [255]. MiRNA-340-5p downregulation was seen to be correlated with tumor size, recurrence, poor survival, as well density of TAMs and M2-polarized TAMs. On the contrary, overexpression of miRNA-340-5p leads to attenuation of tumor growth and is also associated with good prognosis. For exerting its function, miRNA-340-5p regulates its downstream targets which include Periostin (POSTN), Latent Transforming Growth Factor Beta Binding Protein 1 (LTBP-1), TGF β -1, and HMGA2. Indeed, miRNA-340-5p- macrophage feedback loop regulates the progression and tumor microenvironment of glioblastoma multiforme [256]. Also, miRNA-211 has been proven to exert onco-suppressor function in GBM [257], and its overexpression resulted in tumor cell growth and EMT suppression mediated by Akt/ β -catenin and then HMGA2 suppression [258]. In addition, it seems that miRNA-98 plays critical roles in glioblastoma. For instance, upregulation of miRNA-98 is associated with inhibition of glioma cell invasion via downregulating Inhibitor Of Nuclear Factor Kappa B Kinase Subunit Epsilon (IKK ϵ) [259]. Besides, lncRNA NEAT1 suppresses miRNA-98-5p to upregulate Basic leucine zipper and W2 domain-containing protein 1 (BZWI1) in increasing glioma progression [260]. Furthermore, miRNA-98 directly targets PBX3 to attenuate glioma cell invasion and metastasis [261]. Moreover, miRNA-98 exerts the same function and attenuates glioblastoma cell proliferation and invasion by targeting HMGA2 [262].

As an example of the circRNA/miRNA/HMGA2 axis, circABCC1 upregulates HMGA2 by sponging miRNA-591 to promote glioma cell progression [263]. Furthermore, FOXD2-AS1, an oncogenic lncRNA, promotes glioma tumorigenesis and progression by acting as a sponge for miRNA-185-5p to upregulate HMGA2 and further affecting PI3K/Akt signaling pathway [264]. Similarly, LINC00152 inhibits miRNA-107 to increase HMGA2, thereby promoting glioblastoma cell proliferation and invasion [265]. Intriguingly, various studies have indicated activity of LINC00152 in brain tumors as an oncogene. For instance, Wang et al. have suggested a prognostic role for LINC00152 in

patients with high-grade glioma [266]. In addition, knocking down of LINC00152 leads to glioblastoma suppression. However, upregulation of LINC00152 leads to sponging miRNA-612, and then augmentation of the AKT2/NF- κ B signaling pathway which in turn promotes mesenchymal phenotype-induced glioblastoma malignancy [267]. It bears noting that as miRNA/HMGA2 axis is broadly studied in brain cancer, it could be speculated that use of the miRNAs which inhibits HMGA2 in brain tumors could be a promising miRNA-based therapy and it might be the subject of future investigations.

10. Regulatory role of miRNA/HMGA2 axis in squamous cell carcinoma

In squamous cell carcinoma, increased HMGA2 induces angiogenesis and metastasis to distant tissues and is also associated with poor prognosis [268-270]. Also, in head and neck squamous cell carcinoma (HNSCC) HMGA2 interaction with Snai2 enhances tumorigenesis and stemness [271]. In addition, HMGA2 was elucidated to increase in approximately 90% of ESCC samples and its overexpression is accompanied by malignant phenotype [272]. Also, high expression level of HMGA2 in OSCC cells was associated with decreased recurrence-free survival and was correlated with poor overall survival [273]. Moreover, angiogenin directly regulates HMGA2 overexpression to mediate lung squamous cell carcinoma proliferation, invasion, and metastasis [274]. It was also elucidated that HMGA2 expression is a promising biomarker in UV-induced cutaneous squamous cell carcinoma tumorigenesis [275].

