https://doi.org/10.15407/exp-oncology.2023.04.421

V. Chekhun [1,*], T. Borikun [1], O. Mushii [1], T. Zadvornyi [1], O. Martyniuk [1], E. Kashuba [1], V. Bazas [1,3], S. Hrybach [4], M. Krotevych [2], S. Lyalkin [2], N. Lukianova [1]

[1] R.E. Kavetsky Institute of Experimental Pathology, Oncology and Radiobiology, NAS of Ukraine, Kyiv, Ukraine
[2] National Cancer Institute, Ministry of Health of Ukraine, Kyiv, Ukraine
[3] Kyiv City Clinical Oncology Center, Kyiv, Ukraine
[4] Kyiv Regional Oncology Dispensary, Kyiv, Ukraine

* Correspondence: Email: chekhun@onconet.kiev.ua

EXPRESSION PROFILE OF miR-145, -182, -21, -27a, -29b, and -34a IN BREAST CANCER PATIENTS OF YOUNG AGE

Background. Breast cancer (BC) in young women remains a significant public health concern. While progress has been made in understanding the etiology, diagnosis, and treatment of BC in this population, challenges persist. The identification and utilization of prognostic biomarkers offer valuable tools for tailoring treatment strategies and improving outcomes for BC patients. **Aim.** To evaluate the relationship between the expression of tumor-associated microRNAs and the clinical and pathological features of BC in young patients. **Materials and Methods.** The work is based on the results of the examination and treatment of 50 women younger than 45 years with stage I—II BC. miR-145, -182, -21, -27a, -29b, and -34a expression in tumor samples was analyzed by the real-time reverse transcription polymerase chain reaction. **Results.** Higher expression of miR-182, -21, and -29b and lower levels of miR-27a were associated with tumor stage in young BC patients. Patients without lymph node metastases (N0) had significantly higher levels of miR-182, -27a, and -34a and lower levels of miR-29b compared to N1 cases ($p < 0.05$). Expression of miR-145, -182, -21, -27a, and -29b was associated with molecular BC subtypes. **Conclusion.** Obtained results show that a high malignancy degree of BC in young women is associated with an increase in the miR-182, -21, -29b, and -34a expressions and a decrease in the miR-27a level in the tumor tissue, which indicates the prospects of the use of them for predicting the aggressiveness of the disease.

Keywords: breast cancer, young women, epidemiology, microRNA, prognosis.

Citation: Chekhun V, Borikun T, Mushii O, Zadvornyi T, Martyniuk O, Kashuba E, Bazas V, Hrybach S, Krotevych M, Lyalkin S, Lukianova N. Expression profile of miR-145, -182, -21, -27a, -29b, and -34a in breast cancer patients of young age. *Exp Oncol.* 2023; 45(4): 421-431. https://doi.org/10.15407/exp-oncology.2023.04.421

Breast cancer (BC) remains the most common cancer among women worldwide, accounting for approximately 25% of all female cancer cases. While it is more prevalent in older women, it can also occur in younger women, representing a significant public health concern. BC is the leading cause of cancer death among women under the age of 44 [1].

The incidence of BC in young women has been increasing in recent decades. This rise is likely attributed to a combination of factors, including changes in lifestyle, environmental exposures, and reproductive history [2]. For instance, the increasing prevalence of obesity, physical inactivity, and late-in-life childbearing have been linked to an elevated risk of BC in young women. Additionally, exposure to certain environmental toxins, such as pesticides and chemicals found in personal care products, has also been associated with an increased risk of BC [3].

The diagnosis of BC in young women can be challenging due to the higher likelihood of dense breasts, which can obscure tumors on mammograms. Moreover, young women are more prone to hormone receptor-positive BC, a subtype that presents treatment challenges [4].

With early detection and individualized treatment approaches, the prognosis for young women with BC is favorable. The 5-year survival rate for women under the age of 45 with BC exceeds 90% [5].

Prognostic biomarkers play a crucial role in guiding treatment decisions and predicting disease outcomes in young BC patients. Several prognostic biomarkers are currently employed in BC, including estrogen receptor (ER), progesterone receptor (PR), Ki-67, *BRCA* mutation status, lymphovascular invasion, tumor size, and tumor grade [6—8].

Researchers continue to investigate novel prognostic biomarkers that may provide further insights into disease progression and survival in young women with BC. These emerging biomarkers include microRNAs (miRNAs), both tumor-derived and exosomal [9]. The assessment of these prognostic biomarkers helps clinicians tailor treatment plans to the individual patient's risk profile, optimizing treatment efficacy and improving outcomes for young women with BC [10].

miRNAs have emerged as promising prognostic markers for BC in young women due to their unique properties and potential to provide valuable insights into tumor biology and patient outcomes. miRNAs are small, non-coding RNA molecules that regulate gene expression by binding to messenger RNA (mRNA) and promoting mRNA degradation or translational inhibition. Their dysregulation has been implicated in various malignancies, including BC [9, 11].

The use of miRNAs as prognostic markers in BC holds several advantages. miRNAs are relatively stable and can be easily detected in various biological fluids, including blood, plasma, and urine, making them non-invasive and readily accessible for clinical assessment. Additionally, miRNAs exhibit tissue-specific and cancer-specific expression patterns, offering the potential for early detection and discrimination between benign and malignant tumors [12].

Studies have demonstrated the association of specific miRNAs with clinical outcomes in BC. For instance, miRNA-21 and miRNA-155 are upregulated in BC tissues and associated with poor prognosis. In contrast, miRNA-126 and miRNA-34a are downregulated and associated with a more favorable prognosis [13, 14].

Despite the potential of miRNAs as prognostic markers, further research is needed to validate their clinical utility in large-scale prospective studies. Additionally, the development of standardized miRNA detection methods and the identification of miRNA targets and their functional roles in BC progression are crucial for translating miRNA-based prognostic information into effective clinical applications.

Up-to-date, miRNAs represent a promising avenue for prognostication in BC, particularly in

young women. Their unique properties and ability to provide insights into tumor biology hold promise for improving risk stratification, guiding treatment decisions, and monitoring treatment response.

Thus, ongoing development and validation of these emerging prognostic biomarkers hold promise for further improving risk stratification and treatment personalization for young women with BC. Therefore, our aim was to evaluate the relationship between the expression of a panel of tumor and circulating microRNAs and the clinicopathological features of BC patients in young women.

