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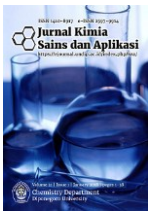

The Effect of miR-10b Mimic Transfection on Invasion and Proliferation Gene Expression as the Direct Target of the miR-10b Pathway in T47D Breast Cancer Cell Lines

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Abstract

Breast cancer remains one of the leading causes of death in women worldwide, with high incidence and mortality rates. The abnormal expression of the small non-coding RNA, microRNA-10b (miR-10b), has been associated with breast cancer progression. miR-10b is involved in various biological processes, including proliferation, metastasis, and drug resistance. However, the underlying mechanism by which miR-10b contributes to breast cancer progression remains unclear. This study aimed to investigate the effect of miR-10b on the expression of HOXD10 and PI3K genes, as well as its impact on cell viability and proliferation in breast cancer cells. In this study, T47D breast cancer cells were transfected with mimic miR-10b using the FANA-oligo transfection method at concentrations of 1, 2.5, and 5 µM. Cell viability was assessed using the MTT assay, while HOXD10 and PI3K gene and protein expression levels were measured using RT-qPCR and ELISA. Data were analysed using ANOVA with SPSS, and results were considered statistically significant at $p < 0.05$. The results showed that mimic miR-10b induced a dose-dependent increase in cell proliferation. Notably, only HOXD10 gene and protein expression were significantly affected by the transfection, whereas PI3K expression remained unchanged. Cells transfected with 5 µM miR-10b mimic exhibited the highest proliferation rate compared to non-transfected controls ($p < 0.05$). In conclusion, miR-10b promotes breast cancer cell proliferation by downregulating HOXD10 expression, independent of PI3K, suggesting it is a potential target for further investigation.

1. Introduction

Breast cancer remains the most common malignancy among women worldwide and is one of the leading causes of cancer-related death [1, 2]. In developing countries such as Indonesia, the incidence and mortality of breast cancer have increased significantly over recent decades [3]. While improved living standards and early detection have contributed to higher diagnosis rates in developed nations, the persistently high mortality in developing regions underscores the importance of advancing our understanding of the molecular mechanisms underlying breast cancer. Such molecular insights are essential for improving disease diagnosis, prognosis, and treatment outcomes [3, 4].

Over the past decade, significant advances have been made in understanding gene regulation in normal and malignant cells. Messenger RNA (mRNA) serves as an essential intermediate that conveys genetic information for protein synthesis [5, 6]. In addition to mRNA, cells also produce thousands of non-coding RNAs that do not

encode proteins but exert regulatory functions [5, 6, 7, 8]. Among these, microRNAs (miRNAs), small ~22-nucleotide RNAs, play crucial roles in post-transcriptional regulation by binding to complementary sequences in target mRNAs, leading to mRNA degradation or translational inhibition [5, 9]. Although only a subset of miRNAs has well-defined biological functions, they are known to regulate key cellular processes such as differentiation, apoptosis, and adhesion [7, 10, 11]. Consequently, dysregulation of miRNAs has been implicated in tumor initiation, progression, metastasis, and other cancer-related features [6, 12]. Thus, miRNA biomarkers can be used for early disease diagnosis and for intervention during disease progression, as changes in mRNA levels are often associated with alterations in gene expression.

One of the miRNAs most consistently associated with breast cancer metastasis is miR-10b, which is identified as a critical regulator of tumor invasion and progression in several cancers [13, 14, 15]. Bioinformatics analyses have revealed that miR-10b has complementary binding sites in the 3' untranslated regions (3' UTRs) of Homeobox D10 (HOXD10) and Phosphatidylinositol-3 kinase (PI3K) genes (www.miRBase.org), both of which are linked to cancer proliferation and invasion [15].

PI3K is a plasma membrane-bound enzyme activated by tyrosine kinase receptors (TKRs) or G protein-coupled receptors (GPCRs) [7, 16]. They are involved in various cellular processes, including development, proliferation, differentiation, motility, survival, and intracellular trafficking, all of which are associated with cancer progression [16, 17, 18]. Hyperactivation of the PI3K/Akt pathway has been shown in several studies to promote cell proliferation and confer resistance to chemotherapy and HER2-targeted therapies [19, 20]. In breast cancer, HER2-driven activation of PI3K has been reported to increase AKT levels, highlighting the involvement of the PI3K/Akt/mTOR (mammalian target of rapamycin) signaling axis [7, 15].