In laryngeal squamous cell carcinoma (LSCC), overexpression of miRNA-98 negatively regulates HMGA2 to suppress EMT. HMGA2 expression is reversely correlated with miRNA-98 and its upregulation increases LSCC cell stem cell-like features. Indeed, HMGA2 regulates POSTN to increase EMT, and miRNA-98 inhibits EMT by suppressing HMGA2/POSTN axis [276]. In addition, it was elucidated that let-7a and HMGA2 expression in LSCC is decreased and increased, respectively, and downregulation of let-7a was shown to be associated with lymph node metastasis, as well high proliferation and invasion. However, overexpression of let-a reverses these cancer hallmarks via down regulating HMGA2 [277].

In HNSCC, tumor cell proliferation, migration and EMT was demonstrated to be suppressed after let-7c overexpression which resulted from HMGA2 downregulation [278]. In addition, hsa_circ_0000264 overexpression has been seen to be accompanied by HNSCC progression. For applying its function, hsa_circ_0000264 acts as a sponge for has-let-7b-5p to increase its downstream target, HMGA2 [279].

Another type of squamous cell carcinoma affects vulva tissue. HMGA2 was found to be critical in genesis and/or progression of vulva tumors [280]. Moreover, aberrant expression of HMGA2 in squamous cell vulvar carcinoma has been revealed to be associated with an aggressive phenotype [281]. Progression of squamous cell carcinoma of vulva could be suppressed by miRNA-30c and let-7a upregulation. These two miRNAs decrease HMGA2 expression, thereby inhibiting cancer progression [282].

11. Regulatory role of miRNA/HMGA2 axis in osteosarcoma

In osteosarcoma, circUBAP2 is a tumor promoting ncRNA whose overexpression is in favor of cancer development [283]. For instance, it promotes osteosarcoma proliferation and invasion by suppressing miRNA-641 and increasing YAP1 [284]. Also, another study has confirmed this oncogenic role for circUBAP2 by targeting miRNA-143 [285]. More importantly, circUBAP2 targets miRNA-204-3p/HMGA2 [286] and miRNA-637/HMGB2 [287] axes to serve its functions. It bears noting that miRNA-204-5p inhibitory role in osteosarcoma was seen to be exerted through targeting EBF2 [288]. In addition, lncRNA CCDC144NL-AS1 promotes HMGA2 by serving as a sponge for miRNA-490-3p to augment proliferation, growth, invasion, and

migration of osteosarcoma cells [289]. Likewise, regulation of miRNA-497-5p/HMGA2 axis by LINC01410 results in increasing the tumorigenesis of osteosarcoma cells [290]. Other studies also have revealed the onco-suppressor function of miRNA-497 in osteosarcoma [291]. miRNA-497 targets MAPK/ERK in osteosarcoma to suppress cancer progression [292]. In addition, by targeting PI3K/Akt, miRNA-497 inhibits osteosarcoma cell growth and cisplatin resistance [293]. Besides the miRNA-497, LINC01410 also plays a key role in osteosarcoma. For instance, LINC01410 facilitates osteosarcoma cell proliferation and invasion by functioning as a sponge for miRNA-3128 [294]. Also, proliferation and metastasis in osteosarcoma could be also regulated by LINC01410 via targeting miRNA-122-5p/NDRG3 axis [295].