Materials and Methods

The study includes the results of the clinical examination and treatment of 50 female patients younger than 45 years hospitalized at the National Cancer Institute of the Ministry of Health of Ukraine, Kyiv City Clinical Oncology Center, and Kyiv Regional Oncology Dispensary during 2015—2019. The patients gave informed consent to using clinical data for scientific purposes. The

Table 1. **Clinical characteristics of BC cases**

Characteristics	Number of patients	
	n	%
Total number of patients	50	100
Average age, years (range)	37.5 ± 5.6 (28—45)	
Stage		
I	18	36.0
II	32	64.0
Category N by T NM		
N0	35	70.0
N1	15	30.0
Histological type		
Infiltrative ductal cancer	33	66.0
Infiltrative lobular cancer	17	34.0
Differentiation grade		
G1 (high)	5	10.0
G2 (moderate)	31	62.0
G3 (low)	14	28.0
Molecular subtype		
Luminal A	15	30.0
Luminal B	12	24.0
Basal	23	46.0

Table 2. **Monoclonal antibodies used**

Molecular marker	Clone	Dilution	Manufacturer
ER	1D5	1:50	DakoCytomation, Denmark
PR	PgR636	1:50	DakoCytomation, Denmark
Her2/ neu	e2-4001	1:50	Thermo Scientific, USA

Table 3. **Primer sequences used for assessing the expression of miRNAs**

miRNA	Stem-loop primer	Forward primer
miR-145-5p (miR-145)	5'-GTGTCCAGTTTTCCCAGGA-3'	5' - GTGAACCCGTAGATCCGAA - 3'
miR-182-5p (miR-182)	5'-GTTGTTTGGCAATGGTAGAACT-3'	5'-GTGTCCAGTTTTCCCAGGA-3'
miR-21-5p (miR-21)	5'-GTTTGGTAGCTTATCAGACTGA-3'	5' - GTTTCCCTGAGACCCTAAC - 3'
miR-27a-3p (miR-27a)	5'-GTGGTTCACAGTGGCTAAG-3'	5' - GTTTCCCTGAGACCCTAAC - 3'
miR-29b-3p (miR-29b)	5'-GTTGGTAGCACCATTTGAAATC-3'	5' - GTTTCCCTGAGACCCTAAC - 3'
mir-34a-5p (miR-34a)	5'-GTGTGGCAGTGTCTTAGCT-5'	5' - GTTTGGTAATACTGCCTGGTAA - 3'

stage of the tumor process was determined according to the international classification (TNM Classification of Malignant Tumours, 8th edition (2016)).

All patients underwent general clinical, biochemical, and laboratory examinations, ultrasound examination of abdominal organs, mammography, X-ray of chest organs, and puncture biopsy of breast tumors according to the standards of diagnosis and treatment of oncological patients approved by the orders of the Ministry of Health of Ukraine. The characteristics of the patients are presented in Table 1. Stage II BC dominated. The metastatic lesions in the regional lymph nodes were diagnosed in 30% of patients, while distant metastases were not identified during the complex examination of patients before surgical treatment.

Immunohistochemical studies. Histological sections (thickness 5—7 μm) of paraffin blocks of surgical material were used to assess the molecular subtype of BC. They were subjected to an immunohistochemical (IHC) study of the expression of ER, PR and epidermal growth factor type 2 (Her2/neu). IHC of the expression of the studied markers was carried out using an Ultra Vision LP Detection System (Thermo Scientific, USA) using monoclonal antibodies to determine the molecular subtypes of BC (Table 2). The sections were stained with Mayer's hematoxylin. The expression of molecular markers was evaluated by the H-Score method as described earlier [15].

Real-time RT-PCR. MicroRNA levels were estimated in 50 samples of BC tissue and 10 samples of normal adjacent breast tissue. Total RNA from paraffin blocks with tumor tissue and was isolated using the commercial RNeasy FFPE Kit (QIAGEN, Germany) by the manufacturer's protocol.

Quantitative PCR was performed on a QuantStudio 5 Dx Real-Time PCR System (Thermo Scientific, USA) with a commercial Luna Universal qPCR Master Mix (2X) (New England Biolabs, USA) by the manufacturer's protocol. A reverse transcription was performed using a High Capacity cDNA Reverse Transcription Kit (Thermo Scientific, USA). Relative expression of miRNAs was identified by the comparative Ct method as described earlier [16] and presented as fold change (dCT).

Sequences of primers were obtained by using the resource genomics.dote.hu:8080/mirnadesigntool (Table 3).

Bioinformatics research methods. Comparison of the expression levels of the studied genes in the tumor tissue of patients with BC and in non-malignant cells of the mammary gland was carried out using the resource of the University of Alabama at Birmingham CANcer data analysis portal — UALCAN (http://ualcan.path.uab.edu/index.html). UALCAN contains online information on gene expression levels, miRNAs, long non-coding RNAs, methylation promoter DNA from TCGA, et al. for 33 types of cancer [17].

Statistical analysis. Statistical analysis was performed using GraphPad Prism v. 8.00 software (GraphPad Software Inc., USA). All data were obtained in triplicates. The values were expressed as means ± standard deviation. Mann — Whitney test was used to evaluate the significance of the differences between the groups. A value of $p < 0.05$ was accepted as statistically significant.

Results and Discussion

The fundamental studies of the role of microRNAs in biological processes and their importance in the development of pathologies have allowed the formation of databases that contain information on the verified and experimentally confirmed target genes of most miRNAs, as well as the signaling pathways in which they are involved. In addition, there are many resources in which *in silico*, on the basis of already known data on the regulatory role of microRNAs, potential target mRNAs are predicted (www.mirdb.org, www.microrna.org, www.microrna.gr/tar-

base, www.targetscan.org/vert_72, DianaTools, etc.). There are also resources where experimentally confirmed data on the role of miRNA in tumor growth have been collected (http://www.mirbase.org, http://www.oncomir.org).

With the help of the above resources, we selected a panel of microRNAs, for which a connection with carcinogenesis in the mammary gland had been established, and their oncogenic (miR-182, -21, -27a) and tumor suppressor (miRNA -145, -29b, -34a) properties in BC had been proven.

We used the UALCAN database to evaluate the association of the mentioned miRNAs with the clinicopathological characteristics of BC (Figs. 1—6). Despite the limitations of this database, it is clear that the chosen miRNAs represent a promising diagnostic and prognostic set of BC biomarkers. As seen in Fig. 5, b and Fig. 6, b, the miR-29b and -34a levels in cancer tissue are age-dependent and lower in younger patients. Also, we found an association of miR-27a and -29b with lymph node metastasis (Fig. 4, *c*, Fig. 5, *c*).