One gene of particular interest in breast cancer development is HOXD10, whose expression and dysregulation have been associated with tumor growth and malignant progression [21, 22, 23]. In breast cancer, HOXD10 has been identified as a tumor suppressor gene and is a critical target of miR-10b [22]. Loss of HOXD10 expression can trigger phenotypic changes that drive invasive behavior in breast cancer cells [24]. Importantly, previous studies have demonstrated that downregulation of HOXD10 leads to activation of the RhoC/PI3K/Akt signaling pathway, linking HOXD10 suppression to enhanced cancer cell motility and invasiveness [22, 25].

To better understand the molecular mechanism of miR-10b in breast cancer, we examined its regulatory effect on HOXD10 and PI3K in T47D breast cancer cells, a luminal A subtype. In this study, cells were transfected with miR-10b mimic, a synthetic RNA duplex that increases the intracellular abundance of miR-10b and thereby simulates its overexpression. The resulting changes in HOXD10 and PI3K gene and protein expression were evaluated to elucidate the potential role of miR-10b in regulating invasion and proliferation pathways in T47D breast cancer cells.

2. Experimental

2.1. Cell Culture

T47D breast cancer cells were cultured in DMEM supplemented with 10% FBS and 1% penicillin-streptomycin at 37°C in a 5% CO_2 atmosphere. The growth medium was changed every two days until the cells reached 70-85% confluency. Cells were harvested using a 0.1% trypsin/EDTA solution and sub-cultured twice a week.

2.2. miR-10b FANA-oligo Mimic Transfection on T47D Breast Cancer Cells

T47D cells (20,000 cells per well) were seeded in a 96-well microplate. After 24 hours, the medium was removed, and cells were exposed to modified FANA-oligo miR-10b mimics at different concentrations (1, 2.5, and 5 µM). Cells were then incubated for an additional 72 hours. Untreated mimic miR-10b FANA-oligonucleotides were used as a control (C-) to represent baseline cell viability (100%). This approach was chosen to evaluate the direct biological effect of miR-10b overexpression compared with normal cellular conditions.

2.3. MTT Assay (Cell Viability Assay)

Cell viability was assessed using the MTT [3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide] assay. Cells seeded at a density of 6×10^5 were incubated with MTT reagent for 2 hours at 37°C in the dark. After incubation, the formazan crystals formed by metabolically active cells were dissolved in DMSO and incubated for an additional 15 minutes at room temperature. Absorbance was measured at 490 nm using an xMark™ Microplate Spectrophotometer (Bio-Rad, USA). Cell viability (%) was calculated relative to the negative control group using Equation (1).

$$Cell\ viability\ (\%) = \frac{A_{treated} - A_{medium}}{A_{solvent} - A_{medium}} \times 100\% \quad (1)$$

Where, A_{treated} is the absorbance of cells treated with the test sample, A_{solvent} is the absorbance of cells treated with the solvent (negative control), and A_{medium} is the absorbance of the medium without cells (blank). Cell viability is expressed as a percentage relative to the solvent control, which is set at 100% viability.

2.4. RNA Extraction and cDNA Synthesis

RNA was extracted using the PureLink RNA Mini Kit (Ambion, USA), following the manufacturer's protocol. Briefly, cells were lysed using Trizol reagent (Invitrogen, Carlsbad, CA), and chloroform was added. The aqueous phase was transferred to a sterile 1.5 ml tube, and RNA was precipitated with 2-propanol. The RNA pellet was washed with 75% ethanol and dissolved in nuclease-free water. RNA concentration was quantified using a NanoDrop spectrophotometer (Thermo, USA).