12. Regulatory role of miRNA/HMGA2 axis in other type of cancers

In laryngeal cancer, an interaction between let-7 and HMGA2 was elucidated. It was demonstrated that let-7 inhibits laryngeal cancer progression by negatively regulating HMGA2 [296]. It is of importance to mention that HMGA2, but not HMGA1, is upregulated in larynx carcinoma which highlights the fact that HMGA2 could play a key role in this cancer [297]. In addition, transcriptome profiling has revealed HMGA2 as a biomarker of progression and prognosis in melanoma [298]. miRNA/HMGA2 axis has also been shown in melanoma. It was proved that let-7a attenuates tumor cell migration by inhibiting HMGA2 expression [299]. In retinoblastoma, a common primary intraocular tumor in children, HMGA2 overexpression was seen to be associated with invasiveness [300]. As mentioned before, miRNA-98 is an onco-suppressor ncRNA which targets HMGA2 in different cancers. Also in retinoblastoma, miRNA-98 suppresses HMGA2 expression to inhibit cancer progression through regulating Wnt/ β -catenin [301]. In nasopharyngeal carcinoma, HMGA2 mediates EMT-induced invasion and migration for cancer progression and its overexpression is associated with poor prognosis [302,303]. Furthermore, let-7a suppresses EMT, invasion, and migration of nasopharyngeal carcinoma by targeting HMGA2 [304]. The critical role of miRNA-383-3p in suppressing cell proliferation and radio-resistance in nasopharyngeal carcinoma has been proved in a study through targeting RBM3 [305]. Besides, lncRNA HOXC13 modulates miRNA-383-3p/HMGA2 axis to promote nasopharyngeal carcinoma cell proliferation and invasion [306]. In addition, miRNA-26a directly affects HMGA2 to suppress cell proliferation in gallbladder cancer [307]. In CCRC, miRNA-599 attenuates cancer cell proliferation and invasion by negatively regulating HMGA2 [308]. Also, lncRNA SNHG1 enhances tumor progression via sponging miRNA-103a and increasing HMGA2 in renal cell carcinoma [309].

13. Therapy response

13.1. Regulation of therapy response by miRNAs

Inevitable emergence of resistance to therapy is the major obstacle in cancer therapy. Cancer cells employ different mechanisms to offset therapeutic efficacy of drugs. Due to their plasticity, cancer cells are able to develop resistance to therapies. For this purpose, cancer cells use various mechanisms including [1] alterations in the target through mutations in the drug target or amplification of the target, [2] reactivation of the drug targets via alterations in the upstream or downstream factors of target, [3] activation of other alternative signaling pathways, and [4] the crosstalk between cancer cells and tumor microenvironment (TME) through their adhesive interactions and transmission of signals between them [310]. In addition, TME attenuates drug penetration into tumor cells, preventing clearance of cancer cells by the immune system, promotes proliferation and augments anti-apoptotic pathways to enhance resistance to therapy, without inducing genetic mutations and epigenetic alterations [311,312]. Also, cancer

cells inactivate drug, use transporters such as ATP-binding cassette sub-family B member 1 (ABCB1; also known as P-gp) for drug efflux, repair drug-induced DNA damage, and increases epigenetic changes (including DNA methylation, chromatin remodeling, and histone modification) to promote drug resistance. In addition, EMT is one of the cancer hallmarks and drug resistance can also arise following EMT promotion [313–316].

Interestingly, various approaches are in progress to overcome drug resistance in cancer therapy. For instance, it was found that nanotherapeutics could significantly overcome the drug resistance mediated by P-gp for optimal chemotherapy performance [317]. Also, targeting DNA methylation, histone deacetylation, demethylation and methylation is of importance in reversing drug resistance. In addition, combination therapies such as combination of immunotherapy with epigenetics could be efficient in this way [318]. Also, ferroptosis is an iron-dependent cell death that could be targeted for overcoming drug resistance. There are compounds that induce ferroptosis to reverse resistance to immunotherapy and chemotherapeutic drugs [319]. Recently, it was suggested that CRISPR/Cas9 could improve the effectiveness of anti-tumor drugs by targeting critical genes involved in mechanisms of drug resistance. Interestingly, CRISPR/Cas9 is also applicable for detecting drug resistance-related genes and understanding the underlying mechanisms of drug resistance. Also, the CRISPR/Cas9 system has some limitations in which off-target mutagenesis and anti-SpCas9 antibodies are among them [320].

