

Peripheral blood microRNAs: A novel tool for diagnosing disease?

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Summary

Peripheral blood microRNAs (miRNAs) are endogenous, noncoding small RNAs present in blood. Because of their size, abundance, tissue specificity, and relative stability in peripheral circulation, they offer great promise of becoming a novel noninvasive biomarker. However, the mechanism by which they are secreted, their biological function, and the reason for the existence of extracellular miRNAs are largely unclear. This article describes advances in the study of the mechanism of origin and biological function of extracellular miRNAs along with approaches adopted by research and questions that remain. This work also discusses the potential for peripheral blood miRNAs to serve as a diagnostic tool.

Keywords: Peripheral blood miRNAs, diagnosis, biomarker, biological function

1. Introduction

The traditional method for diagnosing disease was to find pathological tissue. This method was highly specific but lacked sensitivity and involved greater harm to the patient. Therefore, the pressing need was to find a type of noninvasive and highly accurate method of diagnosing disease. MicroRNAs (miRNAs) are endogenous noncoding RNA molecules of 21-23 nucleotides that negatively regulate gene expression by binding to sites in the 3' untranslated regions of target mRNAs, causing a degradation or blockade of the translation. Since their discovery in the early 1990s, miRNAs have been found to play important regulatory roles in a wide range of biological and pathological processes. In recent years, rapid advances in sequencing techniques have greatly improved the sensitivity of their detection, and many miRNAs have been noted in serum and plasma. Studies have found that miRNAs are highly stable in peripheral blood containing ribozymes and some miRNAs, and their levels differ significantly in patients with different diseases

(1,2). Furthermore, levels of expression of specific peripheral blood miRNAs are correlated with certain clinicopathological variables and could serve as a novel diagnostic biomarker for detection of disease and could be used clinically to monitor disease progression (3-8). However, some researchers began to question their diagnostic value given that peripheral blood miRNAs have not been found to play a functional role in the etiology or progression of disease (9). There are doubts about whether levels of expression of peripheral blood miRNAs can be regarded as diagnostic targets and the diagnostic value they may have.

2. miRNAs in peripheral blood

As an existing form of miRNAs, peripheral blood miRNAs come directly from exosomes, which are vesicles 30-100 nm in diameter. Since Johnstone *et al.* discovered that exosomes perform a number of activities (10), as exemplified by the reticulocyte plasma membrane in sheep reticulocytes cultured *in vitro*, exosomes have been gradually emerged from the shadows. Researchers found that purified exosomes contain functional miRNAs and originate from endocytic compartments that are released by many cell types (11,12). A study concerning the mechanism of exosome secretion found that miRNAs increased through overexpression of neutral sphingomyelinase 2 (nSMase2) (13). Decreasing the activity of nSMase2 with a chemical inhibitor, GW4869,

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and specific small interfering RNA resulted in the reduced secretion of miRNAs, so exosomes are released *via* ceramide-dependent secretion. Moreover, a study examining mammary epithelial cells releasing miRNAs revealed that mammary epithelial cells typically release similar exosomes (14). That study measured the level of expression of CD63 and CD81, endosomal marker proteins, and the authors considered extracellular miR-16 to be a surrogate marker for the abundance of endosomal miRNAs.

In addition, levels of miRNAs and exosomes in peripheral circulation are correlated with breast cancer (5), osteoarthritis (15), lung cancer (16,17), and ovarian cancer (18). The relative expression of some miRNAs is closely associated with clinicopathological features of cancer, such as their histologic grade and pathology. In short, these studies have highlighted the potential for use of exosomal miRNAs profiles as diagnostic biomarkers of disease through noninvasive testing. Nonetheless, cells selectively release miRNAs. Pigati *et al.* found that the bulk of miR-451 and miR-1246 produced by malignant mammary epithelial cells was released but that most of the miRNAs produced by non-malignant mammary epithelial cells were retained (14). In addition, Tanaka *et al.* found a high level of miR-92a expression in tissue samples from patients with acute leukemia but a reduced level of miR-92a in plasma (19). Lodes *et al.* also found that the expressional profiles of serum miRNAs did not directly correspond to tissue profiles (20). Therefore, some types of cells selectively release miRNAs, and other pathways of miRNAs secretion must exist.

