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ЕЖЕМЕСЯЧНЫЙ НАУЧНЫЙ ЖУРНАЛ

Медицинские новости Грузии

საქართველოს სამედიცინო სიახლენი

GEORGIAN MEDICAL NEWS

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GMN: Georgian Medical News is peer-reviewed, published monthly journal committed to promoting the science and art of medicine and the betterment of public health, published by the GMN Editorial Board since 1994. GMN carries original scientific articles on medicine, biology and pharmacy, which are of experimental, theoretical and practical character; publishes original research, reviews, commentaries, editorials, essays, medical news, and correspondence in English and Russian.

GMN is indexed in MEDLINE, SCOPUS, PubMed and VINITI Russian Academy of Sciences. The full text content is available through EBSCO databases.

GMN: Медицинские новости Грузии - ежемесячный рецензируемый научный журнал, издаётся Редакционной коллегией с 1994 года на русском и английском языках в целях поддержки медицинской науки и улучшения здравоохранения. В журнале публикуются оригинальные научные статьи в области медицины, биологии и фармации, статьи обзорного характера, научные сообщения, новости медицины и здравоохранения. Журнал индексируется в MEDLINE, отражён в базе данных SCOPUS, PubMed и ВИНИТИ РАН. Полнотекстовые статьи журнала доступны через БД EBSCO.

GMN: Georgian Medical News – საქართველოს სამედიცინო სიახლენი – არის ყოველთვიური სამეცნიერო სამედიცინო რეცენზირებადი ჟურნალი, გამოიცემა 1994 წლიდან, წარმოადგენს სარედაქციო კოლეგიისა და აშშ-ის მეცნიერების, განათლების, ინდუსტრიის, ხელოვნებისა და ბუნებისმეტყველების საერთაშორისო აკადემიის ერთობლივ გამოცემას. GMN-ში რუსულ და ინგლისურ ენებზე ქვეყნდება ექსპერიმენტული, თეორიული და პრაქტიკული ხასიათის ორიგინალური სამეცნიერო სტატიები მედიცინის, ბიოლოგიისა და ფარმაციის სფეროში, მიმოხილვითი ხასიათის სტატიები.

ჟურნალი ინდექსირებულია MEDLINE-ის საერთაშორისო სისტემაში, ასახულია SCOPUS-ის, PubMed-ის და ВИНИТИ РАН-ის მონაცემთა ბაზებში. სტატიების სრული ტექსტი ხელმისაწვდომია EBSCO-ს მონაცემთა ბაზებიდან.

WEBSITE

www.geomednews.com

К СВЕДЕНИЮ АВТОРОВ!

При направлении статьи в редакцию необходимо соблюдать следующие правила:

1. Статья должна быть представлена в двух экземплярах, на русском или английском языках, напечатанная через **полтора интервала на одной стороне стандартного листа с шириной левого поля в три сантиметра**. Используемый компьютерный шрифт для текста на русском и английском языках - **Times New Roman** (**Кириллица**), для текста на грузинском языке следует использовать **AcadNusx.** Размер шрифта - **12**. К рукописи, напечатанной на компьютере, должен быть приложен CD со статьей.

2. Размер статьи должен быть не менее десяти и не более двадцати страниц машинописи, включая указатель литературы и резюме на английском, русском и грузинском языках.

3. В статье должны быть освещены актуальность данного материала, методы и результаты исследования и их обсуждение.

При представлении в печать научных экспериментальных работ авторы должны указывать вид и количество экспериментальных животных, применявшиеся методы обезболивания и усыпления (в ходе острых опытов).

4. К статье должны быть приложены краткое (на полстраницы) резюме на английском, русском и грузинском языках (включающее следующие разделы: цель исследования, материал и методы, результаты и заключение) и список ключевых слов (key words).

5. Таблицы необходимо представлять в печатной форме. Фотокопии не принимаются. **Все цифровые, итоговые и процентные данные в таблицах должны соответствовать таковым в тексте статьи**. Таблицы и графики должны быть озаглавлены.

6. Фотографии должны быть контрастными, фотокопии с рентгенограмм - в позитивном изображении. Рисунки, чертежи и диаграммы следует озаглавить, пронумеровать и вставить в соответствующее место текста **в tiff формате**.

В подписях к микрофотографиям следует указывать степень увеличения через окуляр или объектив и метод окраски или импрегнации срезов.

7. Фамилии отечественных авторов приводятся в оригинальной транскрипции.

8. При оформлении и направлении статей в журнал МНГ просим авторов соблюдать правила, изложенные в «Единых требованиях к рукописям, представляемым в биомедицинские журналы», принятых Международным комитетом редакторов медицинских журналов - http://www.spinesurgery.ru/files/publish.pdf и http://www.nlm.nih.gov/bsd/uniform_requirements.html
В конце каждой оригинальной статьи приводится библиографический список. В список литературы включаются все материалы, на которые имеются ссылки в тексте. Список составляется в алфавитном порядке и нумеруется. Литературный источник приводится на языке оригинала. В списке литературы сначала приводятся работы, написанные знаками грузинского алфавита, затем кириллицей и латиницей. Ссылки на цитируемые работы в тексте статьи даются в квадратных скобках в виде номера, соответствующего номеру данной работы в списке литературы. Большинство цитированных источников должны быть за последние 5-7 лет.

9. Для получения права на публикацию статья должна иметь от руководителя работы или учреждения визу и сопроводительное отношение, написанные или напечатанные на бланке и заверенные подписью и печатью.