MiRNAs highly affect therapy response in cancer cells through different mechanisms. For instance, miRNA-17 is highly expressed in CRC. Also, SRY-related HMG box transcription factor 4 (SOX4) upregulates miRNA-17 expression, and miRNA-17 reduces CYLD expression to promote cancer progression and resistance to 5-fluorouracil [321]. Also, it was shown that extracellular vesicles derived from mesenchymal stem cells containing miRNA-301b-3p were able to suppress Thioredoxin interacting protein (TXNIP) in gastric cancer cells to promote drug resistance and tumor cell proliferation and migration [322]. In gemcitabine-resistant bladder cancer cells, miR-99a-5p exert tumor suppressor function by inhibiting SMARCD1 to increase cellular senescence [323]. It was found that miRNA-485-5p overexpression inhibits cell progression and resistance towards cisplatin and carboplatin in OSCC. For this purpose, miRNA-485-5p repressed Keratin 17 (KRT17) which ultimately inhibits integrin β 4/ α 6/FAK/Src/ERK/ β -catenin signaling pathway [324]. Table 2 provides more miRNAs with regulatory function on drug resistance.

13.2. MiRNAs delivery to cancer cells

As mentioned previously, use of miRNA mimics or miRNA inhibitors is a promising approach for cancer therapy. However, administration of nucleic acid-based molecules have limitations such as being degraded or removed rapidly from the body, poor cell membrane penetration, unwanted off-target effects, unfavorable pharmacokinetics, and activation of immune response. Thus, application of delivery systems is of importance to minimize the limitations of miRNA-based therapies [343,344]. There are various miRNA delivery systems which include lipid-based nanocarriers (liposome, micelles and nanoemulsion), viral carriers (Adenovirus and retrovirus), and inorganic materials (gold nanoparticles, iron oxide, and quantum dots). In addition, exosomes, apoptotic bodies, platelet-derived microparticles, and microvesicles are cell-derived membranes with capacity for delivering miRNAs [345]. Also, polymer-based carriers are applicable for delivering miRNAs. These polymers are divided into natural and synthetic nanocarriers. Natural polymers could be based on proteins (Albumin, Gelatin, and Atelocollagen), peptides (Cationic peptides and Tachyplesin), and polysaccharides (Chitosan, Cyclodextrin, Dextran, and Hyaluronic acid). Synthetic polymer-based carriers which widely used for delivering therapeutic miRNAs are produced from poly(lactic-co-glycolic acid) (PLGA), polyethylene glycol (PEG), polyethyleneimine (PEI), and poly

Table 2
miRNAs which regulates response to chemotherapeutics in cancer.

Function	miRNA	Cancer	Drug	Mechanism	Ref
Drug sensitivity	miRNA-205	Liver cancer	Doxorubicin	PTEN/PI3K/Akt/P-gp	[325]
	miRNA-199a-3p	TNBC	Cisplatin	BRCA1	[326]
			Veliparib	Suppressing DNA repair	
				Apoptosis induction	
	miRNA-140	Breast cancer	Doxorubicin	FEN1	[327]
				Suppressing DNA repair	
	miRNA-20a-5p	Ovarian cancer	Cisplatin	DNMT3B)-mediated DNA methylation of RBP1	[328]
	miRNA-146a	Ovarian cancer	Taxane	LAMC2/PI3K/Akt	[329]
			Docetaxel		
	miRNA-5195-3p	TNBC	Paclitaxel	EIF4A2	[330]
	miRNA-552	CRC	5-fluorouracil	SMAD2	[331]
	miRNA-200b and miRNA-200c	Estrogen receptor-positive breast cancer	Tamoxifen	c-MYB	[332]
	miRNA-195	Glioma	Temozolomide	Cyclin E1	[333]
	miRNA-302c	Glioma	Temozolomide	P-gp	[334]
Drug resistance	miRNA-769-5p	Gastric cancer	Cisplatin	Caspase9/caspase3/apoptosis	[335]
				Ubiquitination and degradation of p53	
	miRNA-181b-5p	Breast cancer	Doxorubicin	BCLAF1/p53/p21	[336]
	miRNA-23b/27b/24-1 cluster	CRC	Oxaliplatin	EMT markers (vimentin and SNAI2)	[337]
	miRNA-155-5p	OSCC	5-fluorouracil	TP53INP1	[338]
	miRNA-620	TNBC	Gemcitabine	DCTD	[339]
	miRNA-27a-3p	Glioma	Temozolomide	NF1	[340]
	miRNA-19b	CRC	Oxaliplatin	NR3C1/PI3K/AKT/mTOR	[341]
	miRNA-96-5p	CCRCC	Sunitinib	PTEN	[342]