A study of the secretory pathway of let-7, a tumor-suppressive miRNAs, that targeted oncogenes such as *RAS* and *HMG42* found that not all types of cells secreted exosomes (21). Moreover, another study did not detect exosomal miRNAs in serum from normal controls (20). However, a variety of tissue-derived miRNAs exist in the peripheral circulation of healthy people (22). So where do these miRNAs come from? Some researchers believe that cell death or cell injury is the mechanism of miRNAs release (7,23,24). Alternatively, the release of miRNAs in exosomes is correlated with housecleaning, whereby cells release damaged components and other cellular components into the environment (25). Regardless, none of the hypotheses can sufficiently explain the mechanism of miRNAs release. Therefore, the mechanisms involved in miRNAs release and whether different cells have the same mechanism are questions that still need to be determined.

3. Functions of peripheral blood miRNAs

As an important regulator in the post-transcriptional control of gene expression, miRNAs are involved in major biological processes of cancers, including metastasis, differentiation, apoptosis, and proliferation. In the blood, cellular interactions between erythrocytes,

leukocytes, platelets, and endothelial cells are regulated by complex mechanisms that involve multiple molecules. Interestingly, exosome-derived miRNAs are one such molecule. Circulating miRNAs exist in the form of exosomes (26), which play an important role in intercellular communication, and mature miRNAs can be transferred between circulating cells through exosomes (12).

Many recent studies have noted that miRNAs are important participants in erythropoiesis (27-30), lymphopoiesis (31-33), the modulation of innate immune response (34-36), adaptive immune response (37-39), and the differentiation of leukocytes (40) and dendritic cells (DCs) (41,42). These findings show that exosomal miRNAs are crucial to the functioning of blood cells, and miRNAs could be manufactured into drugs to correct for autoimmune diseases or other diseases related to blood cells.

As miRNAs transporters, exosomes contain inactive miRNAs. Instead of a single messenger, exosomes can deliver multiple miRNAs at one time to neighboring cells and simultaneously suppress related genes (43). Thus, exosomes are a potential way to treat complex and uncontrollable diseases. However, the mechanism by which exosomes bind to the cellular surface and exosomal miRNAs enter into cells is not known. Also unknown is whether exosomes selectively bind to neighboring cells. Other pathways through which miRNAs enter cells need to be determined.

4. The potential use of peripheral blood miRNAs as a diagnostic tool

To deduce miRNAs involved in the progression of non-small-cell lung cancer (NSCLC), one study examined exosomes, another examined serum, and the third examined plasma (16,44,45). The three studies came up with different results. Other studies found that different techniques lead to different results (46,47). This suggests that appropriate specimens and techniques must be used for results to be generalizable and valid.

Whole blood, serum, and plasma can be used to study peripheral blood. Given its relation to erythrocytes, leukocytes, and platelets, whole blood is often chosen when studying immune diseases, inflammatory diseases, or coagulation factor deficiencies, while other studies choose serum or plasma. In actuality, the best specimens are ones that characterize the status of disease; in most diseases, exosomes are the best choice because their origin is known.

The qualitative and quantitative analysis of miRNAs is essential. Microarrays are often used to that end, as are quantitative real-time polymerase chain reaction (qRT-PCR) systems. Real-time PCR using the TaqMan Array Human MicroRNA panel is a novel and practical means of high-throughput investigation of serum RNA samples (48). Lodes *et al.* invented a type of microarray platform

that enables the simultaneous analysis of all human microRNAs *via* either fluorescent or electrochemical signals (20). This platform could easily be redesigned to include newly identified miRNAs without the need for amplification. Further developments have taken place. For example, Lusi *et al.* manufactured an electrochemical genosensor that is able to directly detect miRNAs without the need for PCR and a labeling reaction; their technique is simple, fast, and ultrasensitive (49). Heneghan *et al.* developed a reverse-transcription qRT-PCR assay that can detect circulating miRNAs in serum without RNA isolation (9). To improve accuracy, Moltzahn *et al.* invented a multiplex qRT-PCR technique involving purification of multiplex PCR products followed by uniplex analysis on a microfluidic chip to evaluate 384 human miRNAs (3).