10. В конце статьи должны быть подписи всех авторов, полностью приведены их фамилии, имена и отчества, указаны служебный и домашний номера телефонов и адреса или иные координаты. Количество авторов (соавторов) не должно превышать пяти человек.

11. Редакция оставляет за собой право сокращать и исправлять статьи. Корректура авторам не высылается, вся работа и сверка проводится по авторскому оригиналу.

12. Недопустимо направление в редакцию работ, представленных к печати в иных издательствах или опубликованных в других изданиях.

При нарушении указанных правил статьи не рассматриваются.

REQUIREMENTS

Please note, materials submitted to the Editorial Office Staff are supposed to meet the following requirements:

1. Articles must be provided with a double copy, in English or Russian languages and typed or compu-ter-printed on a single side of standard typing paper, with the left margin of **3** centimeters width, and **1.5** spacing between the lines, typeface - **Times New Roman** (**Cyrillic**), print size - **12** (referring to Georgian and Russian materials). With computer-printed texts please enclose a CD carrying the same file titled with Latin symbols.

2. Size of the article, including index and resume in English, Russian and Georgian languages must be at least 10 pages and not exceed the limit of 20 pages of typed or computer-printed text.

3. Submitted material must include a coverage of a topical subject, research methods, results, and review.

Authors of the scientific-research works must indicate the number of experimental biological species drawn in, list the employed methods of anesthetization and soporific means used during acute tests.

4. Articles must have a short (half page) abstract in English, Russian and Georgian (including the following sections: aim of study, material and methods, results and conclusions) and a list of key words.

5. Tables must be presented in an original typed or computer-printed form, instead of a photocopied version. **Numbers, totals, percentile data on the tables must coincide with those in the texts of the articles.** Tables and graphs must be headed.

6. Photographs are required to be contrasted and must be submitted with doubles. Please number each photograph with a pencil on its back, indicate author's name, title of the article (short version), and mark out its top and bottom parts. Drawings must be accurate, drafts and diagrams drawn in Indian ink (or black ink). Photocopies of the X-ray photographs must be presented in a positive image in **tiff format**.

Accurately numbered subtitles for each illustration must be listed on a separate sheet of paper. In the subtitles for the microphotographs please indicate the ocular and objective lens magnification power, method of coloring or impregnation of the microscopic sections (preparations).

7. Please indicate last names, first and middle initials of the native authors, present names and initials of the foreign authors in the transcription of the original language, enclose in parenthesis corresponding number under which the author is listed in the reference materials.

8. Please follow guidance offered to authors by The International Committee of Medical Journal Editors guidance in its Uniform Requirements for Manuscripts Submitted to Biomedical Journals publication available online at: http://www.nlm.nih.gov/bsd/uniform_requirements.html
http://www.icmje.org/urm_full.pdf
In GMN style for each work cited in the text, a bibliographic reference is given, and this is located at the end of the article under the title "References". All references cited in the text must be listed. The list of references should be arranged alphabetically and then numbered. References are numbered in the text [numbers in square brackets] and in the reference list and numbers are repeated throughout the text as needed. The bibliographic description is given in the language of publication (citations in Georgian script are followed by Cyrillic and Latin).

9. To obtain the rights of publication articles must be accompanied by a visa from the project instructor or the establishment, where the work has been performed, and a reference letter, both written or typed on a special signed form, certified by a stamp or a seal.

10. Articles must be signed by all of the authors at the end, and they must be provided with a list of full names, office and home phone numbers and addresses or other non-office locations where the authors could be reached. The number of the authors (co-authors) must not exceed the limit of 5 people.

11. Editorial Staff reserves the rights to cut down in size and correct the articles. Proof-sheets are not sent out to the authors. The entire editorial and collation work is performed according to the author's original text.

12. Sending in the works that have already been assigned to the press by other Editorial Staffs or have been printed by other publishers is not permissible.

Articles that Fail to Meet the Aforementioned Requirements are not Assigned to be Reviewed.

ავტორთა საყურადღებოდ!

რედაქციაში სტატიის წარმოდგენისას საჭიროა დავიცვათ შემდეგი წესები:

1. სტატია უნდა წარმოადგინოთ 2 ცალად, რუსულ ან ინგლისურ ენებზე,დაბეჭდილი სტანდარტული ფურცლის 1 გვერდზე, 3 სმ სიგანის მარცხენა ველისა და სტრიქონებს შორის 1,5 ინტერვალის დაცვით. გამოყენებული კომპიუტერული შრიფტი რუსულ და ინგლისურენოვან ტექსტებში - **Times New Roman (Кириллица)**, ხოლო ქართულენოვან ტექსტში საჭიროა გამოვიყენოთ **AcadNusx.** შრიფტის ზომა – 12. სტატიას თან უნდა ახლდეს CD სტატიით.

2. სტატიის მოცულობა არ უნდა შეადგენდეს 10 გვერდზე ნაკლებს და 20 გვერდზე მეტს ლიტერატურის სიის და რეზიუმეების (ინგლისურ, რუსულ და ქართულ ენებზე) ჩათვლით.

3. სტატიაში საჭიროა გაშუქდეს: საკითხის აქტუალობა; კვლევის მიზანი; საკვლევი მასალა და გამოყენებული მეთოდები; მიღებული შედეგები და მათი განსჯა. ექსპერიმენტული ხასიათის სტატიების წარმოდგენისას ავტორებმა უნდა მიუთითონ საექსპერიმენტო ცხოველების სახეობა და რაოდენობა; გაუტკივარებისა და დაძინების მეთოდები (მწვავე ცდების პირობებში).

