

The role of microRNAs in *Helicobacter pylori* pathogenesis and gastric carcinogenesis

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Jennifer M. Noto, Division of Gastroenterology, Department of Medicine, Vanderbilt University Medical Center, 2215 Garland Avenue, 1030C MRB IV, Nashville, TN 37232-0252, USA. e-mail: jennifer.noto@vanderbilt.edu Gastric carcinogenesis is a multistep process orchestrated by aberrancies in the genetic and epigenetic regulation of oncogenes and tumor suppressor genes. Chronic infection with *Helicobacter pylori* is the strongest known risk factor for the development of gastric cancer. *H. pylori* expresses a spectrum of virulence factors that dysregulate host intracellular signaling pathways that lower the threshold for neoplastic transformation. In addition to bacterial determinants, numerous host and environmental factors increase the risk of gastric carcinogenesis. Recent discoveries have shed new light on the involvement of microRNAs (miRNAs) in gastric carcinogenesis. miRNAs represent an abundant class of small, non-coding RNAs involved in global post-transcriptional regulation and, consequently, play an integral role at multiple steps in carcinogenesis, including cell cycle progression, proliferation, apoptosis, invasion, and metastasis. Expression levels of miRNAs are frequently altered in malignancies, where they function as either oncogenic miRNAs or tumor suppressor miRNAs. This review focuses on miRNAs dysregulated by *H. pylori* and potential etiologic roles they play in *H. pylori*-mediated gastric carcinogenesis.

Keywords: gastric cancer, Helicobacter pylori, microRNA, cell cycle, proliferation, apoptosis

INTRODUCTION

Microbial infections are among the most significant causes of cancer worldwide with nearly one in five malignancies resulting from infectious agents (Parkin, 2006). Gastrointestinal cancers represent a major global health concern and account for nearly 20% of all cancer-related deaths (Ferlay et al., 2007). Despite the decreasing incidence of gastric cancer in developed countries, it remains the second leading cause of cancer-related death throughout the world, with ~700,000 deaths attributed to this malignancy annually (Parkin et al., 2005). The major contributing factor to the development of gastric cancer is colonization and chronic infection by the bacterial pathogen, Helicobacter pylori. H. pylori selectively colonizes the gastric epithelium of over 50% of the world's population and typically persists for the lifetime of the host. Among colonized individuals, however, only a fraction develop gastric adenocarcinoma, emphasizing the importance of understanding the pathogenic mechanisms by which H. pylori promotes chronic inflammation and the progression to gastric cancer.

VIRULENCE FACTORS THAT MEDIATE *HELICOBACTER PYLORI* PATHOGENESIS

Chronic gastric inflammation induced by the bacterial pathogen, *H. pylori*, is the strongest known risk factor for the development of atrophic gastritis, metaplasia, dysplasia, and ultimately gastric adenocarcinoma (**Figure 1**). *H. pylori* is a Gram-negative, helical-shaped bacterium specifically adapted to persist within the human gastric niche. *H. pylori* possesses numerous elements to successfully colonize the gastric mucosa, establish chronic infection, and induce gastric pathology. *In vivo*, approximately 20% of *H. pylori*

adhere to the gastric epithelium (Hessey et al., 1990). The large repertoire of adhesins expressed by *H. pylori* likely contribute to its specific adaptation to the gastric niche, allowing flexibility to target specific host cells and to exert a dynamic range of effector functions on host cells. *H. pylori* expresses a number of adhesins that have been linked to virulence. SabA (sialic acid-binding adhesin), which binds host sialyl-Lewis^x, contributes to *H. pylori* persistence and mediates chronic gastric inflammation and injury (Mahdavi et al., 2002). The presence of blood group antigen-binding adhesin (BabA), which binds the host Lewis^b blood group antigen, increases the risk of gastric cancer in a synergistic fashion with other virulence factors, such as CagA (Ilver et al., 1998; Gerhard et al., 1999).

Following adherence and colonization of the gastric mucosa, H. pylori induces chronic gastritis and gastric injury, which are characterized by both neutrophilic and lymphocytic inflammation (Marshall et al., 1985; Goodwin et al., 1986). H. pylori expresses a number of factors capable of modulating the host immune system and eliciting proinflammatory immune responses. Some of these virulence factors include vacuolating cytotoxin (VacA) and the cag (cytotoxin associated gene) pathogenicity island. VacA is coded by the gene vacA, which is present in all strains of H. pylori, and which exhibits vacuolating activity (Leunk et al., 1988; Cover and Blaser, 1992; Cover et al., 1994; Phadnis et al., 1994; Schmitt and Haas, 1994; Telford et al., 1994). Additionally, VacA can induce apoptosis of host cells (Kuck et al., 2001; Xia and Talley, 2001) and suppress proliferation of T and B lymphocytes (Boncristiano et al., 2003; Gebert et al., 2003; Sundrud et al., 2004), which may contribute to the persistence of *H. pylori* through dysregulation of the host immune response. The cag pathogenicity island is present in



~60% of all H. pylori strains and its presence is strongly associated with an increased risk of severe gastritis, ulcer disease, and gastric cancer (Censini et al., 1996; Tomb et al., 1997; Akopyants et al., 1998; Alm et al., 1999). The *cag* island encodes a type 4 secretion system (T4SS), which injects effector molecules, such as CagA, into host cells. CagA is a 120- to 140-kD protein that contains a number of tyrosine phosphorylation motifs (Covacci et al., 1993; Tummuru et al., 1993). Following its injection into host cells, CagA exerts a wide range of phosphorylation-dependent and independent effects, such as cytoskeletal rearrangements, disruption of cell polarity, and mitogenic and proinflammatory responses (Polk and Peek, 2010). Cumulatively, these bacterial factors contribute to adherence, persistence, host immune modulation, and virulence of *H. pylori* within the gastric niche, ultimately resulting in *H*. pylori-mediated chronic inflammation and a series of pathological outcomes that facilitate the development of gastric cancer.

HOST FACTORS THAT CONTRIBUTE TO GASTRIC CARCINOGENESIS

In addition to microbial factors that potentiate gastric disease, there are a number of host factors that contribute to chronic gastritis and the progression to gastric adenocarcinoma. Cyclooxygenases (COX) are key enzymes that catalyze prostaglandin synthesis. Of the three isoforms identified, COX-2 is upregulated in gastric epithelial cells upon co-culture with *H. pylori* (Romano et al., 1998; Juttner et al., 2003; Meyer et al., 2003; Wu et al., 2005) and within the gastric mucosa of *H. pylori*-infected individuals (Sawaoka et al., 1998; Fu et al., 1999; McCarthy et al., 1999). *In vivo* studies show that COX-2 is further upregulated in *H. pylori*-mediated adenocarcinoma (Ristimaki et al., 1997; Sung et al., 2000). COX-2 expression levels are considered an independent factor for poor prognosis and correlate with reduced patient survival, suggesting that *H. pylori*-induced COX-2 overexpression is a risk factor for the development of gastric cancer.