For cDNA synthesis, 5 µg of total RNA was mixed with 1× RT buffer, 20 pmol oligo(dT), 4 mM dNTPs, 10 mM DTT, and 40 U of SuperScript™ II reverse transcriptase in a final volume of 20 µl using DEPC-treated water. The

reaction was performed at 52°C for 50 minutes according to the manufacturer's protocol (iScript cDNA Synthesis Kit, Bio-Rad). The final cDNA concentration was also measured using NanoDrop.

2.5. Amplification of Targeted Genes by RT-PCR

Quantitative real-time PCR (RT-qPCR) was performed to determine the relative mRNA expression levels of HOXD10, PI3K, and the housekeeping gene GAPDH, using cDNA synthesized. Primers were designed using Primer-BLAST (NCBI) from human reference sequences in GenBank and synthesized by Integrated DNA Technologies (IDT, Singapore). The primer sequences were as follows:

HOXD10: Forward 5'-AGCTGCCTGACTTCTACAGC-3',

Reverse 5'-TCTGCCTGTAGCTTCTGCTG-3'

PI3K: Forward 5'-GGTTGGTGCTGGGAATTTGT-3',

Reverse 5'-CTTGGCTGGAGTGGATGTTG-3'

GAPDH: Forward 5'-AGAAGGCTGGGGCTCATTTG-3',

Reverse 5'-AGGGGCCATCCACAGTCTTC-3'

Target genes were amplified using the SYBR Green PCR master mix (Bio-Rad). PCR cycling conditions were as follows: pre-denaturation at 95°C for 3 minutes, denaturation at 95°C for 5 seconds, annealing at 50-60°C (gradient) for 5 seconds, repeated for 39 cycles. Melt curve analysis was performed to confirm amplification specificity. Relative gene expression levels were calculated using the $2^{-\Delta\Delta Ct}$ method, with GAPDH serving as the reference gene.

2.6. Statistical Analysis

Statistical analysis was performed using one-way ANOVA to assess the differences among groups treated with various concentrations of mimic miR-10b. Post hoc analysis was conducted using Tukey's test to determine pairwise significance. All data were expressed as mean ± SD, and $p < 0.05$ was considered statistically significant.

2.7. Protein Expression Quantification

The protein expression levels of HOXD10 and PI3K in T47D cells were quantified using a human-specific sandwich Enzyme-Linked Immunosorbent Assay (ELISA) method, following the standard manufacturer's protocol. HOXD10 levels were measured using the Human Homeobox Protein HOXD10 ELISA Kit (Code: E4772), and PI3K levels were measured using the Human Phosphatidylinositol 3-Kinase (PI3K) ELISA Kit (Code: E0896Hu).

After treatment, cells were washed twice with ice-cold phosphate-buffered saline (PBS) and lysed in RIPA buffer supplemented with a protease inhibitor cocktail. Lysates were centrifuged at 12,000 × g for 15 minutes at 4°C, and the supernatants were collected for analysis. Standards and samples were added to pre-coated 96-well plates and incubated according to the manufacturer's instructions. Following incubation, the wells were washed, and horseradish peroxidase (HRP)-conjugated detection antibodies were added. After adding the substrate solution, the enzymatic reaction was terminated, and absorbance was measured at 450 nm using an ELISA plate reader (xMark™ Microplate Spectrophotometer, Bio-Rad, USA). Protein concentrations were calculated from standard curves and normalized to total protein content.

3. Results and Discussion

3.1. Cell Viability

miR-10b has been recognized as an important regulator of tumor cell proliferation and invasion [26, 27, 28, 29]. To evaluate whether miR-10b overexpression influences breast cancer cell survival, cell viability was assessed using the MTT assay after transfection with miR-10b mimics at varying concentrations. As shown in Figure 1, cell viability increased progressively from the control group (C-, 0 µM) to the highest mimic concentration (5 µM). The control cells exhibited 100% viability, indicating that all cells remained metabolically active under untreated conditions. Cells exposed to 1 µM and 2.5 µM of miR-10b mimic displayed higher metabolic activity, with the maximum viability observed at 5 µM.

