# MicroRNA-454 functions as an oncogene by regulating PTEN in uveal melanoma

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## ARTICLE INFO

## ABSTRACT

MicroRNAs (miRNAs) regulate gene expression by targeted repression of transcription and translation, and are involved in carcinogenesis. In this study, we demonstrated that the expression of miR-454 was up-regulated in uveal melanoma tissues compared to normal tissues. Ectopic expression of miR-454 resulted in significant promotion of cell proliferation, colony formation, invasion and induction of cell cycle in uveal melanoma cells. Furthermore, we identified PTEN as a direct target of miR-454. Our data revealed that ectopic expression of PTEN restored the effects of miR-454 on cell proliferation and invasion in uveal melanoma cells. These findings support an oncogene role of miR-454 in development of uveal melanoma.

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## 1. Introduction

Uveal melanoma is the most common malignancy of the eye. It is arising out of pigmented cells including the ciliary body, choroid, or iris [1–4]. The annual incidence of uveal melanoma is five to seven cases per million populations [5–7]. Metastatic disease of the liver accounts for the high death rate of uveal melanoma, with up to 50% of patients having liver metastases [8–11]. Currently, the etiology and pathogenic mechanism of uveal melanoma are still not elucidated. Therefore, it is important to identify the new crucial biomarkers for early prognosis and therapeutic targets [12–14].

MicroRNAs (miRNAs) are a class 18–22 nucleotide-length non-coding RNAs that are involved in posttranslational regulation of gene expression by repressing translation or cleaving RNA transcripts in a sequence-specific manner [15–18]. A growing body of evidence suggests that miRNAs play crucial roles in various physiological and pathological processes, including development, cell differentiation, proliferation, apoptosis, migration and signal transduction [19–22]. Recent evidence also identifies muted or aberrantly expressed miRNAs in various human cancers such as gastric cancer, bladder cancer, breast cancer, osteosarcoma, hepatocellular carcinoma and Ewing's sarcoma, indicating that miRNAs can function as tumor suppressors or oncogenes [23–29].

The expression of miR-454 was reported to be upregulated in human colorectal cancer tissues and cell lines, functioning as a novel oncogenic miRNA contributing to colon tumorigenesis by regulating TGF-b/Smad signaling by targeting Smad4 [30]. Moreover, another study showed that the expression of miR-454 was downregulated in the TGF-β1-treated LX-2 cells and miR-454 could inhibit the activation of hepatic stellate cells (HSCs) by directly targeting Smad4 [31]. However, the expression and role of the miR-454 in the uveal melanoma development and progression remain unknown. In our study, we demonstrated that miR-454 acted as an oncogene in uveal melanoma. The expression of miR-454 was upregulated in uveal melanoma tissues compared to normal tissues and this was also observed in uveal melanoma cells and human melanocyte cell line. Ectopic expression of miR-454 resulted in significant promotion of cell proliferation, colony formation, invasion and induction of cell cycle in uveal melanoma cells. Furthermore, we identified PTEN as a direct target of miR-454.

## 2. Materials and methods

### 2.1. Ethics statement

All patients provided written informed consent for this study and this study was also approved by the Medical Ethics Committee of The Fourth Hospital of Harbin Medical University.

### 2.2. Tissue specimens and cell lines

Tumor samples and their morphologically normal tissues (located > 0.3 cm from the tumor) were obtained from 25 uveal melanoma patients and were immediately frozen in liquid nitrogen. Human uveal melanoma cell lines (OCM-1A, MUM-2C, C918 and MUM-2B) and human melanocyte cell line (D78) were obtained from the Cell Bank of the Chinese Academy of Sciences (Beijing, People's Republic of China). The OCM-1A, MUM-2C and D78 cells were maintained in Dulbecco's modified Eagle's medium (DMEM) containing 10% fetal bovine serum (FBS), and MUM-2B, C918 in RPMI 1640.

### 2.3. RNA preparation and quantitative real-time PCR (qPCR) assay

Total RNA was extracted from tissues or cells using TRIzol reagent (Invitrogen, Carlsbad, CA, USA) following to the manufacturer's instruction. Quantitative real-time PCR was performed using SYBR Premix Ex Taq II (TaKaRa). TaqMan microRNA assays (Applied Biosystems, Foster City, California, USA) were used to quantify the expression levels of miR-454. Forward and reverse primers were used as follows: PTEN, CACCTATTCCTCAGCCCTTAT and AACCCTCATTCAGACCTTCAC; GAPDH, AATGGGCAGCCGTTAGG AAA and TGAAGGGGTCATTGATGGCA; miR-454, ACCCTATCAA TATTGTCTCTGC and GCGAGCACAGAATTAATACGAC; U6, CGCTTCG GCAGCACATATACTA and CGCTTCACGAATTTGCGTGTCA.