Other host factors that increase the propensity for chronic inflammation and gastric adenocarcinoma are polymorphisms within human *IL-1* β (interleukin-1), *TNF*- α (tumor necrosis factor), and *IL-8* promoters (El-Omar et al., 2000, 2003; Machado et al., 2001; Furuta et al., 2002), which lead to increased expression of the proinflammatory cytokines IL-1 β , TNF- α , and IL-8 (**Figure 1**). These polymorphisms in combination with *H. pylori* virulent genotypes increase the risk of gastric cancer up to 87-fold over baseline (Figueiredo et al., 2002), emphasizing the importance of microbial–host interactions in the development of gastric cancer. Collectively, data demonstrate that *H. pylori* virulence factors, host genetics, and environmental factors interact to induce and maintain the persistent inflammatory immune response that initiates the multistep process leading to gastric cancer.

microRNAs

Recent discoveries have shed new light on the involvement of host microRNAs (miRNAs) in gastric carcinogenesis. miRNAs are small, non-coding RNAs \sim 20–25 nucleotides in length, which function as critical post-transcriptional regulators of gene expression (Bartel, 2009). miRNAs were first characterized in 1993 (Lee et al., 1993), but their distinct role in transcriptional regulation was not recognized until the early 2000s. Most miRNAs are found in intergenic regions and contain their own promoter and regulatory units. Processed miRNAs function by binding to the 3' untranslated region (3'UTR) of messenger RNAs (mRNAs), typically resulting in mRNA degradation and gene silencing or translational repression (Bartel, 2009). It is estimated that the human genome encodes thousands of miRNAs, targeting \sim 30–60% of all protein-coding genes (Lewis et al., 2003). miRNAs are involved in many biological processes, including development, differentiation, angiogenesis, cell cycle progression, proliferation, apoptosis, and signal transduction pathways (Ambros, 2004). Dysregulation of miRNA expression with subsequent disruption of these biological processes can result in disease states. There is an increasing body of evidence regarding the regulatory roles of miRNAs in immune and inflammatory disorders (Wu et al., 2008; Sonkoly and Pivarcsi, 2009), and aberrant expression of miRNAs is observed in many cancers (Lu et al., 2005; Volinia et al., 2006). Thus, recent studies have begun to dissect the mechanisms by which miRNAs function as either oncogenic miRNAs (oncomiRs) or tumor suppressors to promote or prevent tumorigenesis.

DYSREGULATION OF miRNAs IN *H. PYLORI*-INDUCED GASTRIC CARCINOGENESIS

The number of studies analyzing miRNA expression profiles in gastric cancer is rapidly increasing and a comprehensive list of

miRNAs dysregulated in gastric cancer, confirmed mRNA targets, and the biological processes affected is shown in **Tables A1** and **A2** in the Appendix. The first study to address miRNA expression profiles in various cancers, including gastric cancer, was performed in 2005 (Lu et al., 2005). Subsequent studies have not only focused on miRNA expression profiles in gastric cancer, but also those that are altered in response to *H. pylori*.

Matsushima et al. (2011) conducted a study to characterize miRNA expression signatures in H. pylori-infected human gastric mucosa. Using high throughput profiling analysis, 31 miR-NAs were identified as being differentially expressed between H. pylori-infected and H. pylori-uninfected gastric mucosa. The relationship between miRNA expression levels and H. pylori-induced acute inflammation, characterized by neutrophil infiltration, and chronic inflammation, characterized by mononuclear cell infiltration were also determined. Expression levels of many miRNAs correlated with either the degree of acute or chronic inflammation and in some cases both (Tables 1 and 2). The relationship between miRNA expression and extent of glandular atrophy, and intestinal metaplasia was also assessed, but no significant correlations were found (Matsushima et al., 2011). A comprehensive list of miRNAs dysregulated by H. pylori, confirmed mRNA targets, and biological processes affected is shown in Tables 1 and 2. These data suggest that H. pylori infection affects global miRNA expression in human gastric mucosa, and this effect is, in part, linked to H. pylori-induced host inflammatory immune responses.

miRNAs that are dysregulated in response to *H. pylori* infection may not be the same miRNAs that are dysregulated in later stages of gastric disease. A comprehensive review of the literature, however, revealed that there is a select subset of miRNAs dysregulated both following *H. pylori* infection as well asin gastric cancer. These include downregulated miRNAs, *let-7a*, *miR-31*, *miR-101*, *miR-141*, *miR-203*, *miR-210*, *miR-218*, *miR-375*, and *miR-449* as well as upregulated miRNAs, *miR-17*, *miR-20a*, *miR-21*, *miR-146a*, *miR-155*, and *miR-223*. These miRNAs may be more biologically relevant to *H. pylori*-induced gastric inflammation and carcinogenesis and represent fruitful targets for studies focused on cancer that develops in the context of *H. pylori* infection.

The next sections will discuss miRNA dysregulation in *H. pylori*-induced disease and how specific miRNAs control various biological processes related to (1) host inflammatory immune response, (2) cell cycle progression, and (3) apoptosis and proliferation.

HELICOBACTER PYLORI-INDUCED miRNA DYSREGULATION TO CONTROL HOST INFLAMMATORY RESPONSES

Host cells recognize invading pathogens and/or pathogenassociated molecular patterns (PAMPs) through membraneassociated or cytoplasmic pathogen recognition molecules known as Toll-like receptors (TLRs) and Nod-like receptors (NLRs), respectively. PAMPs activate adaptor proteins and transcription factors that mediate host innate immunity through activation of NF- κ B (nuclear factor kappa-light-chain-enhancer of activated B cells) signaling (**Figure 2**). Gastric epithelial cells are the initial host element encountered by *H. pylori*. The innate immune response induced in epithelial cells is characterized by NOD1-dependent activation of NF- κ B in response to *H. pylori* peptidoglycan (PGN), which is injected into host cells via the *cag* T4SS (Viala et al., 2004). Activation of NF- κ B by *H. pylori* leads to induction of the proinflammatory cytokine IL-8 and likely contributes to carcinogenesis through activation of downstream targets that mediate inflammation, cell cycle progression, proliferation, and apoptosis. Myeloid cells constitute a second line of defense and secrete proinflammatory cytokines such as IL-6, IL-1, and TNF- α to establish T and B lymphocyte-mediated adaptive immunity.