Consistent with its proposed oncogenic role, our study demonstrated that transfection of T47D breast cancer cells with a miR-10b mimic led to increased cell viability, suggesting that elevated miR-10b expression supports breast cancer cell growth. This finding is also similar to the reported study by Tian *et al.* [30], who observed that miR-10b upregulation in early-stage hepatocellular carcinoma promotes cell proliferation and metastasis, and is supported by others [30, 31, 32, 33].

3.2. Gene and Protein Expression Analysis

The expression of miR-10b has also been linked to developmental genes such as HOXD10 and PI3K [7, 15, 20, 23]. miR-10b acts by binding to the 3' untranslated region (3'UTR) of target mRNAs and inhibiting translation. Based on data from miRBase.org, miR-10b has potential binding sequences within the HOXD10 and PI3K mRNAs. To evaluate the effect of miR-10b mimic transfection on both gene and protein expression, RT-qPCR and ELISA assays were performed for HOXD10 and PI3K in T47D cells treated with increasing concentrations of miR-10b mimic (1, 2.5, and 5 µM). Untreated cells (0 µM) served as the negative control group (C-) representing baseline expression levels.

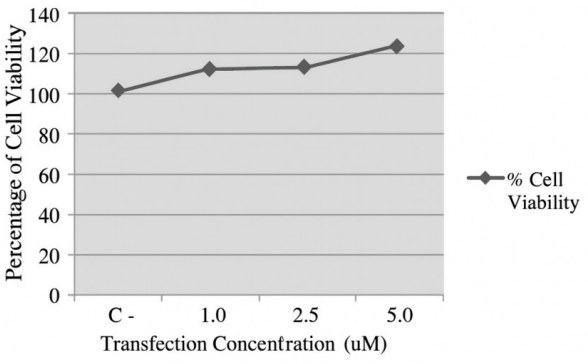

Figure 1. Effect of miR-10b mimic transfection on T47D breast cancer cell viability

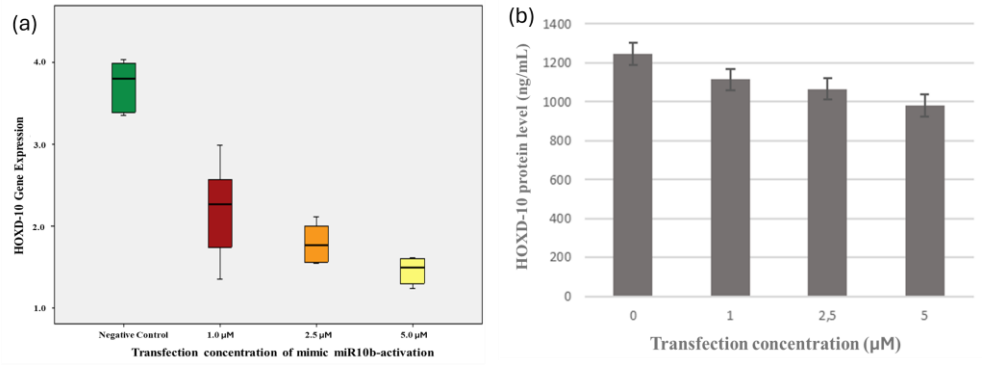

Figure 2. Effect of miR-10b mimic transfection on HOXD10 expression in T47D breast cancer cells. (A) Relative HOXD10 mRNA expression measured by RT-qPCR, and (B) HOXD10 protein concentration measured by ELISA, after transfection with miR-10b mimic at 0 µM (control), 1.0, 2.5, and 5.0 µM