(ϵ -caprolactone) (PCL). Moreover, Dendrimers, vehicles with tree-like structures, offer various advantages as they are lipophilic and well-defined, having notable flexibility, their size is adjustable, and their surface could be modified easily (Fig. 8) [346]. Table 3 provides delivery systems which are used for miRNAs delivery to cancers.

13.3. Regulatory role of miRNA/HMGA2 axis in cancer therapy response

In gastric cancer, it was found that exosomal miRNA-107 increases the sensitivity of gastric cancer cells to chemotherapeutic agents by targeting HMGA2 to suppress mTOR/P-glycoprotein (P-gp) pathway [357]. Similarly, miRNA-33b-5p enhances drug sensitivity in gastric cancer cells by suppressing HMGA2 [358]. In addition, lncRNA HCP5 acts as a sponge for miRNA-128 to promote HMGA2 protein in increasing cisplatin resistance in gastric cancer [359]. In CRC, miRNA-204 and miRNA-9-5p overexpression leads to CRC cell sensitivity to 5-fluorouracil via inhibiting HMGA2 expression [360,361]. lncRNA PCAT6 suppresses miRNA-204 by sponging to increase resistance of CRC cells to 5-fluorouracil [362]. In breast cancer, circFBXL5 upregulation was found to be associated with cancer cells resistance to 5-fluorouracil by suppressing miRNA-216b and increasing HMGA2 expression [363]. Also, circTRIM28 augments breast cancer cells resistance to tamoxifen which is exerted by targeting miRNA-409-3p/HMGA2 axis [364]. Also in NSCLC, miRNA-26a overexpression increases the sensitivity of cancer cells to cisplatin via regulating HMGA2-mediated E2F1-Akt pathway [365]. Moreover, miRNA-219-5p suppresses ovarian cancer cells resistance to cisplatin through suppressing HMGA2-induced Wnt/ β -catenin and autophagy activation [366]. Furthermore, lncRNA ANRIL attenuates cisplatin sensitivity of ovarian cancer cells via regulating let-7a/HMGA2 axis [367]. In addition, miRNA-34a-5p attenuates glioma cell progression and augments temozolomide-induced cytotoxicity via targeting HMGA2 [368]. Interestingly, it was revealed that a type of herb named Verbascode promotes the expression level of let-7 g-5p to suppress HMGA2 via Wnt/ β -catenin signaling inhibition (Fig. 9) [369]. Although a body of studies has revealed the critical role of miRNA/HMGA2 axis in regulation of hallmarks of cancer progression, few studies have addressed the issue of the capacity of this axis in regulation of therapy response, and investigating this function could bring new insight to the field of cancer therapy.

