The Molecular Basis and Therapeutic Potential of Let-7 MicroRNAs against Colorectal Cancer

Rei Mizuno, Kenji Kawada, and Yoshiharu Sakai

Department of Surgery, Graduate School of Medicine, Kyoto University, Kyoto, Japan

Correspondence should be addressed to Kenji Kawada; kkawada@kuhp.kyoto-u.ac.jp

Received 22 March 2018; Accepted 6 June 2018; Published 19 June 2018

Academic Editor: Maikel P. Peppelenbosch

Copyright © 2018 Rei Mizuno et al. This is an open access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

Although a number of studies have revealed the underlying mechanisms which regulate the development of colorectal cancer (CRC), we have not completely overcome this disease yet. Accumulating evidence has shown that the posttranscriptional regulation by the noncoding RNAs such as microRNAs plays an important role in the development or progression of CRC. Among a number of microRNAs, the let-7 microRNA family that was first discovered in C. elegans and conserved from worms to humans has been linked with the development of many types of cancers including CRC. The expression level of let-7 microRNAs is temporally low during the normal developmental processes, while elevated in the differentiated tissues. The let-7 microRNAs regulate the cell proliferation, cell cycle, apoptosis, metabolism, and stemness. In CRC, expressions of let-7 microRNAs have been reported to be reduced, and so let-7 microRNAs are considered to be a tumor suppressor. In this review, we discuss the mechanisms regulating the let-7 microRNA expression and the downstream targets of let-7 in the context of intestinal tumorigenesis. The application of let-7 mimics is also highlighted as a novel therapeutic agent.

1. Introduction

Colorectal cancer (CRC) is one of the most common causes of cancer deaths worldwide [1–3], and the number of CRC patients is increasing more and more [4]. Many studies have revealed the molecular mechanisms of the colonic tumorigenesis and have proposed various models such as the adenoma-carcinoma sequence (i.e., multistep carcinogenesis) and colitis-associated carcinogenesis observed in inflammatory bowel diseases (IBD). However, we have not yet completely understood the molecular basis of CRC tumorigenesis. One of the reasons which makes our understanding difficult is that not only genetic changes, such as mutation/deletion of oncogenes or tumor suppressor genes, but also the epigenetic modification or posttranscriptional regulation by RNA binding proteins and microRNAs is involved in the colonic tumorigenesis. The let-7 microRNAs are noncoding RNAs which consist of ~22 nucleotides [5]. They are first discovered in C. elegans as a critical regulator of developmental process [6, 7]. Let-7 microRNAs have been experimentally confirmed to be conserved in a wide range of species including humans [8]. As the let-7 family, 9 members are identified so far: let-7a, let-7b, let-7c, let-7d, let-7e, let-7f, let-7g, let-7i, and miR-98. The mature let-7 negatively regulates the expression of target mRNAs at a posttranslational level via imperfect base pairing to the 3’-UTR of their target mRNAs [9]. During normal developmental process, the expression levels of let-7 microRNAs in stem and progenitor cells are maintained low. As progenitor cells differentiate, let-7 expression is increasing [10].

Let-7 microRNAs are downregulated in various types of cancers such as hepatocellular carcinoma (HCC), gastric adenocarcinoma, pancreatic cancer, ovarian cancer, prostate cancer, Burkitt lymphoma, renal cell carcinoma, breast cancer, and melanoma [11]. In the context of CRC, let-7 microRNAs are also downregulated, which affects the posttranscriptional regulation of target mRNAs resulting in the colonic tumorigenesis and progression.

In this review, we discuss the molecular mechanisms by which let-7 microRNAs regulate the colonic tumorigenesis, tumor progression, and chemotherapy resistance by a posttranscriptional regulation and also highlight the possibility of the application of let-7 targeting therapy against CRC.
Figure 1: A schematic diagram of the let-7 biogenesis. Pri-let-7 microRNA precursors are processed in the nucleus by Drosha to pre-let-7. Pre-let-7 microRNA precursors are exported to the cytoplasm by exportin-5, where they are subsequently processed by Dicer resulting in the mature let-7. RNA binding protein LIN28A or LIN28B binds to either pri-let-7 or pre-let-7 using RNA binding domains, cold shock domain (CSD), and two zinc finger domains (ZFDs) and blocks the processing. Upon binding to pre-let-7, LIN28A or LIN28B recruits TUTase, which causes oligouridylation resulting in the degradation of pre-let-7.