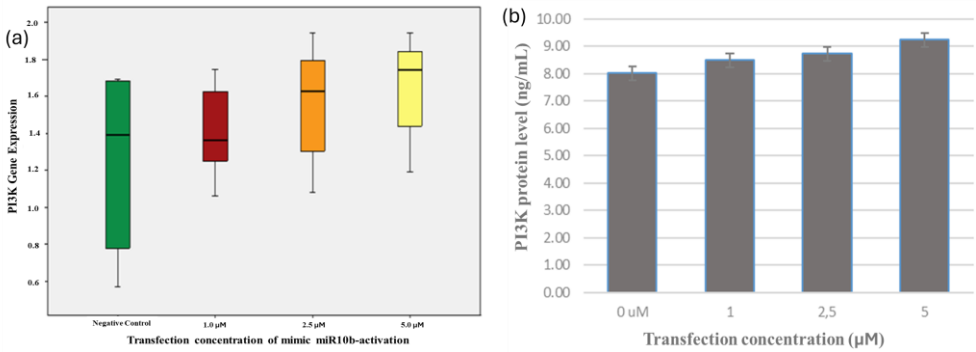

Figure 3. Effect of miR-10b mimic transfection on PI3K expression in T47D breast cancer. (A). Relative PI3K mRNA expression measured by RT-qPCR, and (B) PI3K protein concentration measured by ELISA, after transfection with miR-10b mimic at 0 µM (control), 1.0, 2.5, and 5.0 µM

3.2.1. HOXD10 Expression

The HOXD10 mRNA expression boxplot (Figure 2a) clearly shows that the control group exhibited the highest expression, with median values decreasing stepwise at 1 µM and 2.5 µM and reaching the lowest level at 5 µM. Statistical testing indicated that all mimic-treated groups were significantly reduced compared with the control ($p < 0.05$). This dose-dependent decrease demonstrates that miR-10b strongly suppresses HOXD10 gene expression, consistent with its known role in inhibiting tumor-suppressive pathways. Similarly, at the protein level, HOXD10 expression (Figure 2b) was highest in the control group and declined progressively with increasing mimic concentrations, confirming that miR-10b exerts inhibitory effects at both transcriptional and translational levels. Both mRNA and protein levels of HOXD10 were significantly decreased in a concentration-dependent manner, with the strongest suppression observed at 5 µM.

These results reinforce the post-transcriptional repressive function of miR-10b on HOXD10, which is consistent with previous reports indicating that miR-10b binds to the 3' untranslated region (3'UTR) of HOXD10 mRNA to block its translation and its tumor-suppressive activity [13, 23]. Reduced HOXD10 expression has been associated with enhanced proliferation, migration, and invasion in breast cancer cells [34], which aligns with the increased viability observed in our study. This supports the hypothesis that miR-10b promotes breast cancer progression through HOXD10 downregulation.

3.2.2. PI3K Expression

In contrast, PI3K mRNA expression displayed a different pattern. The boxplot (Figure 3a) showed a slight upward shift in median values across mimic-treated groups, with the highest level at 5 µM. However, these increases were modest, and statistical analysis confirmed that none of the differences reached significance ($p > 0.05$). Consistently, protein-level measurement (Figure 3b) showed a mild increase in PI3K concentration after transfection, although this difference was also modest. The parallel results between mRNA and protein levels indicate that miR-10b does not substantially alter PI3K expression under the tested conditions.

In contrast to HOXD10, the expression of PI3K did not show any significant change at either the mRNA or protein level after transfection with the miR-10b mimic. Although PI3K is frequently overexpressed or mutated in breast cancer [7, 25], our results suggest that it is not a direct downstream target of miR-10b in T47D cells. The slightly changed expression pattern indicates that miR-10b may influence PI3K signaling indirectly through other mediators. Previous studies have reported that miR-10b can modulate PI3K/AKT activation via intermediate molecules, such as FUT8 or the FOXO3a/TWIST-1/CADM2 axis [31, 32]. These observations collectively imply that miR-10b's effect on the PI3K pathway may be context-dependent rather than the result of direct binding to PI3K transcripts.

The differential responses of HOXD10 and PI3K to miR-10b mimic treatment might can be explained by

their distinct regulatory interactions. Previous sequence analyses have identified that the HOXD10 gene contains three potential miR-10b binding sites, whereas PI3K has a single predicted site [13, 16]. This difference in the number of binding sites may explain why HOXD10 expression was significantly reduced in our study, while PI3K expression remained largely unchanged. The presence of several complementary regions likely enhances the efficiency of miR-10b-mediated repression of HOXD10, whereas the limited complementarity in PI3K may lead to weaker or negligible interaction. While this study did not include sequence validation, these reports provide a plausible explanation for the observed expression patterns. These findings collectively suggest that miR-10b primarily regulates HOXD10 directly, while its influence on PI3K may occur indirectly through secondary signaling pathways [13].