### 2.4. Oligonucleotide transfection

miR-454 mimics and scramble were obtained by Genepharma (Genepharm, Shanghai, China). PTEN vector were synthesized by RiboBio (RiboBio, Guangzhou, China). Cells were transfected with oligonucleotides using Lipofectamine 2000 Reagent (Invitrogen Life Technologies) following the manufacturer's instructions.

### 2.5. Cell proliferation, colony formation and cell cycle assay

Cell proliferation was performed using a Cell Counting Kit-8 (CCK-8) (Dojindo, Kumamoto, Japan) according to the manufacturer's instructions and cell numbers were counted by the optical density at 450 nm. For colony formation assay, cells were cultured in a 6-well plate and seeded for 10 days. Colonies were fixed with paraformaldehyde and stained with 1% crystal violet (Sigma–Aldrich) and the numbers of colonies were counted. The fixed cells were incubated with propidium iodide (PI) and ribonuclease A for 30 min, and then detected by flow cytometric analysis using FL2 histogram of a flow cytometer (FACSort; Becton–Dickinson, San Jose, CA, USA).

### 2.6. Cell invasion assay

Invasion assay was performed using Matrigel invasion chamber system (BD Biosciences, Bedford, MA). Cells were cultured on the top of matrigel-coated chambers in a serum-free medium and DMEM containing 10% FBS was used as a chemoattractant. Invasion of cells to the lower side were fixed and stained with % crystal violet (Sigma–Aldrich) and were counted.

### 2.7. Western blot analysis

Proteins were extracted from cells using Protein Extraction Kit (KeyGen, Nanjing, China) and were separated on 10% sodium dodecyl sulfate–polyacrylamide gel electrophoresis (SDS–PAGE) and transferred to nitrocellulose membrane (Bio-Rad, Hercules, California, USA). The membranes were blocked for 1 h with 5% non-fat milk and then detected with primary antibodies recognizing PTEN (Abcam, Cambridge, MA, USA), mouse anti-GAPDH antibody (1:3000; Sigma–Aldrich), respectively. Proteins were detected with enhanced chemiluminescence reagents (Thermo Scientific, Waltham, Massachusetts, USA) after incubation with appropriate horseradish peroxidase (HRP)-conjugated secondary antibodies (Jackson ImmunoResearch).

### 2.8. Luciferase reporter assay

The mutated (MUT) and wild-type (WT) putative miR-454 target on PTEN 3′UTR were cloned into the pGL3 Dual-Luciferase miRNA Target Expression Vector (Invitrogen Corporation). Luciferase activity was performed using the Dual-Luciferase Reporter Assay System (Promega) according to manuscript's instruction.

### 2.9. Statistical analysis

SPSS16.0 (Chicago, IL, USA) was performed for statistical analysis. Data were presented as the mean ± standard deviation (S.D.) from at least three independent experiments. Student's $t$-test or a one-way analysis of variance (ANOVA) was used to evaluate the statistical significance of the results. Differences were considered statistically significant at $P < 0.05$.

## 3. Result

### 3.1. The expression of miR-454 was upregulated in uveal melanoma tissues and cell

The expression of miR-454 was upregulated in uveal melanoma samples compared to their normal samples (Fig. 1A). Further results confirmed that miR-454 was upregulated in uveal melanoma (OCM-1A, MUM-2C, C918 and MUM-2B) compared to human melanocyte cell line (D78) (Fig. 1B).

### 3.2. MiR-454 promoted the uveal melanoma cell proliferation and invasion

To measure the functional role of miR-454 overexpression in uveal melanoma, we transfected uveal melanoma cell line MUM-2B with miR-454 mimic (Fig. 2A). Ectopic expression of miR-454 promoted cell proliferation as compared to cells expressing scramble (Fig. 2B). Cell cycle analysis revealed that overexpression of miR-454 decreased the number of cells in the G0/G1 phase of the cell cycle while the S-phase population increased in MUM-2B cells (Fig. 2C). Colony formation assay also showed that ectopic expression of miR-454 increased the MUM-2B cell colony formation (Fig. 2D). Invasion assay analysis demonstrated that miR-454 overexpression promoted the MUM-2B cell invasion (Fig. 2E).