14. Conclusion and remarks

Cancer therapy is a field in which its challenges are not completely addressed and science increasingly uncovered its gaps and unknown parts. Numerous factors and signaling pathways have been identified and their impact on tumorigenesis established. HMGA2 is a protein belonging to the HMG family of proteins which exerts critical roles in the nucleus. Accumulating evidence has revealed the oncogenic role of HMGA2 in different types of cancers. Interestingly, HMGA2 regulates most of the key oncogenic factors in cells. Also, HMGA2 could be the downstream target of other cancer-related factors which miRNAs are among them. In fact, tumor suppressor miRNAs attenuates HMGA2 expression to inhibit tumor progression. MiRNAs could also be also a downstream target of other ncRNAs including circRNAs and lncRNA. Tumor promoting ncRNAs inhibits miRNAs by acting as a sponge or ceRNA to enhance HMGA2 expression, thereby promoting tumorigenesis and cancer progression. Thus, targeting HMGA2 and suppressing its expression may disrupt further cancer progression and this blocking could result in suppression of cell proliferation, invasion, metastasis, angiogenesis, sensitizing toward therapeutics, or activation of apoptotic pathways. Regarding the critical role of HMGA2 in regulating different cancer hallmarks in many types of cancer, targeting this protein for cancer therapy is of great importance for future studies to study the role of HMGA2 in cancer in more detail and paving the way for clinical studies. Although numerous studies have confirmed the importance of miRNAs/HMGA2 axis, the possible interactions between oncogenic miRNAs and HMGA2 is not evaluated well and future studies could address this issue. Also, another limitation is the lack of supporting data for the oncogenic role of HMGA2. Indeed, as HMGA2 affects the most important cancer hallmarks, further studies should uncover downstream targets of HMGA2 by which it affects cancer progression. In addition, finding these downstream targets could be beneficial in cancer targeted therapy and also might be helpful in reversing therapy resistance in cancer.

Declaration of interest

The authors declare no conflict of interest.

ORCID iD authorship contribution statement

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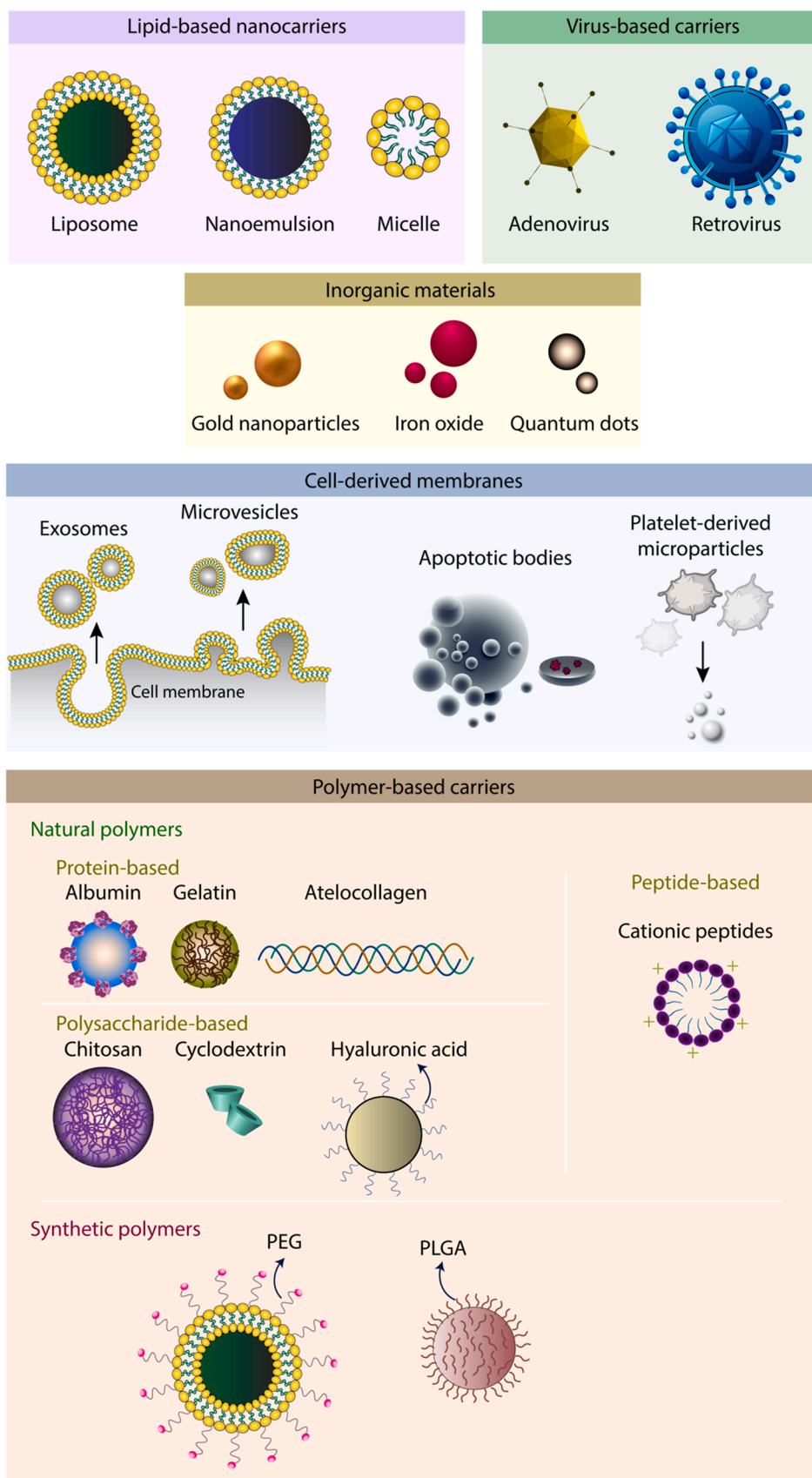