The involvement of miRNAs in modulating both the innate and adaptive immune responses is well established (Chen et al., 2004) and H. pylori can dysregulate miRNA expression to evade host defenses and successfully persist in the gastric niche. miR-146a and miR-155 are specifically involved in H. pylori-induced negative regulation of the proinflammatory immune response (Figure 2). Changes in miR-146a expression occur in the development of gastric cancer and in the negative regulation of the innate inflammatory immune response. Single-nucleotide polymorphisms (SNPs) in miR-146a are associated with an increased susceptibility to gastric cancer (Okubo et al., 2010) and H. pylori upregulates miR-146a in vitro and in vivo in a CagAindependent and an NF-KB-dependent manner (Liu et al., 2010; Li et al., 2011a). miR-146a targets the TLR-signaling adaptor molecules IRAK1 (interleukin-1 receptor-associated kinase) and TRAF6 (TNF receptor-associated factor), resulting in negative regulation of TLR and downstream proinflammatory signaling (Figure 2; Liu et al., 2010; Li et al., 2011a). As a result, miR-146a overexpression negatively regulates H. pylori-induced IL-8, TNF- α , IL-1 β , GRO- α [CXCL1, chemokine (C-X-C motif) ligand], and MIP-3a (macrophage inflammatory protein) expression, all key components to the proinflammatory innate and adaptive immune responses (Liu et al., 2010; Li et al., 2011a).

The second miRNA involved in H. pylori-induced downregulation of the host inflammatory immune response, miR-155, plays a critical role in regulating lymphocyte homeostasis and tolerance (Thai et al., 2007). miR-155 is increased in many malignancies of B cell or myeloid origin (Volinia et al., 2006). In transgenic murine models of *miR-155* overexpression, mice develop spontaneous B cell lymphomas (Costinean et al., 2006). miR-155 is induced during both bacterial and viral infections in myeloid cells through activation of TLR-signaling pathways. H. pylori upregulates miR-155 expression in vitro and in vivo, which occurs in an NF-kB-dependent manner, and ultimately results in decreased induction of the proinflammatory cytokines, IL-8, and GRO-a (Xiao et al., 2009b; Tang et al., 2010). miR-155 targets MyD88 (myeloid differentiation primary response gene), the universal adapter protein used by TLRs to activate NF-KB (Figure 2; Xiao et al., 2009b; Tang et al., 2010). Decreased levels of MyD88 subsequently result in decreased NF-kB activation and dampening of the host inflammatory response (Xiao et al., 2009b; Tang et al., 2010). Therefore, these data demonstrate that H. pylori dysregulates host miRNA expression to manipulate the host inflammatory immune response, which may promote bacterial survival and persistence within the gastric mucosa. Because these miRNAs have established roles in carcinogenesis as well as innate immunity, they could serve as an important link between H. pylori-induced inflammation and carcinogenesis.

Table 1 | miRNAs downregulated in response to H. pylori.

miRNAs	Target mRNAs	Biological process targeted	Reference
let-7a+	RAB40C	Cell cycle progression	Matsushima et al. (2011), Motoyama et al. (2008), Yang et al. (2011
		Proliferation	
	HMGA2	Invasion	
let-7b*	HMGA2	Invasion	Matsushima et al. (2011), Motoyama et al. (2008)
let-7d	HMGA2	Invasion	Matsushima et al. (2011), Motoyama et al. (2008)
let-7e	HMGA2	Invasion	Matsushima et al. (2011), Motoyama et al. (2008)
let-7f	HMGA2	Invasion	Matsushima et al. (2011), Motoyama et al. (2008)
miR-1	ND	Proliferation	Saito et al. (2011)
mi R-31 +	ND	ND	Matsushima et al. (2011)
miR-32	ND	ND	Matsushima et al. (2011)
miR-34b	ND	ND	Suzuki et al. (2010)
miR-34c	ND	ND	Suzuki et al. (2010)
miR-101	COX-2, FOS	Proliferation	Matsushima et al. (2011), Varambally et al. (2008), Wang et al. (2010
	MCL1	Apoptosis	
	EZH2	Invasion migration	
miR-103#	ND	ND	Matsushima et al. (2011)
miR-106b	p21	Cell cycle progression	Kan et al. (2009), Matsushima et al. (2011), Petrocca et al. (2008)
		Proliferation	
	BIM	Apoptosis	
miR-125a	ERBB2	Proliferation	Matsushima et al. (2011), Nishida et al. (2011)
miR-130a	ND	ND	Matsushima et al. (2011)
miR-133	ND	Proliferation	Saito et al. (2011)
miR-141#	FGFR2	Proliferation	Du et al. (2009), Matsushima et al. (2011)
miR-200a+	ZEB1, ZEB2	Epithelial to mesenchymal transition (EMT)	Ahn et al. (2011), Matsushima et al. (2011), Shinozaki et al. (2010)
miR-200b+	, BCL2, XIAP	Apoptosis	Ahn et al. (2011), Matsushima et al. (2011), Shinozaki et al. (2010)
	ZEB1, ZEB2	EMT	Zhu et al. (2011a)
miR-200c+	, BCL2, XIAP	Apoptosis	Matsushima et al. (2011), Shinozaki et al. (2010), Zhu et al. (2011a)
		EMT	
miR-203	ABL1	Proliferation	Craig et al. (2011b), Matsushima et al. (2011)
		Invasion	.
miR-204	EZR	Proliferation	Lam et al. (2011), Matsushima et al. (2011)
miR-210	ND	ND	Matsushima et al. (2011)
miR-214	ND	ND	Matsushima et al. (2011)
miR-218	ECOP	Proliferation	Gao et al. (2010), Tie et al. (2010)
		Apoptosis	
	ROBO1	Invasion and metastasis	
miR-320+	ND	ND	Matsushima et al. (2011)
miR-372	LATS2	Cell cycle progression	Belair et al. (2011)
miR-373	LATS2	Cell cycle progression	Belair et al. (2011)
mi R-375 +	PDK1, 14-3-3	Apoptosis	Ding et al. (2010), Matsushima et al. (2011), Tsukamoto et al. (2010)
	JAK2	Proliferation	
miR-377	ND	ND	Matsushima et al. (2011)
miR-379	ND	ND	Matsushima et al. (2011)
miR-429+	BCL2, XIAP	Apoptosis	Matsushima et al. (2011), Sun et al. (2011), Zhu et al. (2011a)
	MYC	Proliferation	
miR-449	GMNN, CCNE2	Cell cycle progression	Bou Kheir et al. (2011), Lize et al. (2011)
	MET, SIRT1	Proliferation	
miR-455	ND	ND	Matsushima et al. (2011)
miR-455 miR-491-5p	ND	ND	Matsushima et al. (2011) Matsushima et al. (2011)
			Matsushima et al. (2011) Matsushima et al. (2011)
miR-500	ND	ND	ivialouoniiiid et al. (2011)

(Continued)

Table 1 | Continued

miRNAs	Target mRNAs	Biological process targeted	Reference
miR-532#	ND	ND	Matsushima et al. (2011)
miR-652#	ND	ND	Matsushima et al. (2011)

Target criteria included (1) reduced protein expression upon miRNA transfection in gastric cells or expression inversely correlated with miRNA in gastric tissue or (2) presence of miRNA binding site on the 3 UTR of target mRNA confirmed by luciferase reporter assay. ND, target mRNA or biological process not determined. *, miRNA expression correlates with acute inflammation. #, miRNA expression correlates with chronic inflammation. +, miRNA expression correlates with both acute and chronic inflammation. Bold indicates miRNA also downregulated in gastric cancer.