According to the UALCAN data, expression of miR-182, -27a, and -34a can be used as a marker for differential diagnosis of the triple-negative BC (TNBC) molecular subtype. Although the data were obtained *in silico* and on very age-wide samples, our next step was to estimate levels of miR-145, -182, -21, -27a, -29b, and -34a in tumor tissue of young BC patients.

The results of the study of the tumor tissue of 50 young BC patients indicate that the development of BC is accompanied by significant changes in the ratio of oncogenic and oncosupressive microRNAs. Fig. 7 shows that the expression rates of miR-145 were 3.45 times lower while miR-182, -21, and -27a — 2.7, 4.2, and 5.5, respectively, times higher in BC samples compared to the adjacent normal tissue ($p < 0.05$).

We estimated the miRNA profile of BC samples depending on major clinicopathological parameters (Fig. 8). Expression levels of miR-182, -21, and -29b decreased by 3.81, 2.4, and 1.5 times, respectively, while miR-27a increased by 2.1 times when patients with stage II BC were compared to those with stage I. Higher levels of miR-182, -27a, and -34a (by 3.6, 3,0, and 3.5 times, respectively) and lower levels (by 1.3 times) of miR-29b were observed in patients without lymph node metastases, compared to N1 subjects ($p < 0.05$). The relationship between the levels of the studied microRNAs in the cancer tissue of young BC patients and the histological type of tumors, or tumor differentiation grade, has not been established.

Analysis of the expression of tumor miR145, -182, -21, -27a, -29b, and -34a depending on the molecular subtype of tumors revealed that in luminal A cases, expression of miR-182 was 2.1 times higher, and levels of miR-21 and-27a were 1.7 and 4.9 times lower than those in luminal B tumors. Receptor-negative BC was characterized by lower miR-145 (1.4-fold) and higher miR-29b (1.5-fold) expression compared to the luminal A molecular subtype and by lower expression of miR-27a (4.6-fold) compared to the luminal B cases. Both luminal subtypes demonstrated higher expression of miR-182 (by 3.6 and 1.9 times for luminal A and B subtypes, respectively) and miR-21 levels (by 1.3 and 2.2 times for luminal A and B subtypes, respectively).

The obtained results demonstrate that there are several coincidences between *in silico* and *ex vivo* data (association of mir-27a and -29b with lymph node status, miR-182 and -27a with basal molecular subtype), but also there are some discrepancies with the supposedly oncogenic and oncosuppressive role of the studied miRNAs. For example, in most studies, higher levels of miR-182, -21, and -27a and lower levels of miR-145, -29b, and -34a were associated with the advanced stage, presence of lymph node metastases, and negative hormonal receptor status of cancer cells [18].

However, in our study, miR-182, -21, -29b, and -34a levels were more likely associated

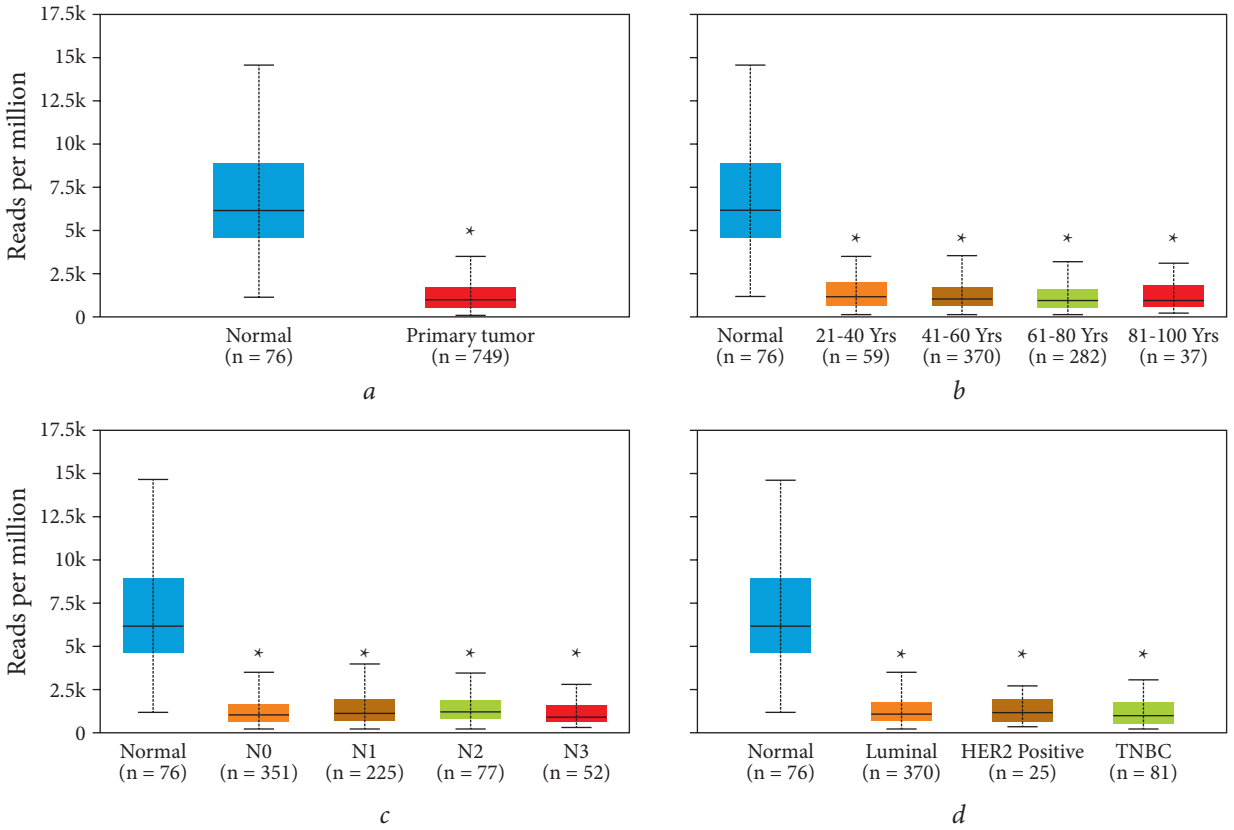

Fig. 1. Expression of miR-145 in normal and malignantly transformed breast tissue (*a*) and its relation to age (*b*), lymph node involvement (*c*), and molecular subtype (*d*) of BC according to UALCAN. * $p < 0.05$ compared to normal tissue