4. სტატიას თან უნდა ახლდეს რეზიუმე ინგლისურ, რუსულ და ქართულ ენებზე არანაკლებ ნახევარი გვერდის მოცულობისა (სათაურის, ავტორების, დაწესებულების მითითებით და უნდა შეიცავდეს შემდეგ განყოფილებებს: მიზანი, მასალა და მეთოდები, შედეგები და დასკვნები; ტექსტუალური ნაწილი არ უნდა იყოს 15 სტრიქონზე ნაკლები) და საკვანძო სიტყვების ჩამონათვალი (key words).

5. ცხრილები საჭიროა წარმოადგინოთ ნაბეჭდი სახით. ყველა ციფრული, შემაჯამებელი და პროცენტული მონაცემები უნდა შეესაბამებოდეს ტექსტში მოყვანილს.

6. ფოტოსურათები უნდა იყოს კონტრასტული; სურათები, ნახაზები, დიაგრამები - დასათაურებული, დანომრილი და სათანადო ადგილას ჩასმული. რენტგენოგრამების ფოტოასლები წარმოადგინეთ პოზიტიური გამოსახულებით **tiff** ფორმატში. მიკროფოტოსურათების წარწერებში საჭიროა მიუთითოთ ოკულარის ან ობიექტივის საშუალებით გადიდების ხარისხი, ანათალების შეღებვის ან იმპრეგნაციის მეთოდი და აღნიშნოთ სურათის ზედა და ქვედა ნაწილები.

7. სამამულო ავტორების გვარები სტატიაში აღინიშნება ინიციალების თანდართვით, უცხოურისა – უცხოური ტრანსკრიპციით.

8. სტატიას თან უნდა ახლდეს ავტორის მიერ გამოყენებული სამამულო და უცხოური შრომების ბიბლიოგრაფიული სია (ბოლო 5-8 წლის სიღრმით). ანბანური წყობით წარმოდგენილ ბიბლიოგრაფიულ სიაში მიუთითეთ ჯერ სამამულო, შემდეგ უცხოელი ავტორები (გვარი, ინიციალები, სტატიის სათაური, ჟურნალის დასახელება, გამოცემის ადგილი, წელი, ჟურნალის №, პირველი და ბოლო გვერდები). მონოგრაფიის შემთხვევაში მიუთითეთ გამოცემის წელი, ადგილი და გვერდების საერთო რაოდენობა. ტექსტში კვადრატულ ფჩხილებში უნდა მიუთითოთ ავტორის შესაბამისი N ლიტერატურის სიის მიხედვით. მიზანშეწონილია, რომ ციტირებული წყაროების უმეტესი ნაწილი იყოს 5-6 წლის სიღრმის.

9. სტატიას თან უნდა ახლდეს: ა) დაწესებულების ან სამეცნიერო ხელმძღვანელის წარდგინება, დამოწმებული ხელმოწერითა და ბეჭდით; ბ) დარგის სპეციალისტის დამოწმებული რეცენზია, რომელშიც მითითებული იქნება საკითხის აქტუალობა, მასალის საკმაობა, მეთოდის სანდოობა, შედეგების სამეცნიერო-პრაქტიკული მნიშვნელობა.

10. სტატიის ბოლოს საჭიროა ყველა ავტორის ხელმოწერა, რომელთა რაოდენობა არ უნდა აღემატებოდეს 5-ს.

11. რედაქცია იტოვებს უფლებას შეასწოროს სტატია. ტექსტზე მუშაობა და შეჯერება ხდება საავტორო ორიგინალის მიხედვით.

12. დაუშვებელია რედაქციაში ისეთი სტატიის წარდგენა, რომელიც დასაბეჭდად წარდგენილი იყო სხვა რედაქციაში ან გამოქვეყნებული იყო სხვა გამოცემებში.

აღნიშნული წესების დარღვევის შემთხვევაში სტატიები არ განიხილება.

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PROGNOSTIC IMPACT OF EGFR2 AND KI-67 OVEREXPRESSION WITH DOWNREGULATION OF *MIR-17* AND *MIR-1307* IN FEMALE BREAST CANCER PATIENTS

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Abstract.

Background: Breast cancer has distinct epidemiological patterns and heterogeneity. EGFR2 and Ki-67 are significant in determining the progression and therapeutic response in breast cancer. Additionally, *miR-17* and *miR-1307* are critical regulators of tumorigenesis. Our research investigates the function of these biomarkers across breast cancer progression, diagnostic and treatment response.

Methods: Fifty-Three women with breast cancer and 25 healthy women were analyzed. ELISA was used to evaluate the concentrations of EGFR2 and Ki-67. For gene expression, qPCR was used to analyze the gene expression of *miR-17* and *miR-1307*. The diagnostic value of the proteins and miRNAs, with significance set at a p-value <0.001 for all tests.

Results: The study found a significant increase in EGFR2 and Ki-67 proteins in patients compared to controls. The concentration of EGFR2 in lobular carcinoma showed a significantly higher concentration compared to Invasive Ductal Carcinoma (IDC) and Mixed carcinoma, with a p-value of 0.001. Regarding Ki-67, Lobular carcinoma had significantly higher levels compared to IDC, with a p-value of 0.03. ROC curve analysis revealed excellent diagnostic accuracy for EGFR2 and Ki-67. Positive correlation was shown between EGFR2 and Ki-67 with each other, also *miR-17* and *miR-1307* showed a positive correlation with other. On the other hand, a negative correlation was seen between the protein level and gene expression.