### 3.3. PTEN was a direct target of miR-454 in uveal melanoma

We used TargetScan to find that 3′UTR of PTEN contained the highly conserved putative miR-454 binding sites (Fig. 3A). Luciferase reporter analysis demonstrated that overexpression of miR-454 reduced luciferase activity in the PTEN wild-type reporter
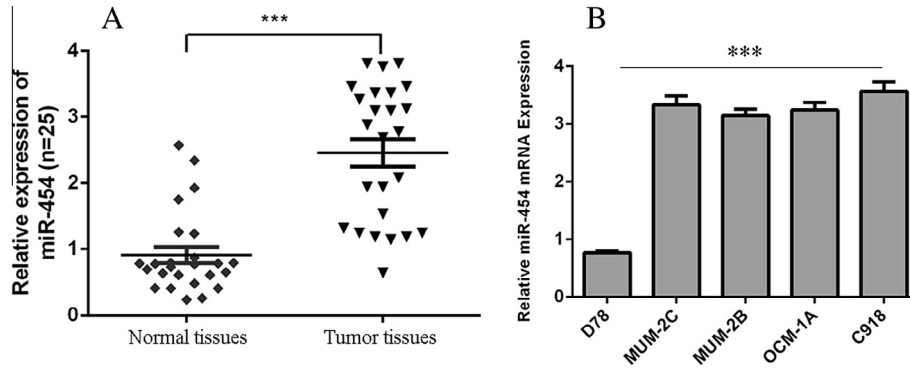
**Fig. 1.** The expression of miR-454 was up-regulated in uveal melanoma tissues and cell. (A) miR-454 was detected in 25 uveal melanoma samples by qRT-PCR. Data demonstrated that the expression of miR-454 was found to be up-regulated in uveal melanoma samples compared to their normal samples. (B) The expression of miR-454 was measured in uveal melanoma (OCM-1A, MUM-2C, C918 and MUM-2B) and uman melanocyte cell line (D78) using qRT-PCR. $^{***}P < 0.001$.
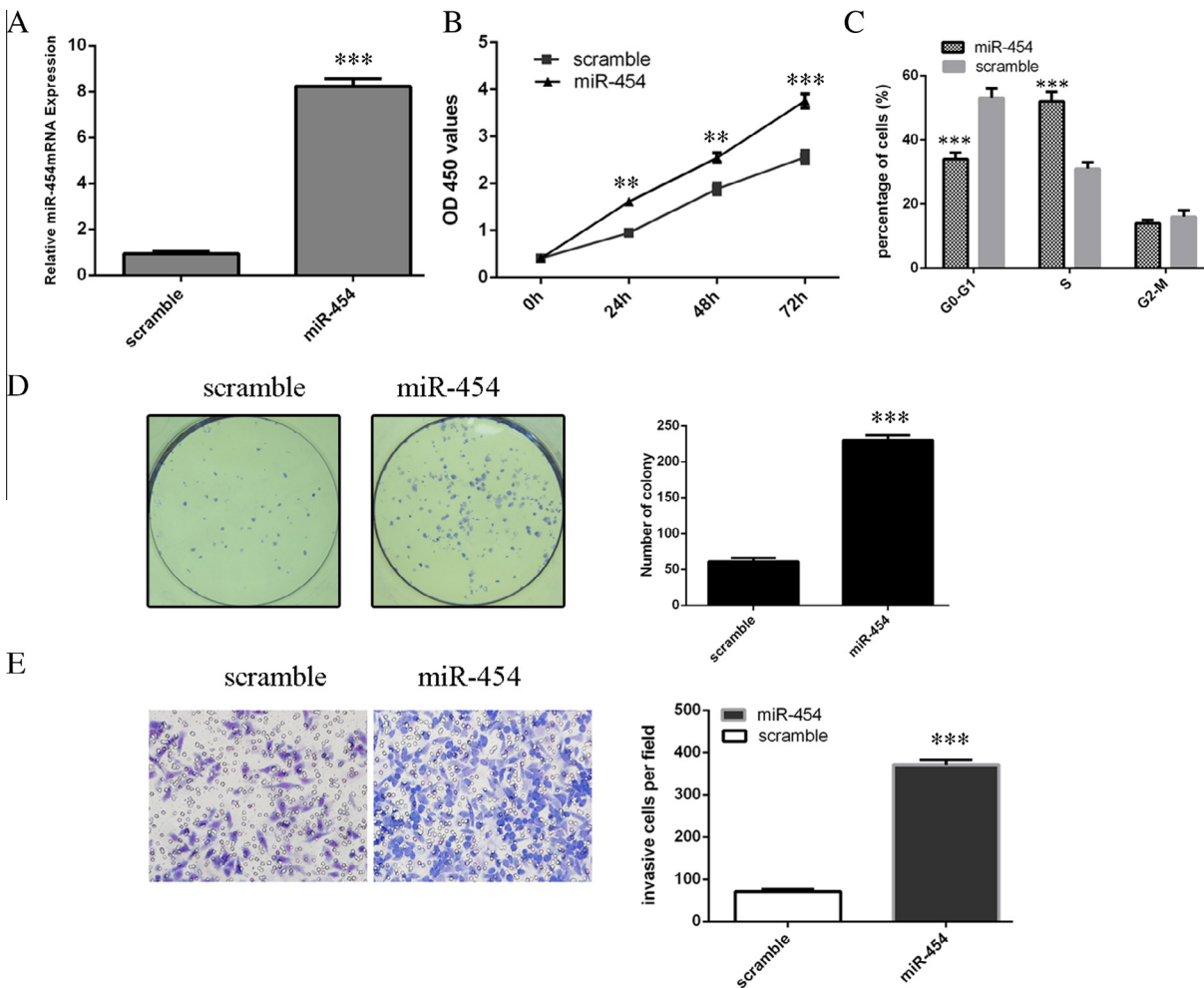