5. Conclusion

Systems biology is defined as a comprehensive quantitative analysis of the manner in which all of the components of a biology system interact functionally over time (50). At the molecular level, the focus of systems biology is to determine the functioning of key molecules in cell signal transduction and gene regulation networks. miRNAs are one class of small, non-coding regulatory molecules, and they play an important role in diverse biological processes such as development, cell proliferation and differentiation, apoptosis, oncogenesis, metabolism, angiogenesis, and inflammation. Therefore, studying the functions of miRNAs is essential to understanding the mechanism of disease and to perceiving the internal workings of biosystems.

As an existing form of miRNAs, peripheral blood miRNAs are encased in exosomes where they are protected from enzymatic degradation. They bind to neighboring cells to regulate the expression of target genes. Most recent studies on peripheral blood miRNAs focused on whether peripheral blood miRNAs can serve as a novel noninvasive biomarker. Surprisingly, almost all found that some (tissue-specific or tissue-nonspecific) circulating miRNAs were correlated with the development and progression of disease. However, the origin and functioning of peripheral blood miRNAs are unclear. miRNAs may exist in another form when they act in peripheral blood.

Peripheral blood miRNAs offer promise in the area of prenatal diagnosis. Evidence has revealed that some placental-specific miRNAs are consistently detected in maternal serum or plasma (2,51). Further research demonstrated that chorionic villous trophoblasts continuously released placenta-specific miRNAs into maternal circulation *via* exosomes (52). The level of expression of placenta-specific miRNAs in maternal peripheral blood is closely related to pre-eclampsia (PE) (3), congenital heart defects (CHD) (53), and fetal growth restriction (54).

In addition, some specific miRNAs have better sensitivity and specificity when distinguishing healthy specimens from those with disease, such as the most common forms of cancers: breast (6,7,55), prostate (47), lung (16,44), and colorectal cancer (56,57). A study of the potential for miRNAs to serve as a biomarker in drug-induced liver injury found that specific miRNAs species exhibited dose- and exposure duration-dependent changes in the plasma that parallel the histopathology of liver degeneration and levels of serum aminotransferase, an earlier biomarker for liver injury, but their changes can be detected significantly earlier (22).

In conclusion, recent studies have shown that tissue-specific miRNAs in peripheral blood may be a potential biomarker because they are noninvasive and reproducible and also because they are accurate (sensitive and specific) and predictable. Therefore, peripheral blood miRNAs may offer a better tool for the diagnosis of disease, though some issues remain.

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References

1. Chen X, Ba Y, Ma L, *et al.* Characterization of microRNAs in serum: A novel class of biomarkers for diagnosis of cancer and other diseases. *Cell Res.* 2008; 18:997-1006.
2. Chim SS, Shing TK, Hung EC, Leung TY, Lau TK, Chiu RW, Lo YM. Detection and characterization of placental microRNAs in maternal plasma. *Clin Chem.* 2008; 54:482-490.
3. Moltzahn F, Olshen AB, Baehner L, Peek A, Fong L, Stöppler H, Simko J, Hilton JF, Carroll P, Blesloch R. Microfluidic based multiplex qRT-PCR identifies diagnostic and prognostic microRNA signatures in sera of prostate cancer patients. *Cancer Res.* 2011; 71:550-560.
4. Melkonyan HS, Feaver WJ, Meyer E, Scheinker V, Shekhtman EM, Xin Z, Umansky SR. Transrenal nucleic acids: From proof of principle to clinical tests. *Ann N Y Acad Sci.* 2008; 1137:73-81.
5. Wang F, Zheng Z, Guo J, Ding X. Correlation and quantitation of microRNA aberrant expression in tissues and sera from patients with breast tumor. *Gynecol Oncol.* 2010; 119:586-593.
6. Roth C, Rack B, Müller V, Janni W, Pantel K, Schwarzenbach H. Circulating microRNAs as blood-based markers for patients with primary and metastatic breast cancer. *Breast Cancer Res.* 2010; 12:R90.
7. Heneghan HM, Miller N, Lowery AJ, Sweeney KJ, Newell J, Kerin MJ. Circulating microRNAs as novel minimally invasive biomarkers for breast cancer. *Ann Surg.* 2010; 251:499-505.
8. Mitchell PS, Parkin RK, Kroh EM, *et al.* Circulating microRNAs as stable blood-based markers for