Fig. 8. miRNA delivery systems. A limitation in miRNA-based therapy is that these molecules are degraded in the body quickly and use of a delivery system is of importance to increase miRNAs efficacy in cancer therapy. MiRNAs could be delivered to the target tissue with lipid-based vehicles, carriers which are produced from inorganic materials, cell-derived membranes, and polymer-based vehicles. PLGA: Poly(lactic-co-glycolic acid), PEG: Polyethylene glycol.

Table 3
miRNAs delivery systems in cancer.

miRNA	Cancer type	Delivery system	Target	Affected cancer hallmarks	Ref
miRNA-205	Breast cancer	Dendrimer (Fifth-poly(amidoamine)) functionalized with human luteinizing hormone releasing hormone and acetic anhydride	-	-Cell proliferation	[347]
miRNA-126	Lung cancer	Chitosan decorated with folic acid	Caspase9 ATG5 BECLIN1 EGF-L7 Bcl-2	-Migration -Apoptosis -Autophagy -Cell cycle arrest	[348]
miRNA-204	Breast cancer	Exosomes derived from bovine milk coated with hyaluronic acid	RAB22A	-Cell proliferation	[349]
miRNA-126	NSCLC	Exosomes derived from breast cancer (MDA-MB-231) cells	PTEN/PI3K/ AKT	-Cell proliferation -Migration	[350]
miRNA-34a	PDAC	Poly(ethylene glycol)-poly[aspartamidoethyl(p-boronobenzyl) diethylammonium bromide]	c-myc	-Cell proliferation -G2/M phase arrest -Colony formation	[351]
miRNA-9	PDAC	Chimeric peptide supramolecular nanoparticle	eIF5A2	-Apoptosis -Autophagy	[352]
miRNA-124	Androgen-independent prostate cancer cells	PEI-functionalized polyhydroxybutyrate nanoparticles	CPT1A	-Cell proliferation -Motility -Colony formation	[353]
miRNA-34a	TNBC	Layer-by-layer assembled PLGA nanoparticles	CCND-1 Notch-1 Bcl-2 Survivin MDR-1	-Cell proliferation -Cell cycle arrest	[354]
miRNA-320a-3p	Lung cancer	Gold nanorod modified with polyethyleneimine	Sp1/PTEN/ MMP9	-Cell proliferation -Metastasis -Apoptosis	[355]
miRNA-660	Lung cancer	Coated Cationic Lipid-nanoparticles	MDM2/p53/ p21	-Tumor growth -Cell proliferation	[356]