Conclusion: This study found elevated EGFR2 and Ki-67 levels in breast cancer patients, indicating tumor aggressiveness, while the downregulation of *miR-17* and *miR-1307* suggests reduced tumor-suppressive activity. Their inverse correlation supports their use in diagnostic and treatment monitoring.

Key words. Breast cancer, epidermal growth factor receptor, Ki-67, MicroRNAs, *miR-17*, *miR-1307*.

Introduction.

The epidemiology and clinical presentation of breast cancer are distinct and highly variable and involve a multitude of molecular and cellular alterations that drive tumor initiation, proliferation, angiogenesis, and metastasis [1]. It's one of the most common cancers that cause death in women [2]. Despite the advances in diagnosis and treatment, early detection and accurate prognosis remain critical for improving survival outcomes and guiding therapeutic strategies [3].

The epidermal growth factor receptor (EGFR2), alternatively referred to as HER2 It is the founder of the broad family of growth factor receptors with intrinsic tyrosine kinase function and is overexpressed in breast cancer, where it enhances cell proliferation, survival, and therapy resistance [4]. Also, EGFR 2 has been detected in approximately 15–30% of breast cancers, particularly in the HER2-positive subtype [5]. Clinically, HER2-positive breast cancer tends to be more aggressive and associated with poor prognosis if left untreated [6].

Ki-67 (also known as Ki67P or MKI67) is a nuclear protein related only to cell proliferation [7]. It is a good indicator of the cell population's growth fraction since it is stimulated during the cell cycle (G1, S, G2, and M phases) but not during resting cells (G0 phase) [8]. Growth, progression, and aggressiveness of tumours are significantly correlated with their expression [9]. The expression of Ki-67 in breast cancer is widely used as a proliferation index to assess tumor aggressiveness and predict clinical consequences [9].

MicroRNAs (miRNAs) are diminutive non-coding RNA transcripts (20–24 nucleotides) that attach to complementary sequences in the 3′-untranslated regions (3′-UTR) of target genes, thereby modulating their expression either negatively or positively. miRNAs influence gene expression in cells, so they play a role in various critical biological processes, including cancer [10].

miR-17, one of the *miR-17-92* cluster, is involved in apoptosis, differentiation, and cell proliferation [11]. Depending on the cancer, the *miR-17-92* cluster can be an oncogene or a tumor suppressor. The target genes inhibited by *miR-17-92* determine its oncogenic/tumour-suppressive effect. In human tumours, *miR-17-92* clusters have various effects, but a single miRNA can target hundreds of genes, even if some of those genes have competing activity. The cancer signature model helps organize and comprehend human carcinogenesis. Published *miR-17-92* targets are associated with human cancer hallmarks [12]. Dysregulated of *miR-17* levels in breast cancer may reflect tumor dynamics and immune evasion mechanisms [13].

Recently discovered cancer-associated miRNA, the *miR-1307*, poses the danger of metastatic malignancies. Early breast cancer diagnosis is possible with elevated serum MiR-1307. Data indicate that *miR-1307* is an oncogenic miRNA that contributes to cancer formation and progression [14]. miR-1307 promotes oncogenic behavior by targeting tumor suppressor genes—one identified target in breast cancer is Protamine 2 (PRM2), where miR-1307 binding reduces PRM2 expression, facilitating angiogenesis and cell survival [15]. Previous studies have found that decreased *miR-1307* expression can be a risk factor for cancers such as colon and rectum, and that decreased expression can lead to reduced programmed cell death, which leads to the development of cancer [16]. Based on these findings, *miR-1307* plays a different role in different cancers [17].

The combined analysis of protein biomarkers (EGFR2, Ki-67) and miRNA profiles (*miR-17, miR-1307*) offers a more comprehensive molecular understanding of breast cancer. It allows for the identification of multi-level dysregulation, both at the protein and genetic levels, which could improve early detection and offer insights into tumor biology. This study, therefore, aims to correlate serum concentrations of (EGFR2, Ki-67) and gene expression of *miR-17, miR-1307*, thereby evaluating their potential as diagnostic tools and treatment monitoring.

Materials and Methods.

Study Design and Sample Collection:

This study was conducted in the postgraduate laboratory at the Department of Biology, College of Science, and in the Molecular Laboratory of the College of Biotechnology, University of Al-Qadisiyah, Iraq. Peripheral blood samples were obtained from 53 patients (Treated) at the Oncology Center in Al-Karama Teaching Hospital, Al-Zahra Teaching Hospital, and external laboratories located in Wasit province, and 25 healthy individuals were collected as a control group. The stage, grade, and type of breast cancer were determined by clinical pathologists based on standard diagnostic criteria and classifications established by renowned cancer organizations. Each patient provided blood samples, from which serum was separated by centrifugation for subsequent analysis. Ethical approval was obtained before sample collection.

Ethics approval:

The study was carried out in line with the Declaration of Helsinki. Approval was granted by the Ethics Committee of the University of Wasit, College of Science – Health Directorate (No. UW.Sci.2025.0723, July 23, 2025). All participants provided informed consent before enrollment.