Table 2 | miRNAs upregulated in response to H. pylori infection.

miRNAs	Target mRNAs	Biological process targeted	Reference
miR-17^	p21	Cell cycle progression	Saito et al. (2010)
<i>miR-20a</i> ^	p21	Cell cycle progression	Saito et al. (2010)
miR-21	PDCD4	Proliferation	Zhang et al. (2008)
	RECK	Apoptosis	
	PTEN	Invasion	
miR-146a	IRAK1, TRAF6	Immune response	Li et al. (2011a), Liu et al. (2010), Xiao et al. (2011)
		Proliferation	
	SMAD4	Apoptosis	
miR-155	IKK-ε, SMAD2	Immune response	Fassi Fehri et al. (2010), Oertli et al. (2011), Tang et al. (2010), Xiao et al. (2009b)
	FADD , ΡΚΙ α	Apoptosis	
miR-223*	EPB41L3	Invasion and metastasis	Li et al. (2011b), Matsushima et al. (2011)

Target criteria included (1) reduced protein expression upon miRNA transfection in gastric cells or expression inversely correlated with miRNA in gastric tissue or (2) presence of miRNA binding site on the 3 UTR of target mRNA confirmed by luciferase reporter assay. ND, target mRNA or biological process not determined. ^, miRNA expression induced by CagA overexpression, not H. pylori infection (Saito et al., 2010). *, miRNA expression correlates with acute inflammation. Bold indicates miRNA also upregulated in gastric cancer.

HELICOBACTER PYLORI AND miRNAS REGULATE CELL CYCLE PROGRESSION

Disruption of cell cycle progression and increased cellular proliferation are common features of malignancies. Cell cycle progression requires coordinated expression of cyclins, which results in sequential activation of cyclin-dependent kinases (CDKs). miRNA dysregulation promotes cell cycle progression by upregulating cyclin expression and/or downregulating expression of CDK inhibitors (p15, p16, p18, p19, p21, p27, p28, p57) in various cancers, including gastric cancer (Figure 3). miR-449, a miRNA downregulated in H. pylori-infected gastric tissue and in gastric cancer, targets GMNN (geminin) and CCNE2 (cyclin E2; Figure 3). Both geminin and cyclin E2 are overexpressed in numerous malignancies and promote M/G1 and G1/Scell cycle progression and cell proliferation (Bou Kheir et al., 2011; Lize et al., 2011). Consequently, downregulation of miR-449, as occurs following H. pylori infection, promotes cell cycle progression and proliferation through upregulation of geminin and cyclin E2.

p42.3, a recently identified protein significantly upregulated in gastric cancer, regulates G2/M cell cycle progression and proliferation in gastric cancer cells (Xu et al., 2007). *miR-29a*, a miRNA significantly downregulated in gastric cancer, targets *p42.3* (Cui et al., 2011; **Figure 3**). Thus, the downregulation of *miR-29a* results in a reciprocal increase in p42.3 expression, promoting increased cell cycle progression and proliferation. The retinoblastoma protein (RB1) is a tumor suppressor dysregulated in many cancers. RB1 functions to prevent excessive cell proliferation by inhibiting G1/S cell cycle progression. RB1 binds and inhibits transcription factors of the E2F family. When RB1 is bound to E2F the complex acts as a growth suppressor and prevents progression through cell cycle. A number of miRNAs target these factors. For instance, *miR-106a* is upregulated in gastric cancer and targets *RB1* (Volinia et al., 2006), while *miR-331-3p* is downregulated in gastric cancer and targets *E2F1* (Guo et al., 2010; **Figure 3**).

TGFβ suppresses gastric cancer cell proliferation via the transcriptional upregulation of the CDK inhibitor, p21 (Yoo et al., 1999). *miR-93* and *miR-106b* directly target p21, resulting in its transcriptional silencing and impairment of the tumorsuppressing activity of TGFβ (Petrocca et al., 2008; Kan et al., 2009; **Figure 3**). In addition, *miR-25* targets the CDK inhibitor, *p57*, while *miR-221* and *miR-222* target the CDK inhibitors, *p27* and *p57* (Kim et al., 2009; **Figure 3**). These oncogenic miRNA clusters are also significantly upregulated in gastric cancer (Volinia et al., 2006; Petrocca et al., 2008; Guo et al., 2009; Kim et al., 2009; Yao et al., 2009). Overexpression of most of these miRNAs results in activation of CDK2, thereby promoting G1/S phase progression. Since numerous reports have described the role of *H. pylori* in the modulation of cyclins, CDKs, and CDK inhibitors and their link to gastric carcinogenesis (Shirin et al., 2001), these



and a proinflammatory immune response. The key adaptor molecule responsible for signaling by TLRs is MyD88. MyD88 and other adaptor proteins (IRAK-1 and TRAF6) in this signaling cascade are targeted by miRNAs to dampen the host immune response.

data suggest that *H. pylori* modulates expression of cyclins, CDKs, and CDK inhibitors through dysregulation of host miRNAs, which may increase the propensity for gastric transformation.

HELICOBACTER PYLORI AND miRNA DYSREGULATION INHIBIT APOPTOSIS AND PROMOTE CELL SURVIVAL

Increased cellular proliferation and evasion of apoptosis are hallmarks of cellular transformation. Apoptosis can be classified as being dependent on either the intrinsic or extrinsic pathways. The intrinsic pathway is initiated within cells and hinges on the balance of activity between pro-apoptotic and anti-apoptotic members of the Bcl-2 (B cell lymphoma 2) superfamily of proteins, which



act to regulate the permeability of the mitochondrial membrane. miRNAs regulate apoptosis by altering expression and balance of members of the pro-apoptotic (e.g., Bax, Bak, Bim, Bad, Bid, and BNIP3L) and anti-apoptotic (e.g., Bcl-2, Bcl-xL, and Mcl-1) Bcl-2 protein family (**Figure 4**).

normal cell cycle progression.