**Fig. 2.** miR-454 promoted the uveal melanoma cell proliferation and invasion. (A) The expression of miR-454 was measured in uveal melanoma cell MUM-2B after transfected by miR-454 mimic or scramble. (B) CCK8 assay was measured the MUM-2B cell proliferation after transfected by miR-454 mimic or scramble. (C) Cell cycle analysis was measured the MUM-2B cell cycle after transfected by miR-454 mimic or scramble. (D) Colony formation analysis was measured the MUM-2B cell colony formation after transfected by miR-454 mimic or scramble. (E) Invasion analysis was measured the MUM-2B cell invasion after transfected by miR-454 mimic or scramble. $^{**}P < 0.01$ and $^{***}P < 0.001$.
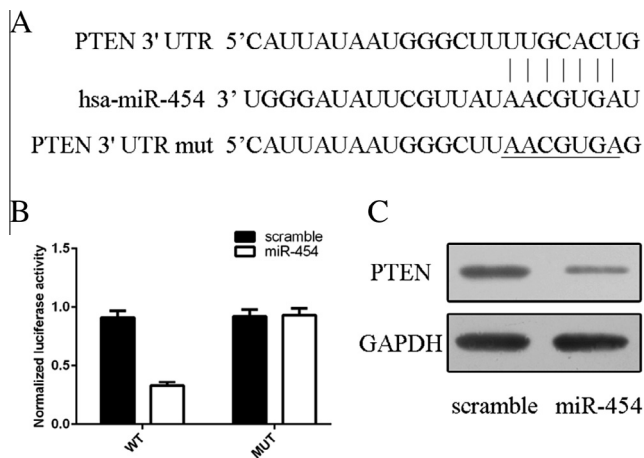
**Fig. 3.** PTEN was a direct target of miR-454 in MUM-2B cell. (A) TargetScan was demonstrated that 3′UTR of PTEN contained the highly conserved putative miR-454 binding sites. (B) Luciferase reporter analysis demonstrated that overexpression of miR-454 reduced luciferase activity in the PTEN wild-type reporter gene but not the mutant type in MUM-2B cell. (C) Ectopic expression of miR-454 inhibited the protein expression of PTEN in MUM-2B cell.

**Fig. 4.** miR-454 inhibited the expression of AKT and MTOR. (A) Western blot analysis was measured the protein level of AKT and phospho-AKT (p-AKT) after transfected by miR-454 mimic or scramble in MUM-2B cell. (B) Western blot analysis was measured the protein level of MTOR and phospho-MTOR (p-MTOR) after transfected by miR-454 mimic or scramble in MUM-2B cell.

gene but not the mutant type, suggesting that miR-454 directly targeted the PTEN 3′UTR (Fig. 3B). Ectopic expression of miR-454 inhibited the expression of PTEN (Fig. 3C).

### 3.4. MiR-454 inhibited the expression of AKT and MTOR

Ectopic expression of miR-454 promoted the expression of AKT, phospho-AKT (p-AKT), MTOR, and phospho-MTOR (p-MTOR) compared to cells expressing scramble (Fig. 4A and B).

### 3.5. Ectopic expression of PTEN restored the effects of miR-454 on cell proliferation and invasion in uveal melanoma cells

Western blot analysis demonstrated that PTEN expression was restored after transfection of cells with the PTEN vector (Fig. 5A). Overexpression of PTEN vector promoted MUM-2B cells proliferation and invasion (Fig. 5B and C).