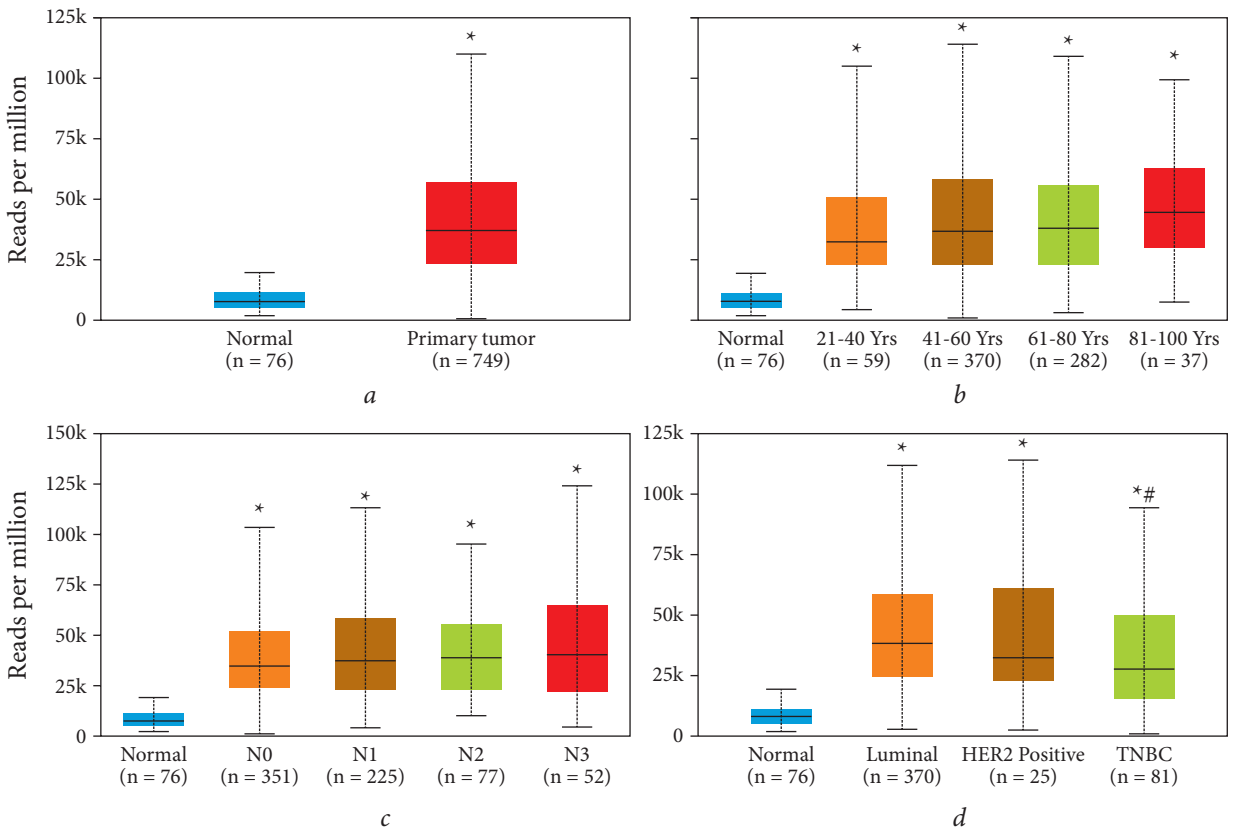

Fig. 1. Expression of miR-182 in normal and malignantly transformed breast tissue (*a*) and its relation to age (*b*), lymph node involvement (*c*), and molecular subtype (*d*) of BC according to UALCAN. * $p < 0.05$ compared to normal tissue, *# $p < 0.05$ compared to luminal BC