Numerous miRNAs overexpressed in gastric cancer function as oncomiRs by targeting members of the pro-apoptotic Bcl-2 protein family. In addition to their role in regulating cell cycle progression, *miR-25*, *miR-93*, and *miR-106b* also inhibit apoptosis by preventing expression of the pro-apoptotic protein, Bim (Kan et al., 2009; **Figure 4**). Overexpression of *miR-130b* also contributes to suppression of Bim and apoptosis by targeting *RUNX3* (runt-related transcription factor; Lai et al., 2010), a known tumor suppressor frequently silenced in gastric cancer (Li et al., 2002). *miR-150* targets the *EGR2* (early growth response protein; Wu et al., 2010), a tumor-suppressive transcription factor that induces apoptosis by direct transactivation of pro-apoptotic factors, Bak, and BNIP3L (Unoki and Nakamura, 2003).

Numerous tumor suppressor miRNAs target members of the anti-apoptotic Bcl-2 protein family and are consequently down-regulated in gastric cancer. *miR-15b*, *miR-16*, *miR-34*, *miR-181b*, *miR-181c*, and *miR-497* directly target anti-apoptotic *BCL2* (Ji et al., 2008; Xia et al., 2008; Zhu et al., 2010b, 2011b; **Figure 4**). These miRNA clusters are downregulated in gastric cancer cells



anti-apoptotic protein XIAP. Other receptors that detect survival factors, such as growth factors and cytokines, induce ERK1/2 and PI3K/Akt signaling cascades that ultimately result in the inhibition of the pro-apoptotic protein, Bad. In contrast, upon removal of survival factors, these receptors can signal via JNK to induce the pro-apoptotic protein, Bax. Pro-apoptotic and results in the release of cytochrome c from the mitochondria and induction of the caspase cascade. Signaling through death receptors initiate the extrinsic pathway of apoptosis, leading to the induction of caspases and cell death. There are numerous miRNAs that regulate each of these pathways and dysregulation of these miRNAs can lead to anti-apoptotic and tumorigenic responses.

(Guo et al., 2009), leading to increased expression of Bcl-2 and inhibition of apoptosis. The *miR-200bc/429* cluster is downregulated in gastric cells, and these miRNAs directly target *BCL2* and *XIAP* (x-linked inhibitor of apoptosis), leading to reduced expression and increased apoptosis (Zhu et al., 2011a; **Figure 4**). *miR-101* and *miR-512-5p* target another anti-apoptotic member of the Bcl-2 family, *MCL1* (myeloid leukemia cell differentiation protein; Saito et al., 2009; Wang et al., 2010; **Figure 4**). Both *miR-101* and *miR-512-5p* are downregulated in gastric cancer, leading to increased levels of Mcl-1 and an anti-apoptotic phenotype. In addition, *miR-101* is downregulated by *H. pylori* (Matsushima et al., 2011). *miR-449* is also likely involved in mediating the intrinsic pathway of apoptosis and has been classified as a potent inducer of cell cycle arrest and cell death. *miR-449* expression is reduced in

H. pylori-infected gastric tissue, and its expression is lost in gastric tumors (Bou Kheir et al., 2011; Lize et al., 2011). Conversely, over-expression of *miR-449* inhibits cellular proliferation and induces significant levels of apoptosis, and since *miR-449* belongs to the family of p53-responsive miRNAs, its overexpression also results in activation of p53 and apoptosis-specific marker, caspase 3.

In contrast to the intrinsic pathway, the extrinsic pathway of apoptosis is initiated on the cell surface through the activation of specific pro-apoptotic, death receptors. Specific pro-apoptotic ligands are known to activate the extrinsic pathway of apoptosis via specific receptor binding. Ligand binding induces receptor clustering and the recruitment of the adaptor protein Fas-associated death domain (FADD), leading to induction of caspases and ultimately cell death. In addition to its role in regulating the host immune response, *miR-155* targets *FADD* (**Figure 4**), leading to decreased expression of this key adaptor molecule (Xiao et al., 2009b). Therefore, the upregulation of *miR-155* by *H. pylori* and during carcinogenesis results in downregulation of FADD and inhibition of apoptosis.

In addition to targeting proteins directly involved in the intrinsic and extrinsic pathways of cell death, miRNAs target other factors that ultimately lead to inhibition of apoptosis and increased proliferation. *miR-375* targets 14-3-3 zeta, an anti-apoptotic protein that mediates cell survival by binding the pro-apoptotic protein Bad and sequestering it to the cytosol (Tsukamoto et al., 2010; **Figure 4**). *miR-375* also targets *PDK1* (3-phosphoinositide dependent protein kinase), a kinase that directly phosphorylates Akt, thereby regulating the PI3K/Akt signaling pathway (**Figure 4**). Overexpression of *miR-375* was shown to substantially reduce cell viability through induction of the caspase-dependent apoptotic pathway. *miR-375* is one of the most highly downregulated miR-NAs in gastric cancer (Tsukamoto et al., 2010), suggesting its role as a potent tumor suppressor that contributes to the development of gastric carcinoma.

In contrast, miR-21, a known oncomir that targets many known tumor suppressors, is consistently upregulated in various human cancers, including gastric cancer (Volinia et al., 2006; Chan et al., 2008; Petrocca et al., 2008; Zhang et al., 2008; Guo et al., 2009), and miR-21 expression is increased in H. pylori-infected gastric tissues (Zhang et al., 2008). Overexpression of miR-21 shifts the balance between proliferation and apoptosis, increasing cellular proliferation and inhibiting apoptosis. Specifically, miR-21 targets PTEN (phosphatase and tensin homolog), a tumor suppressor and negative regulator of the PI3K/Akt signaling pathway (Yamanaka et al., 2009), which is involved in both apoptotic and proliferative pathways (Figure 4). Mutations in PTEN are important in the progression of many cancers, including gastric carcinoma (Kang et al., 2002). miR-21 likely also contributes to apoptosis by targeting PDCD4 (programmed cell death protein 4), which is localized to the nucleus of proliferating cells; however, its direct role in apoptosis has not been elucidated (Lu et al., 2008; Motoyama et al., 2010).