- cancer detection. *Proc Natl Acad Sci U S A.* 2008; 105:10513-10518.
9. Heneghan HM, Miller N, Kerin MJ. Circulating miRNA signatures: Promising prognostic tools for cancer. *J Clin Oncol.* 2010; 28:e573-e574.
 10. Johnstone RM, Adam M, Hammond JR, Orr L, Turbide C. Vesicle formation during reticulocyte maturation. Association of plasma membrane activities with released vesicles (exosomes). *J Biol Chem.* 1987; 262:9412-9420.
 11. Théry C, Ostrowski M, Segura E. Membrane vesicles as conveyors of immune responses. *Nat Rev Immunol.* 2009; 9:581-593.
 12. Zomer A, Vendrig T, Hopmans ES, van Eijndhoven M, Middeldorp JM, Pegtel DM. Exosomes: Fit to deliver small RNA. *Commun Integr Biol.* 2010; 3:447-450.
 13. Kosaka N, Iguchi H, Yoshioka Y, Takeshita F, Matsuki Y, Ochiya T. Secretory mechanisms and intercellular transfer of microRNAs in living cells. *J Biol Chem.* 2010; 285:17442-17452.
 14. Pigati L, Yaddanapudi SC, Iyengar R, Kim DJ, Hearn SA, Danforth D, Hastings ML, Duelli DM. Selective release of microRNA species from normal and malignant mammary epithelial cells. *PLoS One.* 2010; 5:e13515.
 15. Murata K, Yoshitomi H, Tanida S, Ishikawa M, Nishitani K, Ito H, Nakamura T. Plasma and synovial fluid microRNAs as potential biomarkers of rheumatoid arthritis and osteoarthritis. *Arthritis Res Ther.* 2010; 12: R86.
 16. Shen J, Todd NW, Zhang H, Yu L, Lingxiao X, Mei Y, Guarnera M, Liao J, Chou A, Lu CL, Jiang Z, Fang H, Katz RL, Jiang F. Plasma microRNAs as potential biomarkers for non-small-cell lung cancer. *Lab Invest.* 2011; 91:579-587.
 17. Rabinowits G, Gerçel-Taylor C, Day JM, Taylor DD, Kloecker GH. Exosomal microRNA: A diagnostic marker for lung cancer. *Clin Lung Cancer.* 2009; 10:42-46.
 18. Taylor DD, Gerçel-Taylor C. MicroRNA signatures of tumor-derived exosomes as diagnostic biomarkers of ovarian cancer. *Gynecol Oncol.* 2008; 110:13-21.
 19. Tanaka M, Oikawa K, Takanashi M, Kudo M, Ohyashiki J, Ohyashiki K, Kuroda M. Down-regulation of miR-92 in human plasma is a novel marker for acute leukemia patients. *PLoS One.* 2009; 4:e5532.
 20. Lodes MJ, Caraballo M, Suciú D, Munro S, Kumar A, Anderson B. Detection of cancer with serum miRNAs on an oligonucleotide microarray. *PLoS One.* 2009; 4: e6229.
 21. Ohshima K, Inoue K, Fujiwara A, Hatakeyama K, Kanto K, Watanabe Y, Muramatsu K, Fukuda Y, Ogura S, Yamaguchi K, Mochizuki T. Let-7 microRNA family is selectively secreted into the extracellular environment via exosomes in a metastatic gastric cancer cell line. *PLoS One.* 2010; 5:e13247.
 22. Wang K, Zhang S, Marzolf B, Troisch P, Brightman A, Hu Z, Hood LE, Galas DJ. Circulating microRNAs, potential biomarkers for drug-induced liver injury. *Proc Natl Acad Sci U S A.* 2009; 106:4402-4407.
 23. Ji X, Takahashi R, Hiura Y, Hirokawa G, Fukushima Y, Iwai N. Plasma miR-208 as a biomarker of myocardial injury. *Clin Chem.* 2009; 55:1944-1949.
 24. Zernecke A, Bidzhikov K, Noels H, Shagdarsuren E, Gan L, Denecke B, Hristov M, Köppel T, Jahantigh MN, Lutgens E, Wang S, Olson EN, Schober A, Weber C. Delivery of microRNA-126 by apoptotic bodies induces CXCL12-dependent vascular protection. *Sci Signal.* 2009; 2:ra81.