Inclusion Criteria:

Participants were aged between 18 and 65 years. Patients diagnosed with invasive breast carcinoma, categorized into specific grades (I, II, III), stages (I, II, III, IV), and types (IDC, Lobular, Mixed). All patients had received treatment (chemotherapy and hormonal therapy) prior to or during enrollment, as the study aims to explore their relationship with marker concentrations. All participants provide informed consent for participation in the study.

Exclusion Criteria:

Women who are pregnant or breastfeeding. Participants with severe comorbid conditions that might interfere with the study (e.g., autoimmune diseases, severe cardiovascular issues). Patients with conditions unrelated to breast cancer and other cancers.

Enzyme-linked immunosorbent assay (ELISA):

Serum concentrations of EGFR2 and Ki-67 proteins were assessed using commercially available double-antibody sandwich ELISA kits (Elabscience®, China; Cat. No. E-EL-H6083 and E-EL-H5432). In this technique, the target antigen in the sample first binds to a capture antibody fixed on the ELISA plate. A second antibody, conjugated with an enzyme such as horseradish peroxidase, attaches to the antigen–antibody complex. The bound enzyme reacts with a chromogenic substrate, generating a colored product, and the optical density (OD) is measured. The concentration of each marker was calculated by comparing OD values of the samples with the standard curve obtained from the kit's reference antigens. All procedures were conducted in accordance with the manufacturer's instructions to ensure reproducibility and accuracy.

RNA Extraction:

Peripheral blood samples were collected from all participants using standard venipuncture techniques. Whole blood was processed immediately after collection. The red blood cells were lysed, and the remaining white blood cells were isolated by centrifugation at 3000 rpm for 10 minutes. Total RNA, including miRNA, was extracted from the white blood cells using the HiPure Universal miRNA Kit (Magen, China), following the manufacturer's protocol. The homogenized white blood cells were lysed with MagZol Reagent, and phase separation was performed by adding chloroform. The upper aqueous phase, containing RNA, was purified using HiPure RNA Mini Columns, followed by washing with Buffer RWC and Buffer RW2, and finally eluted with RNase-Free Water. The extracted microRNA was preserved at –20°C till use in cDNA synthesis & gene expression analysis.

Primer Design:

Primers for the quantification of target miRNAs (*miRNA 17* and *miRNA-1307*) and the housekeeping gene (*miR-16*) were synthesized by Macrogen, Korea, based on mature miRNA sequences from miRBase as shown in Table 1. All reverse primers shared a common sequence (5′-GAACATGTCTGCGTATCTC-3′), while the forward primers were miRNA-specific.

Complementary DNA (cDNA) synthesis:

cDNA was produced using the AddScript cDNA Synthesis Kit (Addbio, Korea) from extracted RNA. The reaction was prepared at a total concentration of 20 µL per sample. The reaction contained 10 µL of 2x Reaction Buffer, 2 µL of 10 mM dNTP Mix, 2 µL of oligo dT20 or random hexamer, 1 µL of 20x AddScript Enzyme Solution, 1 µL of nuclease-free H_2O, and 4 µL of RNA template. The reaction was performed in a

Table 1. *Primers for the miRNAs gene expression experiment.*

miRNA	Type	Primer name	5'-3'	ACCN	Reference
hsa-*miRNA 17*	Target	F	TGCTTACAGTGCAGGTAG	MIMAT0000070	Origene
		R	GAACATGTCTGCGTATCTC		
hsa-*miRNA-1307*	Target	F	CGTGGCGTCGGTCGT	MIMAT0002853	Origene
		R	GAACATGTCTGCGTATCTC		
hsa-*miRNA-16*	HKG	F	AGCAGCACGTAAATATTGG	MIMAT0000069	Origene

thermal cycler under the following steps: priming at 25°C for 10 minutes, reverse transcription at 50°C for 60 minutes, and RT inactivation at 80°C for 5 minutes. The cDNA that was made was then kept at –20°C until it could be analyzed by qPCR.

qPCR Analysis:

Gene expression was analyzed using the GoTaq® RT-qPCR System (Promega, USA). The PCR reaction mixture included 5 µL of qPCR Master Mix, 0.5 µL each of forward and reverse primers, 0.25 µL of MgCl2, and 1 µL of cDNA template. The reaction was amplified using the following conditions: Initial denaturation at 95°C for 5 minutes, 40 cycles of 95°C for 20 seconds (denaturation), 60°C for *miRNA-17* and *miRNA-1307* for 20 seconds (annealing), and 72°C for 20 seconds (extension). A melting curve analysis was performed from 72°C to 95°C. Gene expression levels were quantified using the Livak Method (ΔΔCT) to determine fold changes in expression.

Statistical analysis.

The results were analyzed using SPSS. Independent t-test, ANOVA (Duncan's test) was used to assess group differences. Correlations were evaluated using Pearson's test, and Receiver Operating Characteristic (ROC) analysis was applied to determine cutoff values and diagnostic performance. Graphs were created using GraphPad Prism. Results are shown as mean ± SD, with significance set at $p \leq 0.05$.

Results.

The mean levels of serum concentration of EGFR2 and Ki-67 proteins and gene expression of *miRNA-17* and *miRNA-1307* in breast cancer patients and control groups are presented in Table 2. The study revealed a noteworthy increase in the mean concentration ± standard deviation (S.D.) (pg/mL) of EGFR2 in patients (1198.22±230.51) compared to the control (182.80±68.12), with a significant difference at (P<0.001) as shown in Figure 1 (A). Similarly, Ki-67 (ng/mL) levels were significantly elevated in patients (12.99±1.46) compared to controls (2.94±0.63) at (P<0.001) as shown in Figure 1 (B). In qPCR analyses presented as 2^-ΔΔCt (controls normalized to 1.00), patients showed a significant reduction in *miR-17-5p* and *miR-1307-3p* relative expression (0.57 and 0.56, respectively; P < 0.001), as shown in Table 2 and Figure 1C–D.