Similar to PI3K/Akt signaling, the NF-kB signaling pathway is important in inhibition of apoptosis and cell survival. The NF-KB signaling cascade is activated during H. pylori-induced gastritis and is constitutively active in gastric cancer (Sasaki et al., 2001). miR-218 expression is reduced in numerous cancers, including gastric cancer. H. pylori infection also reduces the expression of miR-218 in vitro and in vivo. miR-218 induces apoptosis in gastric cancer cells through direct targeting of ECOP (epidermal growth factor receptor-co-amplified and overexpressed protein), a known positive regulator of NF-кВ transcriptional activity. Downregulation of miR-218 leads to overexpression of ECOP, inhibition of NF-KB transcriptional activation, and transcription of a downstream target COX-2, ultimately inhibiting apoptosis, and inducing cell proliferation (Gao et al., 2010). Another miRNA important in regulating NF-KB signal transduction pathways is miR-9, which directly targets NF-KB1, thereby suppressing NFκB transcriptional activity (**Figure 4**). *miR*-9 is downregulated in gastric cancer and in vitro studies have shown that restoration of miR-9 expression suppresses proliferation of gastric cancer cells (Luo et al., 2009; Wan et al., 2010). Cumulatively, these studies demonstrate that aberrant activation of NF-κB signaling as a result of *H. pylori*-induced miRNA dysregulation results in inhibition of apoptosis and increased proliferation, thereby sensitizing cells for subsequent mutagenesis.

miR-451, another downregulated miRNA in H. pylori-infected gastric mucosa and gastric cancer, targets MIF (macrophage migration inhibitory factor; Bandres et al., 2009), a lymphokine involved in cell-mediated immunity that is expressed in response to H. pylori infection and during gastric carcinogenesis (He et al., 2006). Overexpression of miR-451 results in targeted downregulation of MIF, which is accompanied by a decrease in cell proliferation and increased apoptosis (Figure 4). Furthermore, there is an inverse correlation between miR-451 and MIF expression in gastric cancer, suggesting that miR-451 functions as a tumor suppressor by silencing MIF expression, leading to a proliferative and anti-apoptotic phenotype (Bandres et al., 2009). miR-141, another miRNA significantly decreased in H. pylori-infected gastric tissue (Matsushima et al., 2011) as well as gastric carcinoma, targets FGFR2 (fibroblast growth factor receptor), and overexpression of miR-141 leads to decreased FGFR2 expression and inhibition of proliferation (Du et al., 2009; Figure 4). miR-23a functions as a growth-promoting and anti-apoptotic factor. It is significantly upregulated in gastric adenocarcinoma and targets IL-6R (interleukin-6 receptor), which promotes increased proliferation and decreased apoptosis in gastric adenocarcinoma cells (Zhu et al., 2010a; Figure 4).

HELICOBACTER PYLORI AND miRNA DYSREGULATION PROMOTES CELL INVASION AND METASTASIS

Invasion and metastasis are hallmarks of cancer cells. Several intracellular signaling pathways, such as those mediated by TGF β and hepatocyte growth factor/Met signaling, promote metastasis. In addition to its role in regulating cell cycle progression, the *H. pylori* downregulated *miR-449* also targets *Met*, a known proto-oncogene that encodes the hepatocyte growth factor receptor. Aberrant activation of Met triggers oncogenic processes, such as proliferation, angiogenesis, invasion, and metastasis (Bou Kheir et al., 2011; Lize et al., 2011). Thus, the targeted downregulation of *miR-449* by *H. pylori* and during gastric carcinogenesis results in upregulation of Met, increased cell proliferation, and likely other oncogenic processes.

The metastatic potential of cancer cells is also regulated by mechanisms that control cell survival, cytoskeletal changes, as well as the activity of extracellular matrix-degrading proteinases (MMPs). Many miRNAs known to regulate cell cycle progression, proliferation, and apoptosis pathways are also involved in metastasis. For example, overexpression of miR-21 has been shown to increase the invasiveness of gastric cancer cells. In addition to its known tumor suppressor targets, miR-21 also targets RECK (reversion-inducing-cysteine-rich protein with kazal motifs), a tumor and metastasis suppressor that inhibits tumor metastasis and angiogenesis through modulation of matrix metalloproteinases (MMPs; Zhang et al., 2008). H. pylori induces expression of MMPs, including MMP-1, MMP-2, MMP-3, MMP-7, MMP-9, which have been linked to H. pylori-induced disease and carcinogenesis (Elkington et al., 2005). These data suggest that H. pylori has the potential to modulate expression of MMPs through dysregulation of host miRNAs and these disruptions may increase the propensity for gastric transformation.

miR-106a is significantly upregulated in cancer cells (Volinia et al., 2006) and is known to correlate with increased lymphatic and distant metastasis (Xiao et al., 2009a). Conversely, *miR-218*, a tumor suppressor miRNA, is downregulated in gastric cancer (Volinia et al., 2006), which correlates with increased metastasis and invasion. This is thought to occur through direct targeting of *ROBO1* (roundabout homolog), which leads to enhanced signaling through the ROBO1 receptor. The SLIT/ROBO signaling pathway has been implicated in many biological responses through regulation of cell migration (Tie et al., 2010). Thus, disruption of this signaling cascade can result in increased invasion and metastasis.

CONCLUSION

The discovery of miRNAs just over a decade ago has challenged the central dogma of genetic and epigenetic regulation. Although extensive work has been dedicated to identifying miRNAs, mRNA targets, and their contribution to accepted regulatory networks, we have only begun to scratch the surface. With thousands of miR-NAs within the human genome, and the ability of each miRNA to target and regulate numerous protein-coding mRNAs, affected regulatory networks are likely to be modified by countless miRNA contributors and will continue to evolve.

Many questions arise when comparing miRNA expression profiles in different model systems *in vitro* and *in vivo* and when comparing miRNA expression profiles in *H. pylori*-infected gastric tissue and gastric cancer. For example, *miR-106b*, a known oncogenic miRNA, upregulated in various malignancies including gastric cancer, is decreased in *H. pylori*-infected gastric mucosa.

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Similarly, miR-34b, miR-34c, miR-103, miR-200a, miR-200b, miR-214, and miR-372 are all overexpressed in gastric cancer, while in H. pylori-infected gastric mucosa these miRNAs are significantly downregulated. In contrast, miR-146a is significantly decreased in gastric cancer, but upregulated in *H. pylori*-infected gastric tissue. However, a recent report has shown that miR-146a is upregulated in a subset of gastric cancers. Although examining miRNA expression signatures in gastric cancer is clearly important in understanding the disease, development of novel therapeutics requires greater insight into the miRNA profiles in precancerous gastric tissues. Since the majority of gastric cancers arise within the context of chronic inflammation, it will be particularly important to discriminate between preneoplastic and tumor-specific miRNA expression profiles. A more comprehensive understanding of the roles of miRNAs in normal biological processes and disease is needed to fully appreciate miRNA dysregulation by pathogens, such as H. pylori. Furthermore, the relationship between single miRNAs and their targets are important to consider, but many of these relationships are cell and context specific. Thus, it is critically important to dissect these intricate pathways and understand how host-pathogen interactions disrupt these encompassing regulatory pathways.