2. Biogenesis of Let-7 MicroRNAs (Figure 1)

Mature let-7 microRNAs are synthesized through the multiple processing by microprocessors [12]. Let-7 microRNAs are initially transcribed in long transcripts called primary let-7 (pri-let-7), which are processed in the nucleus by Drosha and Pasha to pre-let-7 with hairpin structures of about 70 nucleotides. Next, pre-let-7 are exported to the cytoplasm by exportin-5, where they are subsequently processed by the enzyme Dicer resulting in the mature let-7 [12]. Let-7 is known to be negatively regulated by the RNA binding proteins, LIN28A or LIN28B. LIN28A or LIN28B has two RNA binding domains, cold shock domain (CSD) and two Cys-Cys-His-Cys- (CCHC-) type zinc finger domains (ZFDs) [13–16], which bind to the conserved GGAG motif in the terminal loop of pri-let-7 or pre-let-7, respectively, resulting in the inhibition of the maturation of let-7 [17, 18]. The binding of LIN28A or LIN28B to either pri-let-7 or pre-let-7 inhibits the processing of let-7 precursors by Drosha and Dicer [19]. Upon binding to pre-let-7, LIN28A or LIN28B recruits TUT4/TUT7, which causes oligouridylation at the 3′ terminal of pre-let-7 [20–22]. Under normal conditions, Dicer recognizes the two nucleotides at the 3′ terminal via its PAZ domain; however, oligouridylation elongates the 3′ terminal resulting in the resistance to Dicer cleavage. Oligouridylated pre-let-7 can also be degenerated by the 3′-5′ exonuclease Dis312 [23, 24]. Thus, LIN28A or LIN28B not only inhibits the biogenesis of let-7 family microRNAs, but also induces their degradation. LIN28A and LIN28B are the negative regulators of let-7 microRNAs, and so the expression level of LIN28A is high in the developmental process, while that of LIN28B is low in the adult tissues [10]. LIN28B has two isoforms: LIN28B-long and LIN28B-short isoforms. Both isoforms preserve the binding ability to pre-let-7. However, LIN28B-short isoform lacks the inhibitory ability against the processing by microprocessors. Namely, LIN28B-short isoform functions as a competitor against the LIN28B-long isoform in the context of let-7 maturation [25].

3. Let-7 and Colon Cancer

Regarding the LIN28AB/let-7 axis, the downregulation of let-7 or upregulation of either LIN28A or LIN28B has been reported to be related to the worse prognosis in CRC patients. Stage I/II CRC patients with high expression of LIN28B exhibit poorer prognosis compared to those with no LIN28B expression [26]. King et al. reported that the expression level of LIN28B was inversely correlated to that of mature let-7a in human CRC [27]. Tu et al. examined the expression of LIN28A or LIN28B in the cohort of almost 600 CRC patients and found that LIN28A or LIN28B was highly expressed in 38 % of CRC patients [28]. Importantly, the overall survival was lower in the patients with high expression of LIN28A or LIN28B than in those with low expression of LIN28A or LIN28B. Madison et al. demonstrated that intestinal tumors were spontaneously developed in the transgenic mice with intestinal-specific LIN28B expression (Villin-Lin28b), which suggests that LIN28B functions as an oncogene [29]. Let-7b and let-7c can escape the downregulation by LIN28B in mice. Therefore, they crossed these mice with let-7b and let-7c knock-out mice (let-7bEC-KO and let-7cEC-KO) and found that the additional downregulation of let-7b and let-7c resulted in the increase of tumor incidence [30]. These results suggest that let-7b or let-7c plays an important role in the intestinal tumorigenesis in mice.
4. Let-7 Target mRNAs in Intestine

As let-7 target mRNAs in the intestinal epithelium, Madison et al. revealed that HMGA1, HMGA2, IGF2BP2, HIF3A, ARID3A, and E2F5 were the most highly induced targets of let-7 microRNAs in the context of intestinal homeostasis [31]. Among these target molecules, the protein expression levels of HMGA1, HMGA2, ARID3A, and HIF3A were dramatically increased in the intestinal tumors. They also demonstrated that HMGA2 plays an important role in the downstream of let-7 in the context of colonic tumorigenesis. They found that the forced expression of HMGA2 could increase the colony forming capacity in intestinal organoids and that the haploinsufficiency of HMGA2 significantly decreased the tumor incidence in villin-Lin28b mice. HMGA2 is a member of the High Mobility Group A class of proteins which bind to AT-rich DNA stretches and modulate gene expression by introducing structural alterations in the chromatin landscape [32]. HMGA2-deficiency impaired the growth in mice, whereas the transgenic expression of HMGA2 variants enhanced the formation of benign tumors, indicating that HMGA2 confers a growth advantage and thus promotes tumorigenesis [33]. In fact, overexpression of HMGA2 was reported to promote metastasis and impact the survival of CRC patients [34]. RNA binding protein IGF2BP1 (IMPI) is also considered as a let-7 target molecule and highly expressed during developmental process, and prominent up-regulation and/or de novo synthesis are observed in various tumors [33, 35]. Hamilton et al. demonstrated that enforced expression of IMPI in SW480 cells could increase the growth of xenografts [36], which indicates that IMPI plays an important role in the formation or dissemination of colon cancer.