As shown in Table 3, the analysis of EGFR2 and Ki-67 protein concentrations across different tumor grades revealed no significant differences with p value (0.8 and 0.19, respectively). Similarly, the gene expression of *miRNA-17* and *miRNA-1307* across different tumor grades revealed no significant differences with a p-value of 0.9.

As shown in Table 4, the analysis of biomarker concentrations and gene expression levels across different stages of breast cancer revealed some significant findings. For EGFR2 and Ki-67, no significant differences were observed across stages I to IV, with p-values of 0.16 and 0.4, respectively. Regarding gene expression, *miRNA-17* and *miRNA-1307* showed no significant differences across stages I to IV, with p-values of 0.4 and 0.42, respectively.

As shown in Table 5, the analysis of protein concentrations and gene expression across different breast cancer types revealed several significant findings. For EGFR2, Lobular carcinoma showed a significantly higher concentration (1513.08±346.71) compared to Invasive Ductal Carcinoma (IDC) and Mixed carcinoma (1168.88±199.20 and 1131.33±70.96, respectively) with a p-value of 0.001. Regarding Ki-67, Lobular carcinoma had significantly higher levels (14.41±2.28) compared to IDC (12.80±1.32), with a p-value of 0.03.

Gene expression analysis showed no significant differences for *miRNA-17* and *miRNA-1307* among the BC types, with p-values of 0.9 and 0.95, respectively.

Using ROC analysis in breast cancer patients and healthy controls, the effectiveness of EGFR2 and Ki-67 levels as biomarkers for breast cancer prediction was examined. The results are in Table 6 and Figure 2. In comparing patients with breast cancer to healthy controls, the results showed that the area under the curve (AUC) for EGFR2 and Ki-67 levels was (0.99 and 0.98) respectively, with excellent specificity and sensitivity values. These AUC values determined the cut-off values of EGFR2 and Ki-67 (562.75 and 7.48), respectively, with a significant p value (<0.001) compared to the control. For gene expression, the diagnostic performance of miRNA-17 and miRNA-1307 was poor, with AUC values of 0.2 and 0.22, respectively. Sensitivity ranged from 46% to 47%, indicating a low ability to correctly identify breast cancer patients. However, specificity was high, at 96%, for correctly identifying healthy controls.

Table 2. *Comparison of EGFR2 & Ki-67 concentrations and miRNA-17 & miRNA-1307 expression between patients and controls.*

ELISA	**Groups**	**Concentration (Mean±S.D.)**	**P value**
EGFR2	**Control**	182.80±68.12	<0.001***
	BC Patients	1198.22±230.51	
Ki-67	**Control**	2.94±0.63	<0.001***
	BC Patients	12.99±1.46	
Gene expression	**Groups**	**Relative expression (2^-ΔΔCt)**	**P value**
miR-17-5p	**Control**	1	<0.001***
	BC Patients	0.57	
miR-1307-3p	**Control**	1	<0.001***
	BC Patients	0.56	

Relative expression was calculated using the 2^-ΔΔCt method with the mean of the control group as the calibrator (set to 1.0). Reference: [housekeeper(s) used]. Statistical tests were performed on ΔCt (or log2 fold-change).

Table 3. *Comparison of EGFR2 & Ki-67 concentrations and miRNA-17 & miRNA-1307 expression between patients and controls across cancer grades.*

ELISA	Grade Groups	Concentration (Mean±S.D.)	P value
EGFR2	**I**	1140.59±147.34	0.8 NS
	II	1208.39±253.18	
	III	1196.18±210.6	
Ki-67	**I**	13.24±1.26	0.19 NS
	II	12.72±1.33	
	III	13.44±1.69	
Gene expression	**Groups**	**Fold Expression**	**P value**
miR-17	**I**	2.22±1.81	0.9 NS
	II	2.40±1.89	
	III	2.14±1.77	
miR-1307	**I**	6.14±5.01	0.9 NS
	II	6.63±5.24	
	III	5.90±4.94	

Table 4. *Comparison of EGFR2 & Ki-67 concentrations and miRNA-17 & miRNA-1307 expression between patients and controls across cancer stages.*

ELISA	Stage Groups	Concentration (Mean±S.D.)	P value
EGFR2	**I**	1164.43±142.45	0.16 NS
	II	1168±291.45	
	III	1171.13±188.30	
	IV	1341.48±263	
Ki-67	**I**	12.92±1.14	0.4 NS
	II	12.58±1.12	
	III	13.06±1.62	
	IV	13.58±1.86	
Gene expression	**Groups**	**Fold Expression**	**P value**
miR-17	**I**	2.67±1.63	0.4 NS
	II	1.90±1.66	
	III	2.61±2.20	
	IV	1.83±1.32	
miR-1307	**I**	7.40±4.52	0.42 NS
	II	5.24±4.63	
	III	7.24±6.08	
	IV	5.0±3.70	

NS: Non-Significant; Different letters indicate a significant difference between the groups; Similar letters indicate non-significant differences.