## 4. Discussion

Increasing evidences demonstrate that miRNAs have a regulatory role in the development and progression of human cancers through the suppression of genes involved in cell proliferation, differentiation, invasion and migration [32–39]. Our previous study has shown that miR-144 acts as a tumor suppressor in uveal melanoma [40]. Moreover, Liu et al. demonstrated that miR-9 suppressed uveal melanoma cell migration and invasion partly through downregulation of the NF-κB1 signaling pathway [8]. Yan et al. showed that miR-182 functioned as a potent tumor suppressor in uveal melanoma cells [14]. miR-34b and miR-34c act as tumor suppressor genes in uveal melanoma cell proliferation and migration [11]. In our study, the expression of miR-454 was upregulated in uveal melanoma tissues compared to normal tissues and this was also observed in uveal melanoma cells and human melanocyte cell line. Ectopic expression of miR-454 promoted cell proliferation, colony formation, invasion and induction of cell cycle in uveal melanoma cells. Furthermore, we identified PTEN as a direct target of miR-454. Our data revealed that ectopic expression of PTEN restored the effects of miR-454 on cell proliferation and invasion in uveal melanoma cells. These findings suggest that miR-454 may be an oncogene that controls PTEN expression in uveal melanoma cells.
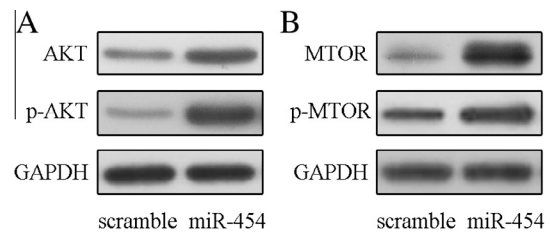
The expression of miR-454 was reported to be upregulated in human colorectal cancer tissues and cell lines, functioning as a novel oncogenic miRNA contributing to colon tumorigenesis by regulating TGF-b/Smad signaling by targeting Smad4 [30]. Moreover, another study showed that the expression of miR-454 was downregulated in the TGF-β1-treated LX-2 cells and miR-454 could inhibit the activation of hepatic stellate cells (HSCs) by directly targeting Smad4 [31]. However, the expression and role of the miR-454 in the uveal melanoma development and progression remain unknown. In our study, the expression of miR-454 was higher in uveal melanoma tissues compared to normal tissues and this was also observed in uveal melanoma cells and human melanocyte cell line. Furthermore, overexpression of miR-454 promoted cell proliferation, colony formation, invasion and induction of cell cycle in uveal melanoma cells. These data suggested that miR-454 acted as an oncogene role in the development and progression of uveal melanoma.

Next, we investigated the molecular mechanism of miR-454 in promoting proliferation and metastasis in uveal melanoma cells. We used TargetScan to find that 3′UTR of PTEN contained the highly conserved putative miR-454 binding sites. Next, we demonstrated that miR-454 overexpression was associated with suppression of luciferase activity. In addition, we observed that the level of PTEN protein was decreased after miR-454 overexpression. We also demonstrated that overexpression of miR-454 enhanced the expression of AKT, phospho-AKT (p-AKT), MTOR, and phospho-MTOR (p-MTOR), which is line with the functional of PTEN downregulation [41]. Functional assays by PTEN vector transfection restored the effects of miR-454 on cell proliferation and invasion in uveal melanoma cells. PTEN was discovered as a tumor suppressor gene and played a critical factor in the development and progression of various cancers including gastric cancer, osteosarcoma, colon cancer, nasopharyngeal carcinoma and prostate cancer [42–46]. Previous studies also showed that PTEN was a tumor suppressor involved in uveal melanoma pathogenesis and might be associated with clinical outcome [47]. Homozygous deletions and intragenic mutations of PTEN occurred more frequently in the metastatic cutaneous melanomas and cell lines [48]. However, the mechanism of PTEN downregulation in uveal melanoma is still unknown. The ability of miR-454 to target PTEN may provide one such mechanism of post-transcriptional control of PTEN.