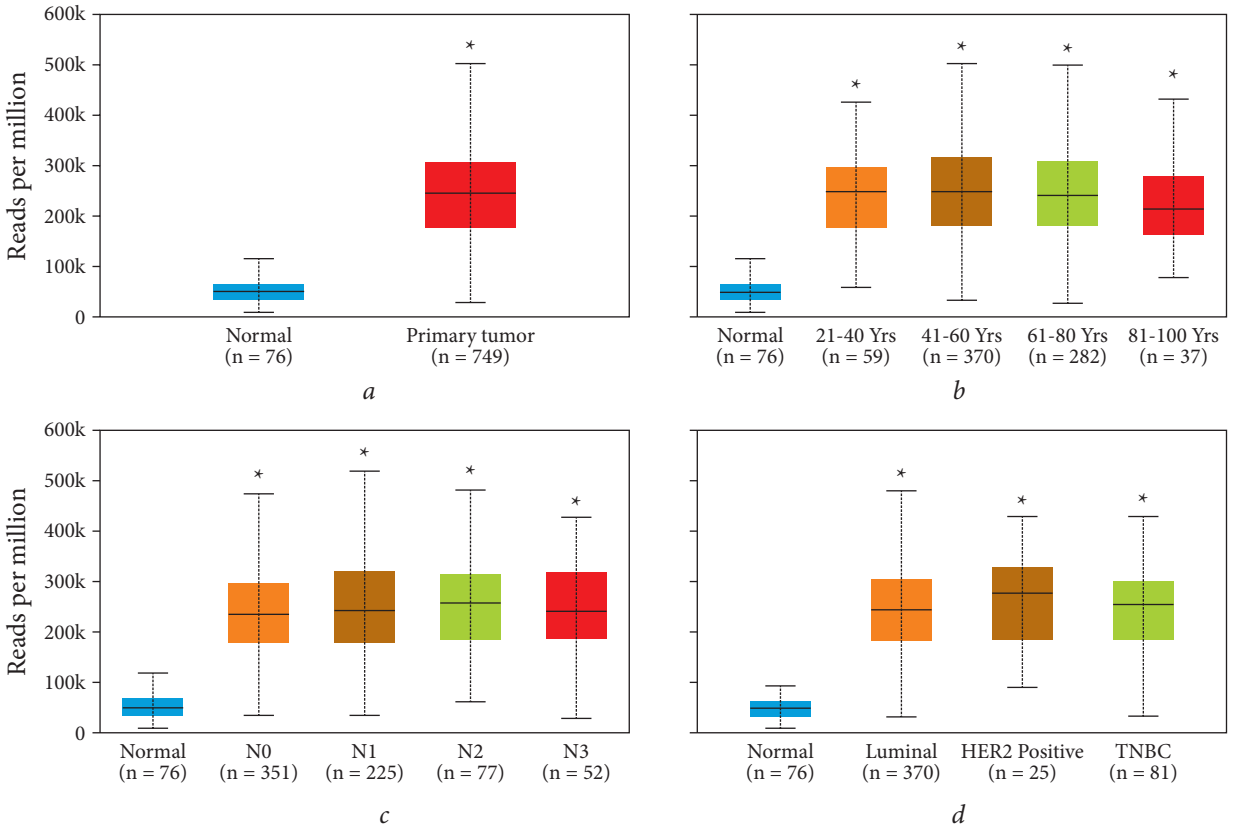

Fig. 3. Expression of miR-21 in normal and malignantly transformed breast tissue (*a*) and its relation to age (*b*), lymph node involvement (*c*), and molecular subtype (*d*) of BC according to UALCAN. * $p < 0.05$ compared to normal tissue

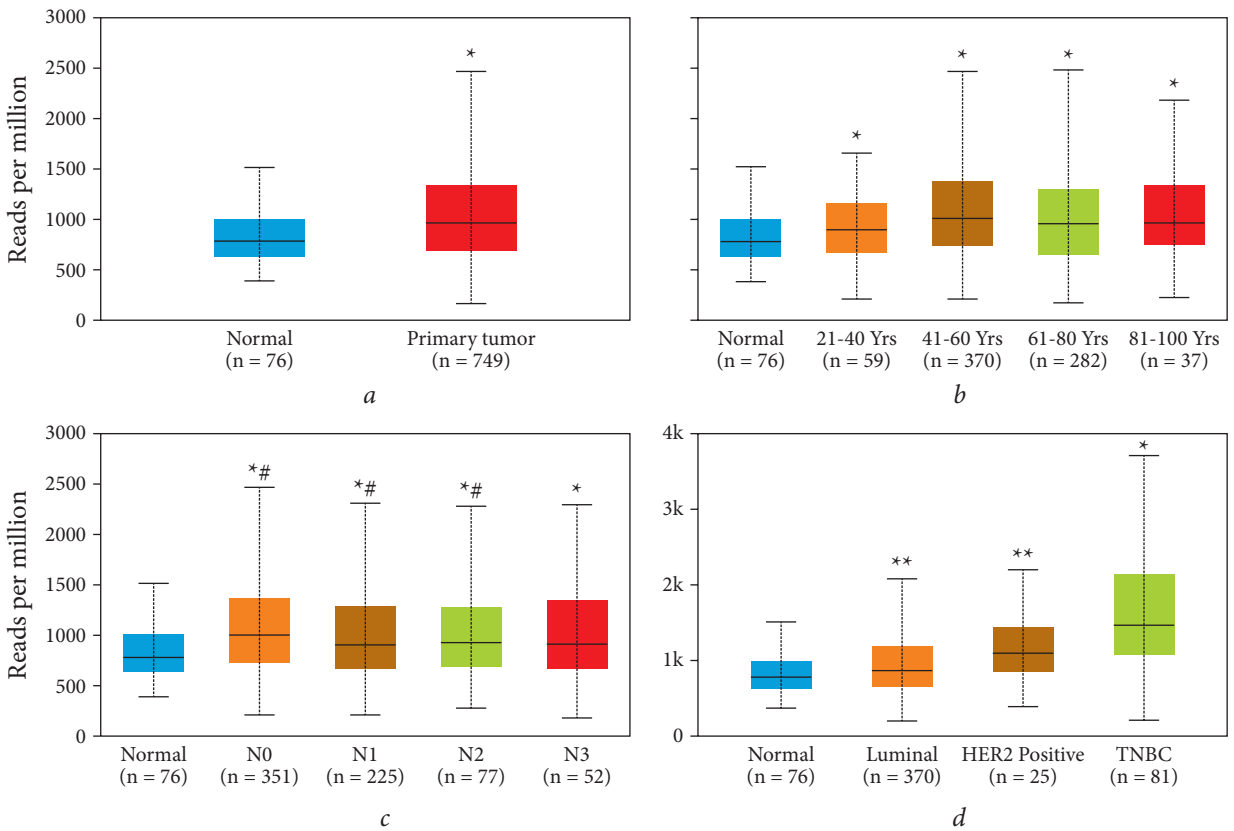

Fig. 4. Expression of miR-27a in normal and malignantly transformed breast tissue (*a*) and its relation to age (*b*), lymph node involvement (*c*), and molecular subtype (*d*) of BC according to UALCAN. * $p < 0.05$ compared to normal tissue, *# $p < 0.05$ compared to N3 BC, ** $p < 0.05$ compared to triple-negative BC