Table 5. *Comparison of EGFR2 & Ki-67 concentrations and miRNA-17 & miRNA-1307 expression between patients and controls across breast cancer types.*

ELISA	BC Type	Concentration (Mean±S.D.)	P value
EGFR2	**IDC**	1168.88±199.20 a	0.001**
	Lobular	1513.08±346.71 b	
	Mixed	1131.33±70.96 a	
Ki-67	**IDC**	12.80±1.32 a	0.03*
	Lobular	14.41±2.28 b	
	Mixed	13.36±0.98 ab	
Gene expression	**Groups**	**Fold Expression**	**P value**
miR-17	**IDC**	2.31±1.78	0.9 NS
	Lobular	2.43±2.41	
	Mixed	2.07±1.94	
miR-1307	**IDC**	6.37±4.95	0.95 NS
	Lobular	6.73±6.66	
	Mixed	5.74±5.37	

NS: Non-Significant; Different letters indicate a significant difference between the groups; Similar letters indicate non-significant differences.

Table 6. *ROC curve results for all studied parameters in breast cancer compared with controls.*

ELISA	AUC	Cut-off	Sensitivity	Specificity	Asymptotic 95% Confidence		P Value
					Lower Bound	Upper Bound	
EGFR2	0.99	562.75	99.8%	100%	0.97	0.99	<0.001***
Ki-67	0.98	7.48	99.7%	100%	0.96	0.98	<0.001***
Gene Expression	**AUC**	**Cut-off**	**Sensitivity**	**Specificity**	**Asymptotic 95% Confidence**		**P Value**
					Lower Bound	**Upper Bound**	
miR-17	0.2	6.68	47%	96%	0.123	0.307	-
miR-1307	0.22	18.52	46%	96%	0.123	0.307	-

Table 7. *Correlation of studied parameters.*

Parameter	Pearson Correlation	P-value
EGFR2 & Ki-67	0.93**	0.001
miR-17 & EGFR2	-0.38**	0.001
miR-1307 & EGFR2	-0.4**	0.001
miR-17 & Ki-67	-0.401**	0.001
miR-1307 & Ki-67	-0.407**	0.001
miR-17 & *miR-1307*	0.97**	0.001

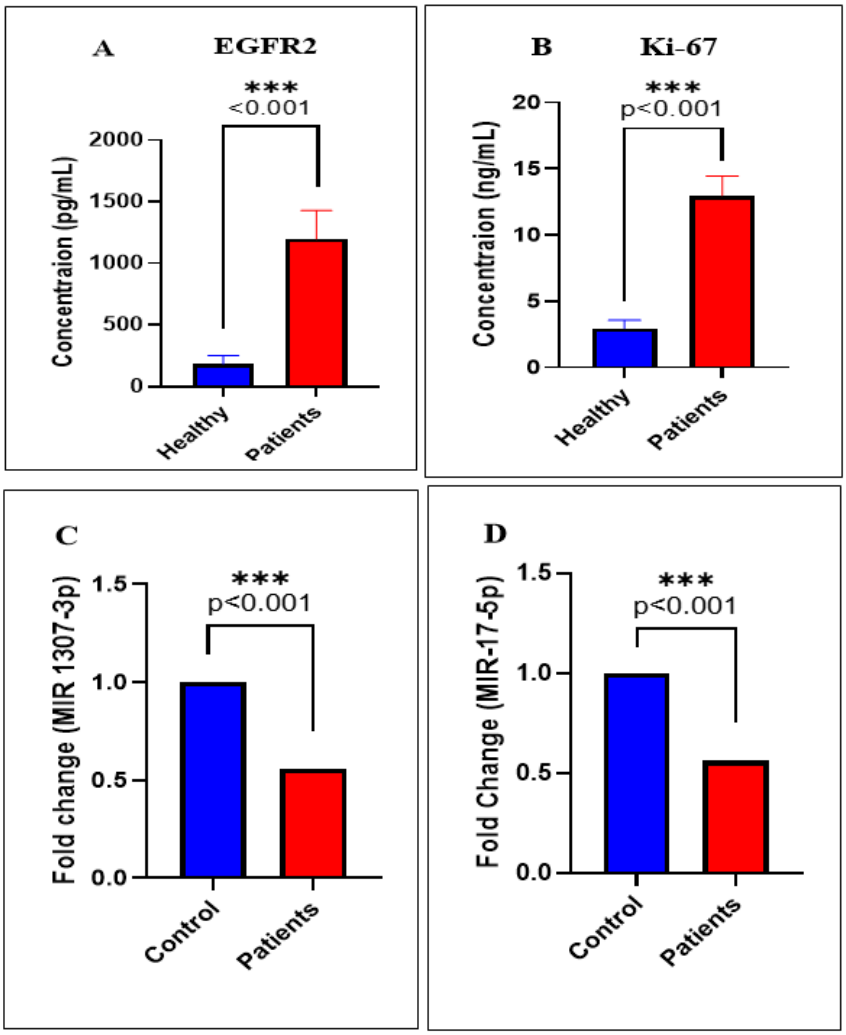

Figure 1. *Differential expression of serum biomarkers in breast cancer patients vs healthy controls. (A) Serum EGFR2 (pg/mL). (B) Serum Ki-67 (ng/mL). (C) miR-1307-3p relative expression (D) miR-17-5p relative expression.*