5. Functions of Let-7 in the Colonic Tumorigenesis

5.1. Cell Cycle, Proliferation, and Apoptosis. The downregulation of let-7 promotes cell proliferation through the activation of a variety of cellular proliferation signaling and cell cycle signaling pathways. For instance, let-7 negatively regulates RAS expression through direct binding, which could down-regulate MAPK pathway and PI3K/AKT pathway [11, 37]. Let-7 also directly downregulates some oncoproteins such as MYC, HMGA2, and IGF1 [38–41] that are known as critical regulators for the growth of CRC.

The downregulation of let-7 upregulates some cell cycle regulators such as cyclin A2, cyclin D1/2, CDK6, CDC34, CDC25A, Aurora A and B kinases, CDK8, PLAGL2, and TRIM71, which results in the activation of cell cycle [11, 42]. Let-7 also inhibits cell proliferation by regulating transcriptional factors such as STAT3, E2F5, E2F6, CBFB, PLAGL2, SOX9, G3Z1, YAP1, GTFT1, and ARID3A [42, 43]. Let-7 microRNAs also suppress cell proliferation by regulating Wnt signaling. The inhibition of Wnt signaling by let-7 is reported in various types of cancers [44–47]. In the context of intestinal tumorigenesis, Tu et al. demonstrated that overexpressed LIN28 could accelerate the growth of intestinal tumors in Apc(−/−) mice and that this tumor-promoting effect was let-7 dependent [28].

The relationship between let-7 microRNAs and apoptosis in CRC is still controversial. Geng et al. reported that let-7 inhibited apoptosis by decreasing the expression of Fas through the direct inhibition against Fas mRNA in HT29 cells [48]. They demonstrated that let-7 inhibition increased Fas expression and the sensitivity to the FAS-related apoptosis. Conversely, Zhang et al. demonstrated that forced expression of let-7c promoted apoptosis in CRC cell lines at least by targeting BCL2L1 [49]. Mongroo et al. showed that the loss of IMPI, a let-7 target, promoted caspase- and lamin-mediated cell death through CYFIP2 by the cross-talk with KRAS in SW480 cells [50]. Another let-7 target in intestine, HMGA2, was reported to inhibit apoptosis [51]. The effect of let-7 microRNAs on apoptosis might be context-dependent and so further investigation will be needed.

5.2. Let-7 and Intestinal Stem Cells. Intestinal stem cell marker LGR5 is known to be upregulated in human colon cancers and sporadic adenomas [67]. The intestinal stem cell markers such as LGR5, ASCL2, SMOC2, Msi1, and Tert are also known to be increased in colitis-associated carcinogenesis [68]. Madison et al. examined the expression levels of let-7 microRNAs and intestinal stem cell markers (e.g., LGR5, EPHB2, and ASCL2) in human CRC tissues and normal adjacent tissues. Let-7a and let-7b were significantly downregulated in CRC specimens, while intestinal stem cell markers were significantly upregulated, which suggests that depletion of let-7a and let-7b may contribute to a stem cell phenotype in CRC [31]. They also demonstrated that tumors from Villin-Lin28b/let-7IEC-KO mice exhibited a significant upregulation of stem cell markers including Bmi1, Lrig1, Olfm4, ASCL2, Prom1, LGR5, Msi1, and SOX9, suggesting an expansion of CRC and +4 stem cell-like compartments. They evaluated the coexpression of let-7 target mRNAs and stem cell markers in mouse samples, and found that HMGA1 and HMGA2 were intensely correlated with stem cell markers. HMGA2 expression was also correlated with LGR5 expression in human CRC samples [31].