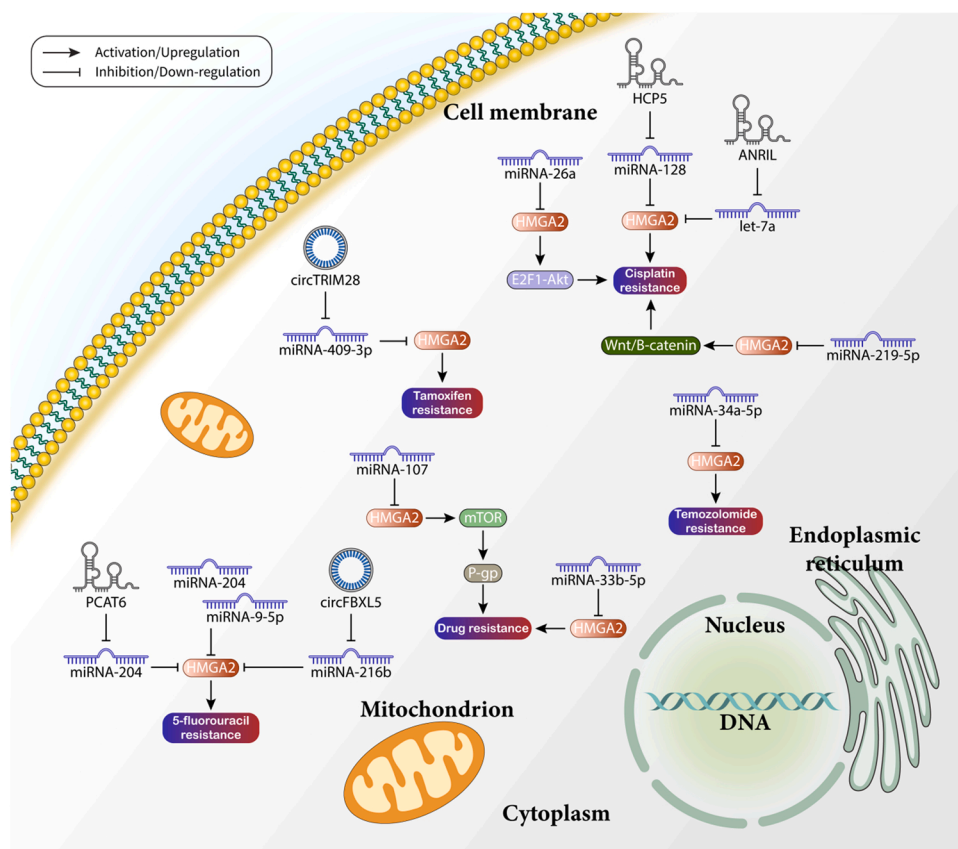


Fig. 9. The miRNA/HMGA2 axis in regulating cancer therapy response. HMGA2 increases drug resistance in cancer directly or through targeting important cellular pathways such as Wnt/ β -catenin and mTOR, or through transporters involving drug efflux such as P-gp. Furthermore, miRNAs that inhibit HMGA2 to increase drug sensitivity could be downstream targets of other ncRNAs including circRNAs and lncRNAs. HMGA2: High mobility group protein AT-hook 2, mTOR: Mammalian target of rapamycin, E2F1: E2F Transcription Factor 1, P-gp: P-glycoprotein.

L.M.ten Hagen: Conceptualization, Literature survey, Writing – original draft preparation. **Shokoo Salimimoghadam, Afshin Taheriazam, Maliheh Entezari, Mojtaba Falahati:** Supervision, Writing – review & editing.

Declaration of Competing Interest

All authors have participated in (a) conception and design, or analysis and interpretation of the data; (b) drafting the article or revising it critically for important intellectual content; and (c) approval of the final version. This manuscript has not been submitted to, nor is under review at, another journal or other publishing venue. The authors have no affiliation with any organization with a direct or indirect financial interest in the subject matter discussed in the manuscript. The following authors have affiliations with organizations with direct or indirect financial interest in the subject matter discussed in the manuscript:

Data availability

No data was used for the research described in the article.

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