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APPENDIX

Table A1 | miRNAs downregulated in gastric cancer.

miRNAs	Target mRNAs*	Biological processes targeted	Reference
let-7a	RAB40C	Cell cycle progression	Li et al. (2010, 2011c), Motoyama et al. (2008), Tsujiura et al.
		Proliferation	(2010), Yang et al. (2011), Zhang et al. (2007), Zhu et al. (2010c)
	HMGA2	Invasion	
miR-9	CDX2	Cell cycle progression	Luo et al. (2009), Rotkrua et al. (2011), Tsai et al. (2011a), Wan
	NFκB1		et al. (2010)
	GRB2, RAB34	Proliferation	
miR-15b	BCL2	Apoptosis	Xia et al. (2008)
miR-16	BCL2	Apoptosis	Shin et al. (2011), Xia et al. (2008)
miR-29a	p42.3	Cell cycle progression	Cui et al. (2011), Lang et al. (2010)
		Proliferation	
	CDC42	Invasion	
miR-29b	CDC42	Proliferation	Lang et al. (2010)
		Invasion	
miR-29c	CDC42	Proliferation	Lang et al. (2010)
		Invasion	
miR-30a	ND	ND	Li et al. (2010)
miR-30b	ND	ND	Ueda et al. (2010)
miR-30c	ND	ND	Ueda et al. (2010)
miR-31	ND	ND	Guo et al. (2009), Zhang et al. (2010b)
miR-33b	ND	ND	Volinia et al. (2006)
miR-34	BCL2	Apoptosis	Ji et al. (2008)
miR-96	ND	ND	Volinia et al. (2006)
miR-101	COX-2, FOS	Proliferation	Varambally et al. (2008), Wang et al. (2010)
	MCL1	Apoptosis	
	EZH2	Invasion migration	
miR-126	CRK	Cell cycle progression	Feng et al. (2010), Li et al. (2010, 2011c), Otsubo et al. (2011)
	O int	Proliferation	
		Invasion and metastasis	
	SOX2	Proliferation	
miR-128b	ND	ND	Katada et al. (2009)
miR-1290	CDK6		
11110-129	CDRO	Cell cycle progression Proliferation	Katada et al. (2009), Shen et al. (2010), Tsai et al. (2011b), Wu
	SOX4		et al. (2010a)
miR-133b	5074 ND	Apoptosis ND	(1)
			Guo et al. (2009), Wu et al. (2011a)
miR-136	ND	ND	Ueda et al. (2010)
miR-138	ND	ND	Volinia et al. (2006)
miR-139-5p	ND	ND	Guo et al. (2009)
miR-141	FGFR2	Proliferation	Du et al. (2009)
miR-143	ND	Proliferation	Li et al. (2011a), Takagi et al. (2009), Wu et al. (2011a)
miR-145	ND	ND	Li et al. (2011a), Takagi et al. (2009), Tchernitsa et al. (2010)
miR-146a	IRAK1, TRAF6	Immune response	Hou et al. (2011), Kogo et al. (2011), Li et al. (2011a,d), Okubo
		Proliferation	et al. (2010), Tchernitsa et al. (2010)
		Apoptosis	
miR-148	ND	ND	Katada et al. (2009)
miR-148a	CCKBR	Proliferation	Chen et al. (2010), Guo et al. (2011), Zheng et al. (2011)
	p27	Cell cycle progression	
	ROCK1	Invasion and metastasis	
miR-148b	CCKBR	Proliferation	Song et al. (2011)
miR-152	CCKBR	Proliferation	Chen et al. (2010), Ueda et al. (2010)

(Continued)

Table A1 | Continued

miRNAs	Target mRNAs*	Biological processes targeted	Reference
miR-181b	BCL2	Apoptosis	Jiang et al. (2011), Li et al. (2011c), Zhu et al. (2010b)
miR-181c	NOTCH4, KRAS	Proliferation	Hashimoto et al. (2010), Zhu et al. (2010b)
	BCL2	Apoptosis	
miR-195	ND	ND	Guo et al. (2009), Wu et al. (2011a)
miR-197	ND	ND	Li et al. (2011c)
miR-203	ABL1	Proliferation	Chiang et al. (2011), Craig et al. (2011b)
		Invasion	
miR-210	ND	ND	Li et al. (2011c)
miR-212	MECP2	Proliferation	Volinia et al. (2006), Wada et al. (2010), Wu et al. (2011a), Xu
	MYC		et al. (2010)
miR-218	ECOP	Proliferation	Gao et al. (2010), Tie et al. (2010), Ueda et al. (2010), Volinia
		Apoptosis	et al. (2006)
	ROBO1	Invasion and metastasis	
miR-331-3p	E2F1	Cell cycle progression	Guo et al. (2010)
		Proliferation	
miR-339	ICAM-1	Immune response	Ueda et al. (2009)
miR-375	PDK1, 14-3-3	Apoptosis	Ding et al. (2010), Tsukamoto et al. (2010), Ueda et al. (2010)
	JAK2	Proliferation	Xu et al. (2011)
miR-378	ND	ND	Guo et al. (2009), Yao et al. (2009)
miR-433	GRB2	Proliferation	Luo et al. (2009)
miR-449	GMNN, CCNE2	Cell cycle progression	Bou Kheir et al. (2011), Lize et al. (2011)
	MET, SIRT1	Proliferation	
miR-451	MIF	Proliferation	Bandres et al. (2009)
		Apoptosis	
miR-497	BCL2	Apoptosis	Guo et al. (2009), Zhu et al. (2011b)
miR-512-5p	MCL1	Apoptosis	Saito et al. (2009)
miR-638	ND	ND	Yao et al. (2009)
miR-768-3p	ND	ND	Guo et al. (2009)

*Target criteria included (1) reduced protein expression upon miRNA transfection in gastric cells or expression inversely correlated with miRNA in gastric tissue or (2) presence of miRNA binding site on the 3 UTR of target mRNA confirmed by luciferase reporter assay. ND, target mRNA or biological process not determined. Bold indicates miRNA also downregulated following H. pylori infection.

Table A2 | miRNAs upregulated in gastric cancer.