5.3. Tumor Progression and Let-7 MicroRNAs in CRC. The downregulation of let-7 promotes migration and invasion of normal intestinal epithelial cells and CRC cells [27]. Xenografts of the DLD-1 cells in which let-7 expression was decreased by LIN28B overexpression developed lung and liver metastases in a mouse model, which suggests that LIN28B/let-7 axis could affect the metastasis in CRC [26]. Some let-7 target oncogenes such as RAS and MYC might contribute to the tumor progression [69, 70]. HMGA2, one of the let-7 target molecules in intestine, is reported to promote epithelial-to-mesenchymal transition (EMT) through the induction of transcription factor Slug [71]. Forced expression of another let-7 target IMP1 in CRC cell line promoted the growth of xenograft tumors and dissemination into the blood in a mouse model. IMP1 overexpression decreased the expression of E-cadherin, suggesting that IMP1 contributes to the tumor progression through the loss of epithelial identity [36].

5.4. Let-7 and Chemoresistance. The downregulation of let-7 has been reported to contribute to the acquisition of
resistance against chemotherapy in many types of cancers such as breast cancer [72], esophageal cancer [43], acute myeloid leukemia [73], pancreatic cancer [74], ovarian cancer [75], and HCC [76]. Although only a single paper reported that the high let-7g expression was significantly associated with the chemoresistance against S-1 in CRC patients [77], most of the studies have shown that the downregulation of let-7 contributes to the chemoresistance in the context of CRC. One of the underlying mechanisms by which the downregulated let-7 contributes to the chemoresistance is that the decreased let-7 induces the expression of DNA excision repair protein, excision repair cross-complementing group 1 (ERCC1), which contributes to the resistance against cisplatin or 5-FU [25].

Let-7 microRNAs play an important role in regulating the response to antiepidermal growth factor receptor (EGFR) therapies in CRC patients. Cappuzzo et al. demonstrated that the KRAS wild-type metastatic CRC patients with high let-7c exhibited better response to EGFR monoclonal antibodies [78]. Although anti-EGFR treatment is not effective in CRC patients with mutated KRAS, Ruzzo et al. reported that the upregulation of let-7a may rescue the sensitivity of anti-EGFR therapies in such CRC patients [79]. A functional variant of a let-7 complementary site (LCS6) in the KRAS 3' UTR mRNA might be a useful biomarker to predict the sensitivity of anti-EGFR therapies in patients with metastatic CRC and, further prospective confirmation is needed [80].

6. Let-7 MicroRNAs as a Therapeutic Target

As discussed above, accumulating evidence has indicated that let-7 microRNAs function as a tumor suppressor in CRC. Therefore, gene replacement therapy which attempts to introduce the analogous let-7 molecules could be effective. Recent advances in genetic engineering have enabled us to make the microRNA mimics, artificial structures of RNA duplexes, that are identical to the mature microRNA sequence. An microRNA mimic is designed to have the function of the endogenous microRNA, attempting to restore its loss of function as a tumor suppressor [81]. However, systemic administration of microRNAs mimics might induce unexpected side effects because microRNAs including let-7 can be functional not only in cancer cells but also in normal cells (i.e., development, cell proliferation, apoptosis, cell cycle control, differentiation, migration, and metabolism [82, 83]). Therefore, alternative delivery systems functionalized with miRNA using nanoparticles have recently gained intense attention [53] and have been investigated in vitro/in vivo and also in clinical trials. Different types of microRNA mimics have been used in the medical field as therapeutic agents loaded on the surface of nanoparticles (Table 1). Let-7 mimics have been proved to have therapeutic efficacy in mouse models of lung and prostate cancers [55, 84]. These delivery systems have been tested on several animal models, and some disadvantages regarding toxicity, immune, and inflammatory responses were observed [85].

For clinical application, gene replacement therapy with microRNA mimics met many obstacles: the instability of therapeutic molecules, nonspecific inflammation, controlled release of therapeutic molecules, specificity and efficiency of the delivery systems [53]. Advanced delivery strategies are still needed.

7. Conclusions

Accumulating evidence has showed that let-7 microRNAs function as tumor suppressor through the posttranscriptional regulation of target mRNAs in CRC. Let-7 microRNAs regulate various biological events such as cell proliferation, cell cycle, migration, progression, stem cell biology, metabolism, and chemoresistance. Gene replacement therapy with let-7 mimics which attempts to restore the tumor suppressive function of let-7 is tested and therapeutic efficacy has been proved in both in vitro experiments and in vivo animal models. However, many obstacles still remain to be overcome for the safe clinical application. Advanced drug delivery strategies are required.

Conflicts of Interest

The authors declare that there are no conflicts of interest regarding this paper.

References


[71] Y. Li, Z. Zhao, C. Xu, Z. Zhou, Z. Zhu, and T. You, “HMG2 induces transcription factor Slug expression to promote epithelial-to-mesenchymal transition and contributes to...