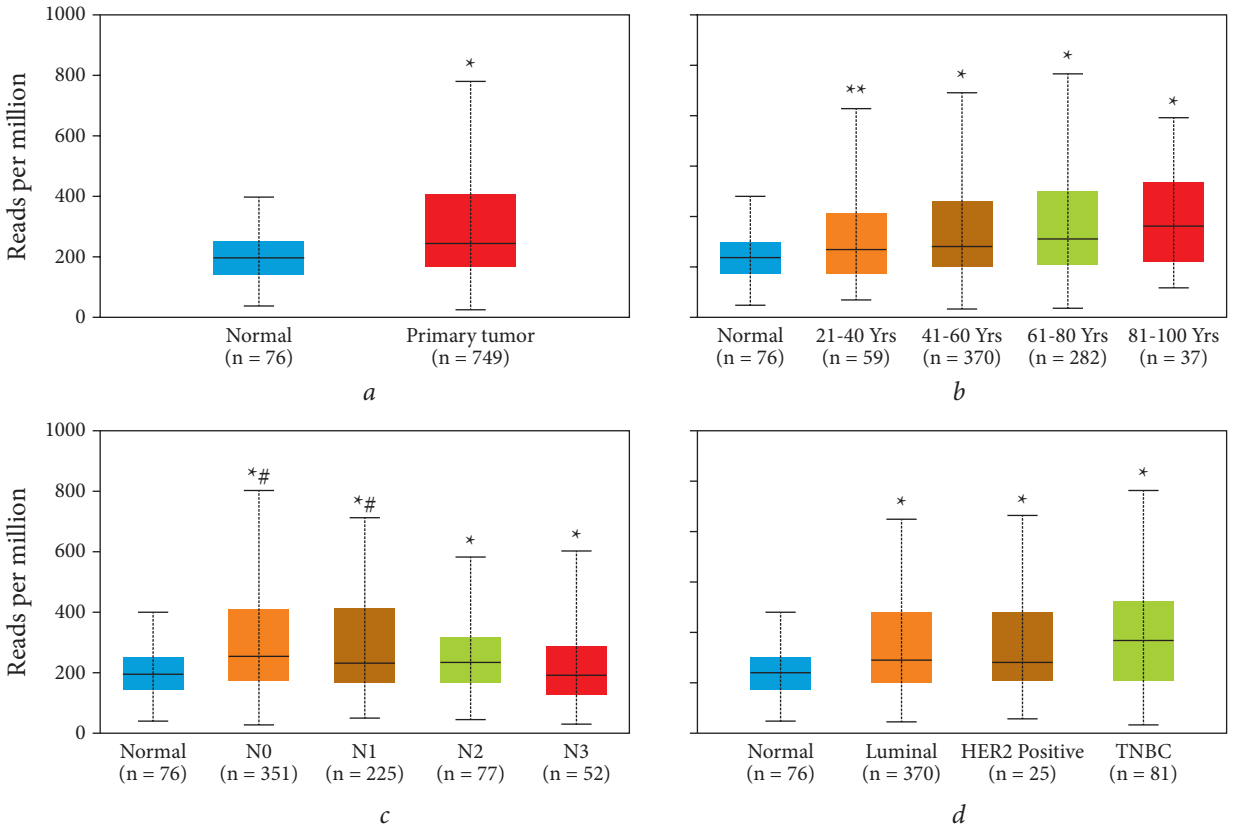

Fig. 5. Expression of miR-29b in normal and malignantly transformed breast tissue (*a*) and its relation to age (*b*), lymph node involvement (*c*), and molecular subtype (*d*) of BC according to UALCAN. * $p < 0.05$ compared to normal tissue, *# $p < 0.05$ compared to ge (81—100 Yrs), ** $p < 0.05$ compared to N3 BC

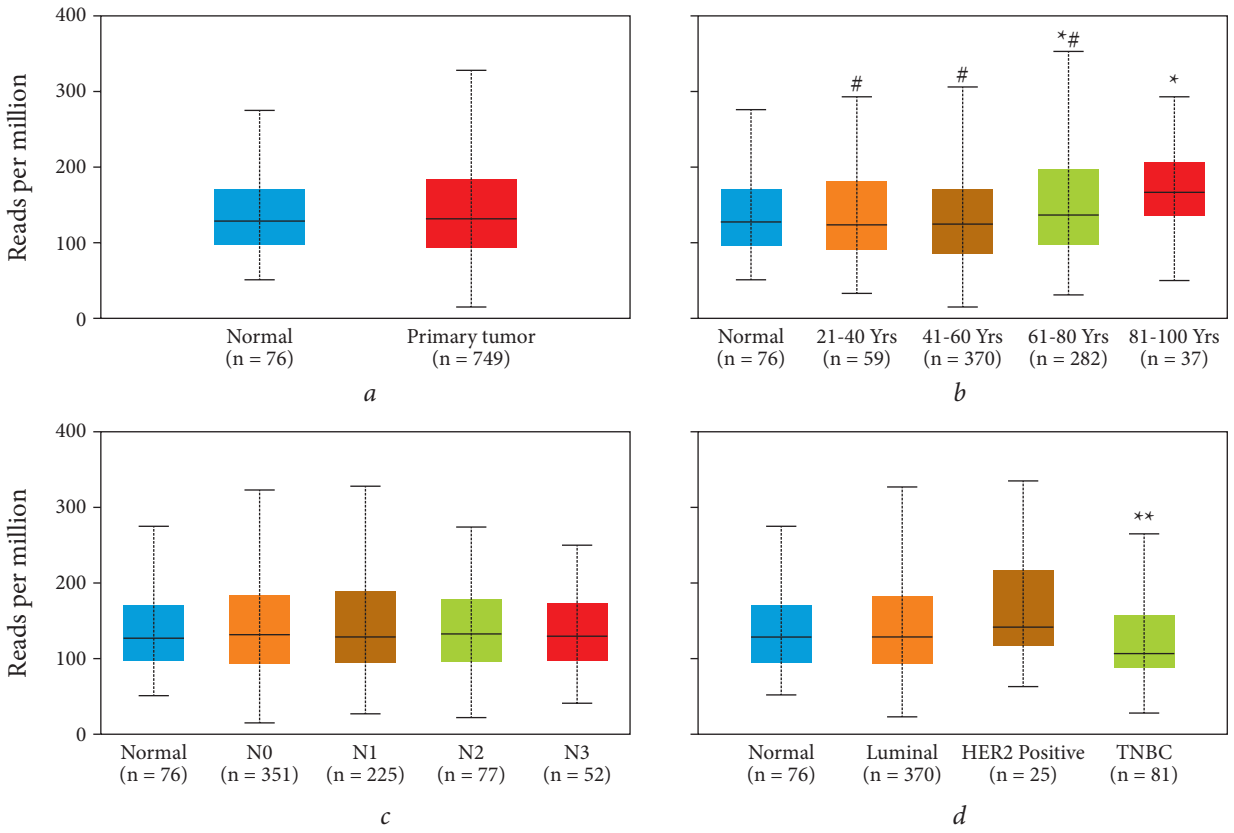

Fig. 6. Expression of miR-34a in normal and malignantly transformed breast tissue (*a*) and its relation to age (*b*), lymph node involvement (*c*), and molecular subtype (*d*) of BC according to UALCAN. * $p < 0.05$ compared to normal tissue, # $p < 0.05$ compared to age (81—100 Yrs), ** $p < 0.05$ compared to HER2-positive tumors