miRNAs	Target mRNAs*	Biological processes targeted	Reference
miR-7	ND	ND	Volinia et al. (2006), Wu et al. (2011b)
miR-17	ND	ND	Guo et al. (2009), Volinia et al. (2006), Yao et al. (2009), Zhou et al. (2010
miR-17-5p	ND	ND	Petrocca et al. (2008), Tsujiura et al. (2010), Ueda et al. (2010), Volini
			et al. (2006)
miR-18a	ND	ND	Guo et al. (2009), Yao et al. (2009)
miR-18b	ND	ND	Guo et al. (2009)
miR-19a	ND	ND	Guo et al. (2009), Ueda et al. (2010)
miR-20a	ND	ND	Guo et al. (2009), Volinia et al. (2006)
miR-20b	ND	ND	Guo et al. (2009), Katada et al. (2009), Ueda et al. (2010)
miR-21	PDCD4	Proliferation	Chan et al. (2008), Guo et al. (2009), Li et al. (2010, 2011c), Lu et al (2008), Motoyama et al. (2010), Petrocca et al. (2008), Shin et al. (2011)
	RECK	Apoptosis	Tsujiura et al. (2010), Ueda et al. (2010), Volinia et al. (2006), Zhang et al
	PTEN	Invasion	(2008)
miR-23a	IL-6R	Proliferation	Li et al. (2011c), Volinia et al. (2006), Zhu et al. (2010a)
		Apoptosis	
miR-23b	ND	ND	Li et al. (2011c)
miR-24	AE1	Proliferation	Chan et al. (2010), Volinia et al. (2006), Wu et al. (2010b)
		Differentiation	
miR-25	p57	Cell cycle progression	Kan et al. (2009), Kim et al. (2009), Li et al. (2011c), Petrocca et al.
	BIM	Apoptosis	(2008), Ueda et al. (2010), Volinia et al. (2006)
miR-27	APC	Epithelial to mesenchymal transition (EMT)	Zhang et al. (2011)
miR-27a	PHB	Proliferation	Katada et al. (2009), Li et al. (2011a); Liu et al. (2009), Sun et al. (2010)
	ZBTB10	Metastasis	Zhao et al. (2011)
miR-34a	SIRT1	Cell cycle progression	Craig et al. (2011a), Yamakuchi and Lowenstein (2009), Yao et al. (2009)
	FOXP1	Proliferation	• · · ·
miR-34b	ND	ND	Katada et al. (2009), Suzuki et al. (2010), Tsai et al. (2011b)
miR-34c	ND	ND	Katada et al. (2009), Suzuki et al. (2010)
miR-92	ND	ND	Li et al. (2011c), Petrocca et al. (2008), Ueda et al. (2010), Volinia et al (2006)
miR-93	p21	Cell cycle progression	Kim et al. (2009), Petrocca et al. (2008), Ueda et al. (2010)
	BIM	Apoptosis	
miR-98	ND	ND	Yao et al. (2009)
miR-99a	ND	ND	Li et al. (2011c)
miR-99b	ND	ND	Volinia et al. (2006)
miR-103	ND	ND	Li et al. (2011c), Tchernitsa et al. (2010), Volinia et al. (2006)
miR-106a	RB1	Cell cycle progression	Guo et al. (2009), Petrocca et al. (2008), Tsujiura et al. (2010), Ueda
	1101	Proliferation	et al. (2010), Volinia et al. (2006), Xiao et al. (2009a), Yao et al. (2009)
miR-106b	p21	Cell cycle progression	Guo et al. (2009), Kim et al. (2009), Petrocca et al. (2008), Tsujiura et al.
	BIM	Apoptosis	(2010), Ueda et al. (2010), Yao et al. (2009)
miR-107	CDK6	Proliferation	Feng et al. (2011), Li et al. (2011b,c), Volinia et al. (2006)
	DICER	Invasion and metastasis	- ong ot an (2011), 21 ot an (20115/0), 10mma ot an (2000)
miR-125b	ND	ND	Li et al. (2011c), Ueda et al. (2010), Volinia et al. (2006)
miR-128a	ND	ND	Katada et al. (2009)
miR-130b	RUNX3	Apoptosis	Li et al. (2002), Lai et al. (2010), Yao et al. (2009)
miR-135a	ND	ND	Ueda et al. (2010)
miR-138	ND	ND	Yao et al. (2009)
miR-146a	SMAD4	Proliferation	Xiao et al. (2011)
1 4 0a	50000	Apoptosis	Nuo ot ul. (2011)
miR-147	ND	ND	Yao et al. (2009)
miR-147	EGR2		Katada et al. (2009), Wu et al. (2010c)
iiin-190	LUNZ	Apoptosis	ולמומטמ כו מו. (2003), אאט פו מו. (20100)

(Continued)

Table A2 | Continued

miRNAs	Target mRNAs*	Biological processes targeted	Reference
miR-155	IKK-ε, SMAD2	Immune response	Fassi Fehri et al. (2010), Oertli et al. (2011), Tang et al. (2010), Tha
	FADD, PKIa	Apoptosis	et al. (2007), Volinia et al. (2006), Xiao et al. (2009b), Yao et al. (2011)
miR-181a-2	ND	ND	Yao et al. (2009)
miR-185	ND	ND	Yao et al. (2009)
miR-191	NDST1	Proliferation	Li et al. (2011c), Shi et al. (2011), Ueda et al. (2010), Volinia et al. (2006)
miR-192	ALCAM	Proliferation	Jin et al. (2011), Volinia et al. (2006)
miR-196a	ND	ND	Okubo et al. (2010), Yao et al. (2009)
miR-200a	ZEB1, ZEB2	Epithelial to mesenchymal transition (EMT)	Ahn et al. (2011)
miR-200b	ZEB1, ZEB2	EMT	Ahn et al. (2011), Zhu et al. (2011a)
	BCL2, XIAP	Apoptosis	
miR-214	ND	ND	Li et al. (2011c), Ueda et al. (2010), Volinia et al. (2006)
miR-215	ALCAM	Proliferation	Jin et al. (2011), Volinia et al. (2006)
		Apoptosis	
miR-221	p27, p57	Cell cycle progression	Chun-Zhi et al. (2010), Kim et al. (2009), Li et al. (2011c), Volinia et al.
	PTEN	Proliferation	(2006), Yao et al. (2009)
miR-222	p27, p57	Cell cycle progression	Chun-Zhi et al. (2010), Kim et al. (2009), Li et al. (2011c), Ueda et al.
	PTEN	Proliferation	(2009), Volinia et al. (2006)
	ICAM-1	Immune response	
miR-223	EPB41L3	Invasion and metastasis	Li et al. (2011c), Petrocca et al. (2008), Volinia et al. (2006), Yao et al. (2009)
miR-302f	ND	ND	Yao et al. (2009)
miR-337-3p	ND	ND	Yao et al. (2009)
miR-340	ND	ND	Guo et al. (2009), Yao et al. (2009)
miR-345	ND	ND	Ueda et al. (2010)
miR-372	LATS2	Cell cycle progression	Cho et al. (2009)
		Apoptosis	
miR-421	CBX7, RBMXL1	Proliferation	Guo et al. (2009), Jiang et al. (2010)
miR-520c-3p	ND	ND	Yao et al. (2009)
miR-575	ND	ND	Yao et al. (2009)
miR-601	ND	ND	Yao et al. (2009)
miR-616	ND	ND	Yao et al. (2009)
miR-650	ING4	Apoptosis	Zhang et al. (2010a)
miR-658	ND	ND	Guo et al. (2009)
miR-1259	ND	ND	Yao et al. (2009)

*Target criteria included (1) reduced protein expression upon miRNA transfection in gastric cells or expression inversely correlated with miRNA in gastric tissue or (2) presence of miRNA binding site on the 3 UTR of target mRNA confirmed by luciferase reporter assay. ND, target mRNA or biological process not determined. Bold indicates miRNA also upregulated following H. pylori infection.

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