Some limitations of our study have to be improved in the further work. First, the sample size of the uveal melanoma tissues was small. Second, both these tumor tissues and control tissues contained melanoma cells and an admixture of stroma cells like macrophages, granulocytes and other matrix cells. The density of these cells may be much higher in the tumor tissues than in the control tissues and this may affect the results. Moreover, it is essential to study the role of miR-454 in more other cancers such as gastric cancer, breast cancer, hepatocellular carcinoma and lung cancer in next work.
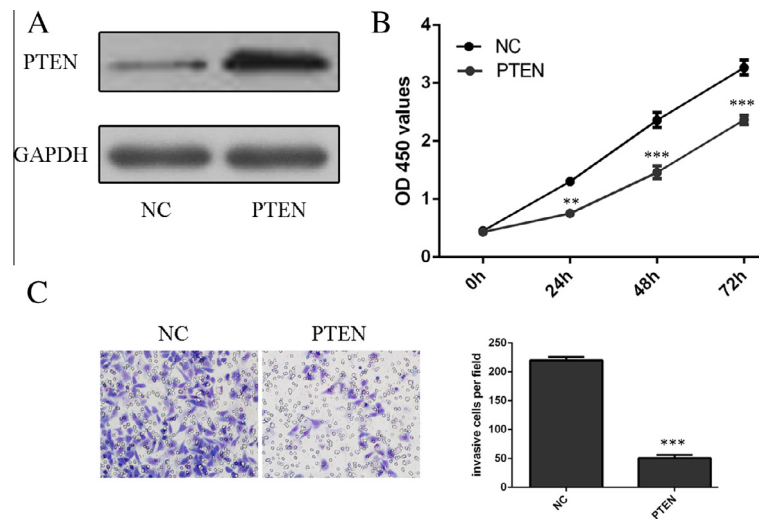
**Fig. 5.** The ectopic expression of PTEN restored the effects of miR-454 on cell proliferation and invasion in uveal melanoma cells. (A) Western blot analysis was measured the protein level of PTEN in the MUM-2B cells after transfection of cells with the PTEN vector. (B) CCK8 assay was measured the miR-454 overexpressing MUM-2B cell proliferation after transfected PTEN vector or control. (C) Invasion assay was measured the miR-454 overexpressing MUM-2B cell invasion after transfected PTEN vector or control. $^{**}P < 0.01$ and $^{***}P < 0.001$.

In conclusion, we demonstrated that miR-454 was frequently overexpressed in uveal melanoma tissues and cell lines. MiR-454 played an important role in the malignant progression of uveal melanoma cells by directly regulating PTEN expression. Our findings suggested that miR-454 might be used as a potential therapeutic target for the treatment of patients with uveal melanoma.

## Acknowledgement

## References

[1] Gardner, F.P., Serie, D.J., Salomao, D.R., Wu, K.J., Markovic, S.N., Pulido, J.S. and Joseph, R.W. (2014) C-MET expression in primary and liver metastases in uveal melanoma. Melanoma Res. 24, 617–620.

[2] Sato, T., Han, F. and Yamamoto, A. (2008) The biology and management of uveal melanoma. Curr. Oncol. Rep. 10, 431–438.

[3] Radhakrishnan, A., Badhrinarayanan, N., Biswas, J. and Krishnakumar, S. (2009) Analysis of chromosomal aberration (1, 3, and 8) and association of microRNAs in uveal melanoma. Mol. Vis. 15, 2146–2154.

[4] Chen, X. et al. (2011) Epigenetics, microRNAs, and carcinogenesis: functional role of microRNA-137 in uveal melanoma. Invest. Ophthalmol. Vis. Sci. 52, 1193–1199.

[5] Harbour, J.W. (2012) The genetics of uveal melanoma: an emerging framework for targeted therapy. Pigment Cell Melanoma Res. 25, 171–181.

[6] Mallikarjuna, K., Pushparaj, V., Biswas, J. and Krishnakumar, S. (2007) Expression of epidermal growth factor receptor, ezrin, hepatocyte growth factor, and c-Met in uveal melanoma: an immunohistochemical study. Curr. Eye Res. 32, 281–290.

[7] Abdel-Rahman, M.H., Boru, G., Massengill, J., Salem, M.M. and Davidorf, F.H. (2010) MET oncogene inhibition as a potential target of therapy for uveal melanomas. Invest. Ophthalmol. Vis. Sci. 51, 3333–3339.

[8] Liu, N. et al. (2012) MicroRNA-9 suppresses uveal melanoma cell migration and invasion through the NF-kappaB1 pathway. Oncol. Rep. 28, 961–968.

[9] Yan, D. et al. (2009) MicroRNA-34a inhibits uveal melanoma cell proliferation and migration through downregulation of c-Met. Invest. Ophthalmol. Vis. Sci. 50, 1559–1565.