4. Conclusion

This study demonstrates that miR-10b promotes breast cancer cell proliferation primarily by directly suppressing HOXD10, whereas its effect on the PI3K/AKT pathway is likely indirect. The inverse relationship between miR-10b and HOXD10 expression observed here reinforces the potential of this regulatory axis as a diagnostic and therapeutic target in breast cancer. Future work involving multiple cell models, additional pathway analyses, and in vivo validation will be valuable for confirming these mechanisms and further elucidating the downstream effects of miR-10b-mediated HOXD10 regulation.

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References

[1] Sergiusz Łukasiewicz, Marcin Czeczelewski, Alicja Forma, Jacek Baj, Robert Sitarz, Andrzej Stanisławek, Breast Cancer—Epidemiology, Risk Factors, Classification, Prognostic Markers, and Current Treatment Strategies—An Updated Review, *Cancers*, 13, 17, (2021), 4287 https://doi.org/10.3390/cancers13174287

[2] Melina Arnold, Eileen Morgan, Harriet Rumgay, Allini Mafra, Deependra Singh, Mathieu Laversanne, Jerome Vignat, Julie R. Gralow, Fatima Cardoso, Sabine Siesling, Isabelle Soerjomataram, Current and future burden of breast cancer: Global statistics for 2020 and 2040, *The Breast*, 66, (2022), 15-23 https://doi.org/10.1016/j.breast.2022.08.010

[3] Freddie Bray, Jacques Ferlay, Isabelle Soerjomataram, Rebecca L. Siegel, Lindsey A. Torre, Ahmedin Jemal, Global cancer statistics 2018: GLOBOCAN estimates of incidence and mortality worldwide for 36 cancers in 185 countries, *CA: A Cancer Journal for Clinicians*, 68, 6, (2018), 394-424 https://doi.org/10.3322/caac.21492

[4] Hannah Arem, Erikka Loftfield, Cancer Epidemiology: A Survey of Modifiable Risk Factors for Prevention and Survivorship, *American Journal of Lifestyle Medicine*, 12, 3, (2018), 200-210 https://doi.org/10.1177/1559827617700600

[5] Tina P. George, Suja Subramanian, M. H. Supriya, A brief review of noncoding RNA, *Egyptian Journal of Medical Human Genetics*, 25, 1, (2024), 98 https://doi.org/10.1186/s43042-024-00553-y

[6] Laura Poliseno, Martina Lanza, Pier Paolo Pandolfi, Coding, or non-coding, that is the question, *Cell Research*, 34, 9, (2024), 609-629 https://doi.org/10.1038/s41422-024-00975-8

[7] Daniela Miricescu, Alexandra Totan, Iulia-Ioana Stanescu-Spinu, Silviu Constantin Badoiu, Constantin Stefani, Maria Greabu, PI3K/AKT/mTOR Signaling Pathway in Breast Cancer: From Molecular Landscape to Clinical Aspects, *International Journal of Molecular Sciences*, 22, 1, (2021), 173 https://doi.org/10.3390/ijms22010173

[8] Eleni Anastasiadou, Leni S. Jacob, Frank J. Slack, Non-coding RNA networks in cancer, *Nature Reviews Cancer*, 18, 1, (2018), 5-18 https://doi.org/10.1038/nrc.2017.99

[9] Jacob O'Brien, Heyam Hayder, Yara Zayed, Chun Peng, Overview of MicroRNA Biogenesis, Mechanisms of Actions, and Circulation, *Frontiers in Endocrinology*, 9, (2018), https://doi.org/10.3389/fendo.2018.00402

[10] Wengong Si, Jiaying Shen, Huilin Zheng, Weimin Fan, The role and mechanisms of action of microRNAs in cancer drug resistance, *Clinical Epigenetics*, 11, 1, (2019), 25 https://doi.org/10.1186/s13148-018-0587-8

[11] Sadegh Babashah, Masoud Soleimani, The oncogenic and tumour suppressive roles of microRNAs in cancer and apoptosis, *European Journal of Cancer*, 47, 8, (2011), 1127-1137 https://doi.org/10.1016/j.ejca.2011.02.008