 25. Johnstone RM, Mathew A, Mason AB, Teng K. Exosome formation during maturation of mammalian and avian reticulocytes: Evidence that exosome release is a major route for externalization of obsolete membrane proteins. *J Cell Physiol.* 1991; 147:27-36.
 26. Pegtel DM, Cosmopoulos K, Thorley-Lawson DA, van Eijndhoven MA, Hopmans ES, Lindenberg JL, de Gruijl TD, Würdinger T, Middeldorp JM. Functional delivery of viral miRNAs via exosomes. *Proc Natl Acad Sci U S A.* 2010; 107:6328-6333.
 27. Grabher C, Payne EM, Johnston AB, Bolli N, Lechman E, Dick JE, Kanki JP, Look AT. Zebrafish microRNA-126 determines hematopoietic cell fate through c-Myb. *Leukemia.* 2011; 25:506-514.
 28. Zhao G, Yu D, Weiss MJ. MicroRNAs in erythropoiesis. *Curr Opin Hematol.* 2010; 17:155-162.
 29. Noh SJ, Miller SH, Lee YT, Goh SH, Marincola FM, Stroncek DF, Reed C, Wang E, Miller JL. Let-7 microRNAs are developmentally regulated in circulating human erythroid cells. *J Transl Med.* 2009; 7:98.
 30. Lu J, Guo S, Ebert BL, Zhang H, Peng X, Bosco J, Pretz J, Schlanger R, Wang JY, Mak RH, Dombkowski DM, Preffer FI, Scadden DT, Golub TR. MicroRNA-mediated control of cell fate in megakaryocyte-erythrocyte progenitors. *Dev Cell.* 2008; 14:843-853.
 31. Xiao C, Calado DP, Galler G, Thai TH, Patterson HC, Wang J, Rajewsky N, Bender TP, Rajewsky K. MiR-150 controls B cell differentiation by targeting the transcription factor c-Myb. *Cell.* 2007; 131:146-159.
 32. Kuchen S, Resch W, Yamane A, *et al.* Regulation of microRNA expression and abundance during lymphopoiesis. *Immunity.* 2010; 32:828-839.
 33. Rao DS, O'Connell RM, Chaudhuri AA, Garcia-Flores Y, Geiger TL, Baltimore D. MicroRNA-34a perturbs B lymphocyte development by repressing the forkhead box transcription factor Foxp1. *Immunity.* 2010; 33:48-59.
 34. Shaked I, Meerson A, Wolf Y, Avni R, Greenberg D, Gilboa-Geffen A, Soreq H. MicroRNA-132 potentiates cholinergic anti-inflammatory signaling by targeting acetylcholinesterase. *Immunity.* 2009; 31:965-973.
 35. Schmidt WM, Spiel AO, Jilma B, Wolzt M, Müller M. *In vivo* profile of the human leukocyte microRNA response to endotoxemia. *Biochem Biophys Res Commun.* 2009; 380:437-441.
 36. Suárez Y, Wang C, Manes TD, Pober JS. Cutting edge: TNF-induced microRNAs regulate TNF-induced expression of E-selectin and intercellular adhesion molecule-1 on human endothelial cells: Feedback control of inflammation. *J Immunol.* 2010; 184:21-25.
 37. Sonkoly E, Janson P, Majuri ML, *et al.* MiR-155 is overexpressed in patients with atopic dermatitis and modulates T-cell proliferative responses by targeting cytotoxic T lymphocyte-associated antigen 4. *J Allergy Clin Immunol.* 2010; 126:581-589.e1-e20.
 38. Curtale G, Citarella F, Carissimi C, Goldoni M, Carucci N, Fulci V, Franceschini D, Meloni F, Barnaba V, Macino G. An emerging player in the adaptive immune response: microRNA-146a is a modulator of IL-2 expression and activation-induced cell death in T lymphocytes. *Blood.* 2010; 115:265-273.
 39. Zhou X, Jeker LT, Fife BT, Zhu S, Anderson MS, McManus MT, Bluestone JA. Selective miRNA disruption in T reg cells leads to uncontrolled