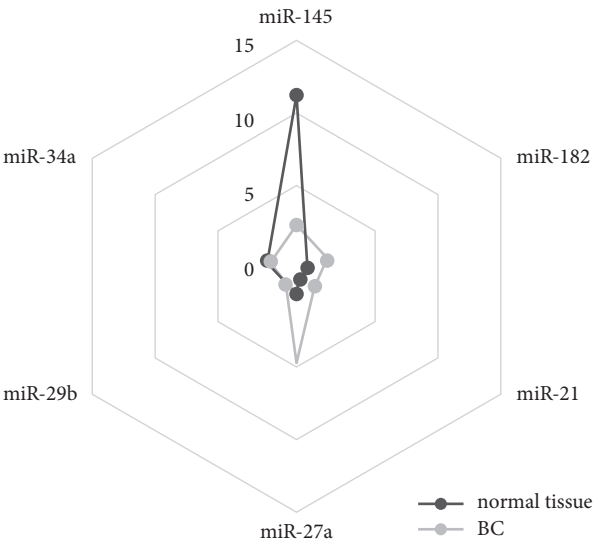

Fig. 7. MicroRNA expression profile in normal breast and BC tissue from young patients, dCT

with the opposite. This suggests that epigenetic changes in the tumor tissue of young BC patients differ from those in other age groups. There are very few studies aimed at comparing the epigenetic profile of BC tumors in younger and older women, or they are focused on much younger subjects [19]. Recently, there has been increasing evidence that age-related differences in gene expression can affect the cancer course [20]. Our data on miRNA profiling are in line with the results of other studies on the age-dependent molecular signatures in BC associated with different age-related biological processes [21].

To sum up, today, women are more likely to be diagnosed with BC at a younger age than a decade ago. This may be due to a combination of factors, including genetic predisposition, environmental exposures, and lifestyle choices. The study of miRNA expression in BC in Ukrainian women is still in its early stages. However, there is some evidence to suggest that miRNA deregulation may play a role in the development of BC at a younger age. The obtained results show that a high malignancy degree of BC in young women is associated with an increase in the miR-182, -21, -29b, and -34a expression and a decrease in the miR-27a level in the tumor tissue and indicate the prospect of the use of these miRNAs for predicting the aggressiveness of the disease course.

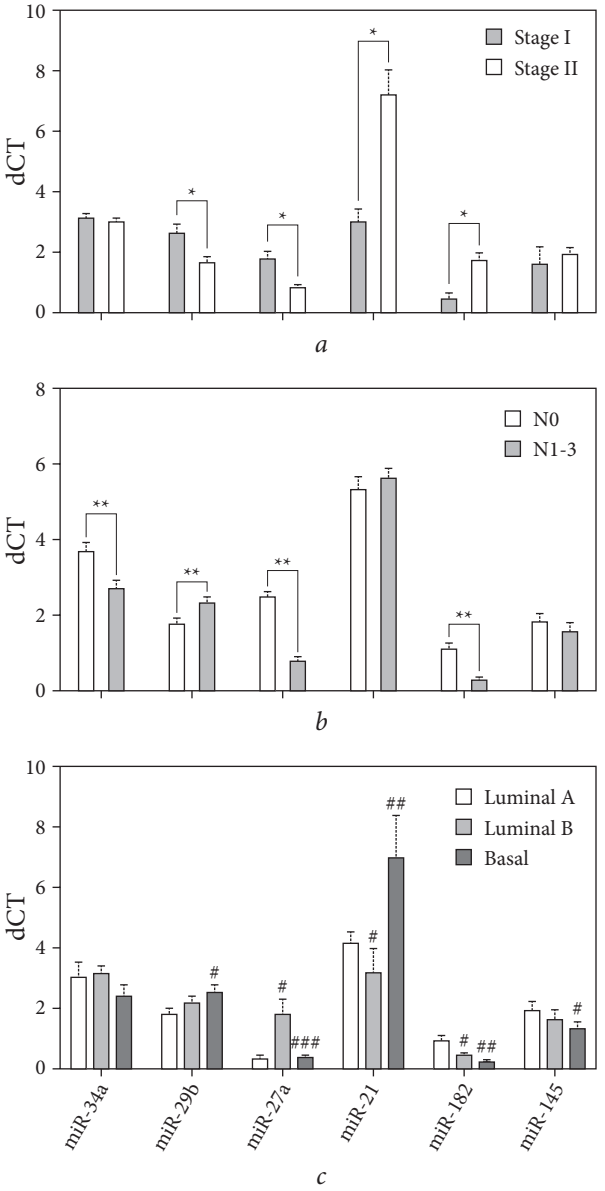

Fig. 8. The relationship between the levels of microRNAs in tumor tissue and the stage (*a*), lymph node involvement (*b*), and molecular subtype (*c*) of young BC patients. * $p < 0.05$ compared to stage I, ** $p < 0.05$ compared to N0, # $p < 0.05$ compared to luminal A subtype, ## $p < 0.05$ compared to luminal A and B subtypes, ### $p < 0.05$ compared to luminal B subtype

Funding

This study was supported by the research program of the Ministry of Education and Science of Ukraine "Development and Validation of Complex Treatment Technology for Breast Cancer Patients of Young Age" (0122U201203)