[12] Yong Peng, Carlo M. Croce, The role of MicroRNAs in human cancer, *Signal Transduction and Targeted Therapy*, 1, 1, (2016), 15004 https://doi.org/10.1038/sigtrans.2015.4

[13] Li Ma, Jennifer Young, Harsha Prabhala, Elizabeth Pan, Pieter Mestdagh, Daniel Muth, Julie Teruya-Feldstein, Ferenc Reinhardt, Tamer T. Onder, Scott Valastyan, Frank Westermann, Frank Speleman, Jo Vandesompele, Robert A. Weinberg, miR-9, a MYC/MYCN-activated microRNA, regulates E-cadherin and cancer metastasis, *Nature Cell Biology*, 12, 3, (2010), 247-256 https://doi.org/10.1038/ncb2024

[14] Francesca Biagioni, Noa Bossel Ben-Moshe, Giulia Fontemaggi, Yosef Yarden, Eytan Domany, Giovanni Blandino, The locus of microRNA-10b, *Cell Cycle*, 12, 15, (2013), 2371-2375 https://doi.org/10.4161/cc.25380

[15] Patrick Sheedy, Zdravka Medarova, The fundamental role of miR-10b in metastatic cancer, *American Journal of Cancer Research*, 8, 9, (2018), 1674

[16] Pixu Liu, Hailing Cheng, Thomas M. Roberts, Jean J. Zhao, Targeting the phosphoinositide 3-kinase pathway in cancer, *Nature Reviews Drug Discovery*, 8, 8, (2009), 627-644 https://doi.org/10.1038/nrd2926

[17] Jeffrey A. Engelman, Ji Luo, Lewis C. Cantley, The evolution of phosphatidylinositol 3-kinases as regulators of growth and metabolism, *Nature Reviews Genetics*, 7, 8, (2006), 606-619 https://doi.org/10.1038/nrg1879

[18] Tiziana Pecchillo Cimmino, Ester Pagano, Mariano Stornaiuolo, Gabriella Esposito, Rosario Ammendola, Fabio Cattaneo, Formyl-peptide receptor 2 signalling triggers aerobic metabolism of glucose through Nox2-dependent modulation of pyruvate dehydrogenase activity, *Open Biology*, 13, 10, (2023), https://doi.org/10.1098/rsob.230336

[19] Ingrid A. Mayer, Clinical Implications of Mutations in the PI3K Pathway in HER2+ Breast Cancer: Prognostic or Predictive?, *Current Breast Cancer Reports*, 7, 4, (2015), 210-214 https://doi.org/10.1007/s12609-015-0197-9

[20] Sherry X. Yang, Eric Polley, Stanley Lipkowitz, New insights on PI3K/AKT pathway alterations and clinical outcomes in breast cancer, *Cancer Treatment Reviews*, 45, (2016), 87-96 https://doi.org/10.1016/j.ctrv.2016.03.004

[21] Hemapreethi Surendran, Thirunavukkarasu Palaniyandi, Sudhakar Natarajan, Rajeswary Hari, Sandhiya Viwanathan, Gomathy Baskar, Mugip Rahaman Abdul Wahab, Maddaly Ravi, Barani Kumar Rajendran, Role of homeobox d10 gene targeted signaling pathways in cancers, *Pathology - Research and Practice*, 248, (2023), 154643 https://doi.org/10.1016/j.prp.2023.154643

[22] Haixia Yang, Jiupeng Zhou, Jianqiang Mi, Ke Ma, Yangwei Fan, Jing Ning, Chuying Wang, Xin Wei, Huadong Zhao, Enxiao Li, HOXD10 acts as a tumor-suppressive factor via inhibition of the RHOC/AKT/MAPK pathway in human cholangiocellular carcinoma, *Oncology Reports*, 34, 4, (2015), 1681-1691 https://doi.org/10.3892/or.2015.4194

[23] N. V. Vardhini, P. Jagan Mohan Rao, P. Balakrishna Murthy, G. Sudhakar, HOXD10 expression in human breast cancer, *Tumor Biology*, 35, 11, (2014), 10855-10860 https://doi.org/10.1007/s13277-014-2324-z