[10] Li, Y., Huang, Q., Shi, X., Jin, X., Shen, L., Xu, X. and Wei, W. (2014) MicroRNA 145 may play an important role in uveal melanoma cell growth by potentially targeting insulin receptor substrate-1. Chin. Med. J. (Engl.) 127, 1410–1416.

[11] Dong, F. and Lou, D. (2012) MicroRNA-34b/c suppresses uveal melanoma cell proliferation and migration through multiple targets. Mol. Vis. 18, 537–546.

[12] Worley, L.A., Long, M.D., Onken, M.D. and Harbour, J.W. (2008) Micro-RNAs associated with metastasis in uveal melanoma identified by multiplexed microarray profiling. Melanoma Res. 18, 184–190.

[13] Coupland, S.E., Lake, S.L., Zeschnigk, M. and Damato, B.E. (2013) Molecular pathology of uveal melanoma. Eye (London) 27, 230–242.

[14] Yan, D. et al. (2012) Role of microRNA-182 in posterior uveal melanoma: regulation of tumor development through MITF, BCL2 and cyclin D2. PLoS One 7, e40967.

[15] Yu, X., Li, Z., Shen, J., Wu, W.K., Liang, J., Weng, X. and Qiu, G. (2013) MicroRNA-10b promotes nucleus pulposus cell proliferation through RhoC-Akt pathway by targeting HOXD10 in intervetebral disc degeneration. PLoS One 8, e83080.

[16] Li, Z., Yu, X., Shen, J. and Jiang, Y. (2015) MicroRNA dysregulation in uveal melanoma: a new player enters the game. Oncotarget.

[17] Ohdaira, H., Sekiguchi, M., Miyata, K. and Yoshida, K. (2012) MicroRNA-494 suppresses cell proliferation and induces senescence in A549 lung cancer cells. Cell Prolif. 45, 32–38.

[18] Li, M., Yu, M., Liu, C., Zhu, H., He, X., Peng, S. and Hua, J. (2013) MiR-34c works downstream of p53 leading to dairy goat male germline stem-cell (mGSCs) apoptosis. Cell Prolif. 46, 223–231.

[19] Yu, X., Li, Z. and Liu, J. (2015) MiRNAs in primary cutaneous lymphomas. Cell Prolif..

[20] Li, Z., Yu, X., Shen, J., Chan, M.T. and Wu, W.K. (2015) MicroRNA in intervertebral disc degeneration. Cell Prolif..

[21] Li, J., You, T. and Jing, J. (2014) MiR-125b inhibits cell biological progression of Ewing's sarcoma by suppressing the PI3K/Akt signalling pathway. Cell Prolif. 47, 152–160.

[22] Luo, X., Dong, Z., Chen, Y., Yang, L. and Lai, D. (2013) Enrichment of ovarian cancer stem-like cells is associated with epithelial to mesenchymal transition through an miRNA-activated AKT pathway. Cell Prolif. 46, 436–446.

[23] Yu, L., Ding, G.F., He, C., Sun, L., Jiang, Y. and Zhu, L. (2014) MicroRNA-424 is down-regulated in hepatocellular carcinoma and suppresses cell migration and invasion through c-Myb. PLoS One 9, e91661.

[24] Li, Z. et al. (2015) DNA methylation downregulated mir-10b acts as a tumor suppressor in gastric cancer. Gastric Cancer 18, 43–54.

[25] Li, Z., Yu, X., Wang, Y., Shen, J., Wu, W.K., Liang, J. and Feng, F. (2014) By downregulating TIAM1 expression, microRNA-329 suppresses gastric cancer invasion and growth. Oncotarget.

[26] Li, Z., Yu, X., Shen, J., Wu, W.K. and Chan, M.T. (2015) MicroRNA expression and its clinical implications in Ewing's sarcoma. Cell Prolif. 48, 1–6.

[27] Zhao, Y., Li, Y., Lou, G., Zhao, L., Xu, Z., Zhang, Y. and He, F. (2012) MiR-137 targets estrogen-related receptor alpha and impairs the proliferative and migratory capacity of breast cancer cells. PLoS One 7, e39102.

[28] Yan, K., Gao, J., Yang, T., Ma, Q., Qiu, X., Fan, Q. and Ma, B. (2012) MicroRNA-34a inhibits the proliferation and metastasis of osteosarcoma cells both in vitro and in vivo. PLoS One 7, e33778.

[29] Luo, J. et al. (2012) A microRNA-7 binding site polymorphism in HOXB5 leads to differential gene expression in bladder cancer. PLoS One 7, e40127.