REFERENCES

1. Lei S, Zheng R, Zhang S, et al. Global patterns of breast cancer incidence and mortality: A population-based cancer registry data analysis from 2000 to 2020. *Cancer Commun (Lond)*. 2021;41:1183-1194. https://doi.org/10.1002/cac2.12207
2. Chekhun V, Martynyuk O, Lukianova Y, et al. Features of breast cancer in patients of young age: search for diagnosis optimization and personalized treatment. *Exp Oncol.* 2023;45:139-150. https://doi.org/10.15407/exp-oncology.2023.02.139
3. Peña-Chilet M, Martínez MT, Pérez-Fidalgo JA, et al, MicroRNA profile in very young women with breast cancer. *BMC Cancer*. 2014;14:1-14. https://doi.org/10.1186/1471-2407-14-529
4. Rossi L, Mazzara C, Pagani O. Diagnosis and treatment of breast cancer in young women. *Curr Treat Options Oncol*. 2019;20:86. https://doi.org/10.1007/s11864-019-0685-7
5. Kim HJ, Kim S, Freedman RA, Partridge AH. The impact of young age at diagnosis (age< 40 years) on prognosis varies by breast cancer subtype: A US SEER database analysis. *Breast*. 2022;61:77-83. https://doi.org/10.1016/j.breast.2021.12.006
6. Zhu JW, Charkhchi P, Adekunte S, Akbari MR. What is known about breast cancer in young women? *Cancers.* 2023;15:1917. https://doi.org/10.3390/cancers15061917
7. Villarreal-Garza C, Ferrigno AS, De la Garza-Ramos C, et al. Clinical utility of genomic signatures in young breast cancer patients: a systematic review. *NPJ Breast Cancer.* 2020;6:46. https://doi.org/10.1038/s41523-020-00188-3
8. Lambertini M, Ceppi M, Hamy AS, et al. Clinical behavior and outcomes of breast cancer in young women with germline BRCA pathogenic variants. *NPJ Breast Cancer*. 2021;7;16. https://doi.org/10.1038/s41523-021-00224-w
9. Jang JY, Kim YS, Kang KN, et al. Multiple microRNAs as biomarkers for early breast cancer diagnosis. *Mol Clin Oncol*. 2021;14:1-1. https://doi.org/10.3892/mco.2020.2193
10. Sopik, V. International variation in breast cancer incidence and mortality in young women. *Breast Cancer Res Treat*. 2021;186:497-507. https://doi.org/10.1038/s41523-021-00224-w
11. Dumanskii YV. Chekhun VF, Lukianova NYu, et al. Chapter 2. The expression profile of tissue and circulating miRNAs for optimization of neoadjuvant therapy of breast cancer patients. In: Hiroto S. Watanabe, eds. *Horizons in Cancer Research*. New York, USA: Nova Science Pub Inc. 2021;80:63-112. ISBN: 978-1-53619-563-7
12. Fang R, Zhu Y, Hu L, et al. Plasma microRNA pair panels as novel biomarkers for detection of early stage breast cancer. *Front Physiol*. 2019;9:1879. https://doi.org/10.3389/fphys.2018.01879
13. Soleimanpour E, Babaei E, Hosseinpour-Feizi MA, Montazeri V. Circulating miR-21 and miR-155 as potential noninvasive biomarkers in Iranian Azeri patients with breast carcinoma. *J Cancer Res Ther*. 2019;15:1092-1097. https://doi.org/10.4103/jcrt.JCRT_1227_16
14. Soofiyani SR, Hosseini K, Ebrahimi T, et al. Prognostic value and biological role of miR-126 in breast cancer. *MicroRNA*. 2022;11:95-103. https://doi.org/10.2174/1876402914666220428123203
15. Lukianova N, Mushii O, Borikun T, et al. Pattern of MMP2 and MMP9 expression depends on breast cancer patients' age. *Exp Oncol*. 2023;45:17-27. https://doi.org/10.15407/exp-oncology.2023.01.017
16. Lukianova N, Zadvornyi T, Kashuba E, et al. Expression of markers of bone tissue remodeling in breast cancer and prostate cancer cells in vitro. *Exp Oncol*. 2022;44:39-46. https://doi.org/10.32471/exp-oncology.2312-8852.vol-44-no-1.17354
17. Chandrashekar DS, Bashel B, Balasubramanya S, et al. UALCAN: a portal for facilitating tumor subgroup gene expression and survival analyses. *Neoplasia*. 2017;19:649-658. https://doi.org/10.1016/j.neo.2017.05.002
18. Adhami M, Haghdoost AA, Sadeghi B, et al. Candidate miRNAs in human breast cancer biomarkers: a systematic review. *Breast Cancer*. 2018;25:198-205. https://doi.org/10.1007/s12282-017-0814-8
19. Hironaka-Mitsuhashi A, Matsuzaki J, Takahashi RU, et al. A tissue microRNA signature that predicts the prognosis of breast cancer in young women. *PLoS One*. 2017;12:e0187638. https://doi.org/10.1371/journal.pone.0187638

20. Huang D, Berglund M, Damdimopoulos A, et al. Sex-and female age-dependent differences in gene expression in diffuse large B-cell lymphoma—possible estrogen effects. *Cancers*. 2023;15:1298. https://doi.org/10.3390/cancers15041298
21. Chatsirisupachai K, Lagger C, de Magalhães JP. Age-associated differences in the cancer molecular landscape. *Trends Cancer*. 2022;8:962-971. https://doi.org/10.1016/j.trecan.2022.06.007

Submitted: October 1, 2023

В. Чехун[1], Т. Борікун [1], О. Мушій [1], Т. Задворний [1], О. Мартинюк [1],
О. Кашуба [1], В. Базась [1,3], С. Грибач [4], М. Кротевич [2], С. Ляльокін [2], Н. Лук'янова [1]

[1] Інститут експериментальної патології, онкології та радіобіології імені Р.Є. Кавецького, Національна академія наук України, Київ, Україна
[2] Національний інститут раку, Міністерство охорони здоров'я України, Київ, Україна
[3] Київський міський клінічний онкологічний центр, Київ, Україна
[4] Київський обласний онкологічний диспансер, Київ, Україна

ПРОФІЛЬ ЕКСПРЕСІЇ MIR-145, -182, -21, -27a, -29b І -34a
У МОЛОДИХ ЖІНОК ХВОРИХ НА РАК МОЛОЧНОЇ ЗАЛОЗИ

Стан питання. Рак молочної залози (РМЗ) у молодих жінок залишається серйозною проблемою здоров'я населення. Незважаючи на прогрес у розумінні етіології, діагностики та лікування РМЗ у молодих жінок, ряд питань, що потребують вирішення, досі залишаються актуальними. Ідентифікація та використання прогностичних біомаркерів є цінними інструментами для адаптації стратегій лікування та покращення прогнозу для молодих жінок з РМЗ. **Мета роботи.** Оцінити зв'язок між експресією мікроРНК пухлини та клініко-патологічними особливостями хворих на РМЗ молодих жінок. **Матеріали та методи.** Робота базується на результатах обстеження та лікування 50 жінок віком до 45 років з I—II стадією РМЗ. Експресію miR-145, -182, -21, -27a, -29b і -34a у зразках пухлини аналізували за допомогою полімеразної ланцюгової реакції зворотної транскрипції в реальному часі. **Результати.** Встановлено, що вища експресія miR-182, -21 і -29b, та нижчі рівні miR-27a пов'язані зі стадією пухлинного процесу. Пацієнти без метастазів у лімфатичні вузли (N0) мали значно вищі рівні miR-182, -27a та -34a, а також нижчі рівні miR-29b порівняно з пацієнтами N1 ($p < 0,05$). Експресія miR-145, -182, -21, -27a і -29b пов'язана з молекулярними підтипами РМЗ у жінок молодого віку. **Висновки.** Отримані результати показують, що високий ступінь злоякісності РМЗ у молодих жінок асоціюється з високим рівнем експресії miR-182, -21, -29b і -34a та низьким рівнем експресії miR-27a в пухлинній тканині та вказують на перспективність використання цих мікроРНК для прогнозування агресивності перебігу захворювання.

Ключові слова: рак молочної залози, епідеміологія, мікроРНК, прогноз.