[24] Meritxell Carrio, Gemma Arderiu, Connie Myers, Nancy J. Boudreau, Homeobox D10 Induces Phenotypic Reversion of Breast Tumor Cells in a Three-Dimensional Culture Model, *Cancer Research*, 65, 16, (2005), 7177-7185 https://doi.org/10.1158/0008-5472.CAN-04-1717

[25] Dessy Arisanty, Wirsma Arif Harahap, Daan Khambri, Rony Rustam, Gestina Aliska, Affifatul Achyar, Juane Plantika Menra, The comparison of *RhoC* and *PI3K* gene expression on the breast cancer tissue and benign tumour tissue, *Open Access Macedonian Journal of Medical Sciences*, 7, 12, (2019), 1911

[26] Yi Shen, Xiaolei Dai, Haibo Chen, Shuwei Zhai, Qiliang Peng, Shang Cai, Yaqun Zhu, Jian Huan, Yuntian Shen, Comprehensive evaluation of microRNA-10b in digestive system cancers reveals prognostic implication and signaling pathways associated with tumor progression, *Journal of Cancer*, 12, 13, (2021), 4011-4024 https://doi.org/10.7150/jca.51303

[27] Ting Yan, Xiaping Wang, Guohua Wei, Hai Li, Leiyu Hao, Yan Liu, Xinqian Yu, Wei Zhu, Ping Liu, Yichao Zhu, Xin Zhou, Exosomal miR-10b-5p mediates cell communication of gastric cancer cells and fibroblasts and facilitates cell proliferation, *Journal of Cancer*, 12, 7, (2021), 2140-2150 https://doi.org/10.7150/jca.47817

[28] Rongxi Quan, Wei Liang, Hong Li, Qian Ning, Dong Shang, Silencing of miR-10b-5p alleviates the mechanical stretch-induced proliferation of HASMCs, *Tissue and Cell*, 74, (2022), 101700 https://doi.org/10.1016/j.tice.2021.101700

[29] Guangyao Dai, Xiaoguang Yao, Yubin Zhang, Jianbin Gu, Yunfeng Geng, Fei Xue, Jingcheng Zhang, Colorectal cancer cell–derived exosomes containing miR-10b regulate fibroblast cells via the PI3K/Akt pathway, *Bulletin du Cancer*, 105, 4, (2018), 336-349 https://doi.org/10.1016/j.bulcan.2017.12.009

[30] Jing Tian, Eric Du, Lan Guo, Mitochondrial Interaction with Serotonin in Neurobiology and Its Implication in Alzheimer's Disease, *Journal of Alzheimer's Disease Reports*, 7, 1, (2023), 1165-1177 https://doi.org/10.3233/adr-230070

[31] Dong Guo, Jia Guo, Xiang Li, Feng Guan, Enhanced motility and proliferation by miR-10b/FUT8/p-AKT axis in breast cancer cells, *Oncology Letters*, 16, 2, (2018), 2097-2104 https://doi.org/10.3892/ol.2018.8891

[32] Long Jin, Jun Zhang, Hui-Qun Fu, Xi Zhang, Yu-Liang Pan, FOXO3a inhibits the EMT and metastasis of breast cancer by regulating TWIST-1 mediated miR-10b/CADM2 axis, *Translational Oncology*, 14, 7, (2021), 101096 https://doi.org/10.1016/j.tranon.2021.101096

[33] Daoliang Wang, Zhuo Wang, Lijun Zhang, Shengrong Sun, LncRNA PDCD4-AS1 alleviates triple negative breast cancer by increasing expression of IQGAP2 via miR-10b-5p, *Translational Oncology*, 14, 1, (2021), 100958 https://doi.org/10.1016/j.tranon.2020.100958

[34] Ai-Ling Liang, Ting-Ting Zhang, Ning Zhou, Cui Yun Wu, Man-Hua Lin, Yong-Jun Liu, miRNA-10b sponge: An anti-breast cancer study in vitro, *Oncology Reports*, 35, 4, (2016), 1950-1958 https://doi.org/10.3892/or.2016.4596