- autoimmunity. *J Exp Med.* 2008; 205:1983-1991.
40. Kasashima K, Nakamura Y, Kozu T. Altered expression profiles of microRNAs during TPA-induced differentiation of HL-60 cells. *Biochem Biophys Res Commun.* 2004; 322:403-410.
 41. Cekaite L, Clancy T, Sioud M. Increased miR-21 expression during human monocyte differentiation into DCs. *Front Biosci (Elite Ed).* 2010; 2:818-828.
 42. Hashimi ST, Fulcher JA, Chang MH, Gov L, Wang S, Lee B. MicroRNA profiling identifies miR-34a and miR-21 and their target genes *JAG1* and *WNT1* in the coordinate regulation of dendritic cell differentiation. *Blood.* 2009; 114:404-414.
 43. Simpson RJ, Lim JW, Moritz RL, Mathivanan S. Exosomes: Proteomic insights and diagnostic potential. *Expert Rev Proteomics.* 2009; 6:267-283.
 44. Silva J, García V, Zaballos A, Provencio M, Lombardía L, Almonacid L, García JM, Domínguez G, Peña C, Diaz R, Herrera M, Varela A, Bonilla F. Vesicle-related microRNAs in plasma of NSCLC patients and correlation with survival. *Eur Respir J.* 2011; 37:617-623.
 45. Hu Z, Chen X, Zhao Y, Tian T, Jin G, Shu Y, Chen Y, Xu L, Zen K, Zhang C, Shen H. Serum microRNA signatures identified in a genome-wide serum microRNA expression profiling predict survival of non-small-cell lung cancer. *J Clin Oncol.* 2010; 28:1721-1726.
 46. Moltzahn F, Olshen AB, Baehner L, Peek A, Fong L, Stöppler H, Simko J, Hilton JF, Carroll P, Belloch R. Microfluidic based multiplex qRT-PCR identifies diagnostic and prognostic microRNA signatures in sera of prostate cancer patients. *Cancer Res.* 2011; 71:550-560.
 47. Brase JC, Johannes M, Schlomm T, Fälth M, Haese A, Steuber T, Beissbarth T, Kuner R, Sültmann H. Circulating miRNAs are correlated with tumor progression in prostate cancer. *Int J Cancer.* 2011; 128:608-616.
 48. Resnick KE, Alder H, Hagan JP, Richardson DL, Croce CM, Cohn DE. The detection of differentially expressed microRNAs from the serum of ovarian cancer patients using a novel real-time PCR platform. *Gynecol Oncol.* 2009; 112:55-59.
 49. Lusi EA, Passamano M, Guarascio P, Scarpa A, Schiavo L. Innovative electrochemical approach for an early detection of microRNAs. *Anal Chem.* 2009; 81:2819-2822.
 50. Aderem A. Systems biology: Its practice and challenges. *Cell.* 2005; 121:511-513.
 51. Gilad S, Meiri E, Yogev Y, Benjamin S, Lebanony D, Yerushalmi N, Benjamin H, Kushnir M, Cholakh H, Melamed N, Bentwich Z, Hod M, Goren Y, Chajut A. Serum microRNAs are promising novel biomarkers. *PLoS One.* 2008; 3:e3148.
 52. Luo SS, Ishibashi O, Ishikawa G, Ishikawa T, Katayama A, Mishima T, Takizawa T, Shigihara T, Goto T, Izumi A, Ohkuchi A, Matsubara S, Takeshita T, Takizawa T. Human villous trophoblasts express and secrete placenta-specific microRNAs into maternal circulation *via* exosomes. *Biol Reprod.* 2009; 81:717-729.
 53. Yu Z, Han S, Hu P, Zhu C, Wang X, Qian L, Guo X. Potential role of maternal serum microRNAs as a biomarker for fetal congenital heart defects. *Med Hypotheses.* 2011; 76:424-426.
 54. Mouillet JF, Chu T, Hubel CA, Nelson DM, Parks WT, Sadovsky Y. The levels of hypoxia-regulated microRNAs in plasma of pregnant women with fetal growth restriction. *Placenta.* 2010; 31:781-784.
 55. Zhu W, Qin W, Atasoy U, Sauter ER. Circulating microRNAs in breast cancer and healthy subjects. *BMC Res Notes.* 2009; 2:89.
 56. Pu XX, Huang GL, Guo HQ, Guo CC, Li H, Ye S, Ling S, Jiang L, Tian Y, Lin TY. Circulating miR-221 directly amplified from plasma is a potential diagnostic and prognostic marker of colorectal cancer and is correlated with p53 expression. *J Gastroenterol Hepatol.* 2010; 25:1674-1680.
 57. Huang Z, Huang D, Ni S, Peng Z, Sheng W, Du X. Plasma microRNAs are promising novel biomarkers for early detection of colorectal cancer. *Int J Cancer.* 2010; 127:118-126.

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