[30] Chang, K.H., Mestdagh, P., Vandesompele, J., Kerin, M.J. and Miller, N. (2010) MicroRNA expression profiling to identify and validate reference genes for relative quantification in colorectal cancer. BMC Cancer 10, 173.

[31] Zhu, D. et al. (2014) Expression of microRNA-454 in TGF-beta1-stimulated hepatic stellate cells and in mouse livers infected with Schistosoma japonicum. Parasit. Vectors 7, 148.

[32] Bier, A. et al. (2013) MicroRNA-137 is downregulated in glioblastoma and inhibits the stemness of glioma stem cells by targeting RTVP-1. Oncotarget 4, 665–676.

[33] Lee, H.K. et al. (2013) Mesenchymal stem cells deliver synthetic microRNA mimics to glioma cells and glioma stem cells and inhibit their cell migration and self-renewal. Oncotarget 4, 346–361.

[34] Hidaka, H. et al. (2012) Tumor suppressive microRNA-1285 regulates novel molecular targets: aberrant expression and functional significance in renal cell carcinoma. Oncotarget 3, 44–57.

[35] Fei, B. and Wu, H. (2013) MiR-378 inhibits progression of human gastric cancer MGC-803 cells by targeting MAPK1 in vitro. Oncol. Res. 20, 557–564.

[36] Zhou, J., Song, S., Cen, J., Zhu, D., Li, D. and Zhang, Z. (2012) MicroRNA-375 is downregulated in pancreatic cancer and inhibits cell proliferation in vitro. Oncol. Res. 20, 197–203.

[37] Wang, K. et al. (2013) Analysis of hsa-miR-30a-5p expression in human gliomas. Pathol. Oncol. Res. 19, 405–411.

[38] Xiao, X., Tang, C., Xiao, S., Fu, C. and Yu, P. (2013) Enhancement of proliferation and invasion by MicroRNA-590-5p via targeting PBRM1 in clear cell renal carcinoma cells. Oncol. Res. 20, 537–544.

[39] Liang, J., Zhang, Y., Jiang, G., Liu, Z., Xiang, W., Chen, X., Chen, Z. and Zhao, J. (2013) MiR-138 induces renal carcinoma cell senescence by targeting EZH2 and is downregulated in human clear cell renal cell carcinoma. Oncol. Res. 21, 83–91.

[40] Sun, L., Bian, G., Meng, Z., Dang, G., Shi, D. and Mi, S. (2015) MiR-144 inhibits uveal melanoma cell proliferation and invasion by regulating c-Met expression. PLoS One 10, e0124428.

[41] Li, D., Xie, X., Wang, J., Bian, Y., Li, Q., Gao, X. and Wang, C. (2015) MiR-486 regulates lactation and targets the PTEN gene in cow mammary glands. PLoS One 10, e0118284.

[42] Roy, S., Yu, Y., Padhye, S.B., Sarkar, F.H. and Majumdar, A.P. (2013) Difluorinated-curcumin (CDF) restores PTEN expression in colon cancer cells by down-regulating miR-21. PLoS One 8, e68543.

[43] Zhang, B.G., Li, J.F., Yu, B.Q., Zhu, Z.G., Liu, B.Y. and Yan, M. (2012) MicroRNA-21 promotes tumor proliferation and invasion in gastric cancer by targeting PTEN. Oncol. Rep. 27, 1019–1026.

[44] Shen, L., Chen, X.D. and Zhang, Y.H. (2014) MicroRNA-128 promotes proliferation in osteosarcoma cells by downregulating PTEN. Tumour Biol. 35, 2069–2074.

[45] Zhang, L.Y. et al. (2013) MicroRNA-144 promotes cell proliferation, migration and invasion in nasopharyngeal carcinoma through repression of PTEN. Carcinogenesis 34, 454–463.

[46] Wu, Z., He, B., He, J. and Mao, X. (2013) Upregulation of miR-153 promotes cell proliferation via downregulation of the PTEN tumor suppressor gene in human prostate cancer. Prostate 73, 596–604.

[47] Abdel-Rahman, M.H., Yang, Y., Zhou, X.P., Craig, E.L., Davidorf, F.H. and Eng, C. (2006) High frequency of submicroscopic hemizygous deletion is a major mechanism of loss of expression of PTEN in uveal melanoma. J. Clin. Oncol. 24, 288–295.

[48] Naus, N.C., Zuidervaart, W., Rayman, N., Slater, R., van Drunen, E., Ksander, B., Luyten, G.P. and Klein, A. (2000) Mutation analysis of the PTEN gene in uveal melanoma cell lines. Int. J. Cancer 87, 151–153.