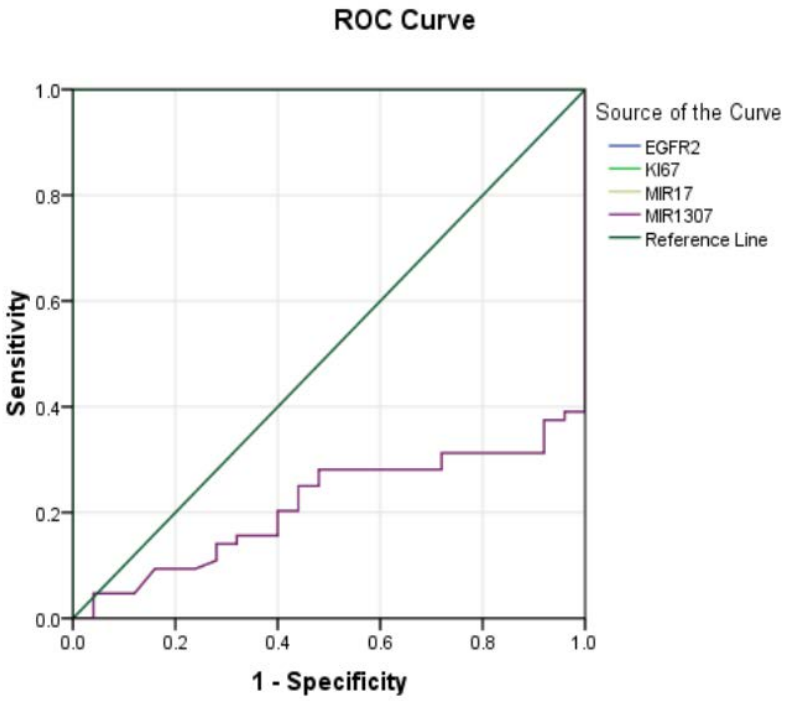

Figure 2. *The ROC Curve for study parameters levels in patients and control groups shows cut-off value, sensitivity, specificity, and area under the curve (AUC).*

The correlation analysis presented in Table 7 revealed several significant associations between protein markers and miRNAs in breast cancer. EGFR2 showed a strong positive correlation with Ki-67 (0.93, p = 0.001). *miRNA-17* and *miRNA-1307* also showed a strong positive correlation (0.97, p = 0.001). Negative correlations were observed between the miRNAs and the protein markers: *miRNA-17* and *miRNA-1307* have negatively correlated with EGFR2 and Ki-67, with correlations ranging from -0.38 to -0.4 (p = 0.001), indicating that lower expression of these miRNAs is associated with high levels of the protein markers.

Discussion.

The disease known as breast cancer is a complicated condition that encompasses several tumor types, each of which is distinguished by its own unique appearance, behavior, and clinical implications [18]. The marked increase in serum EGFR2 (HER2) and Ki-67 levels among breast cancer patients in this study aligns with their established roles as markers of tumor aggressiveness and poor prognosis.

Current data indicate that the level of EGFR2 was found to be significantly increased in patients with breast cancer compared to controls. EGFR family, particularly HER2 (also known as ERBB2), serves a vital function in the pathogenesis and progression of breast cancer [19]. The EGFR2 protein, when overexpressed, promotes cellular proliferation, survival, and angiogenesis through the activation of downstream signaling pathways such as PI3K/AKT and MAPK [20]. These pathways are frequently dysregulated in HER2-positive breast tumors, which are known for their aggressive behavior and poor prognosis if untreated [21]. Several previous studies also found the link between EGFR2 and breast cancer compared with controls, such as a study done by [22] found that plasma EGFR levels reliably reflect the HER2 disease status in patients with metastatic breast cancer, and this may help identify patients, even without visceral involvement, who could benefit from tailored sequential therapies. This supports the concept that serum EGFR2 measurements provide not only diagnostic value but may also contribute to treatment stratification in breast cancer patients, particularly in cases where tissue biopsies are impractical or inconclusive, particularly in patients receiving HER2-targeted treatment. Another study found elevated EGFR2 was correlated with positive estrogen receptor of tumor (ER+), and this finding supports to utilize of EGFR2 in personalised breast cancer therapy to enhance patient outcomes [23]. These results agreed with several previous studies that found that EGFR2 serum levels increase in breast cancer patients compared with controls [24].

EGFR2 levels were notably higher in lobular carcinoma (ILC) compared to IDC and mixed types. This suggests that lobular carcinoma may exhibit stronger HER2/EGFR2 signaling activity, which aligns with findings by [25], who reported that lobular carcinoma, though generally less HER2-amplified than IDC, can exhibit elevated HER2 expression in more aggressive subtypes or specific molecular contexts. Functionally, sHER2 reflects receptor shedding and may track tumor burden and treatment response; its clinical use as a circulating marker is supported by contemporary evidence [26]. Although ILC is typically HER2-negative by amplification, subsets exist with HER2-low expression or activating ERBB2 mutations, providing a biologic rationale for heightened HER2-pathway signaling in some ILCs [27]. hus, elevated sHER2/ECD in ILC may flag a biologically distinct subset (HER2-low or ERBB2-mutant) that warrants tissue confirmation (IHC/ISH) and cautious consideration of HER2-directed strategies in

appropriate contexts; validation in ILC-focused cohorts remains necessary [28].

About the effect of therapy on EGFR2 the serum EGFR2 extracellular domain (sHER2/ECD), effective systemic therapy often coincides with declining circulating ECD, whereas higher or rising sHER2 can be associated with tumor burden and poorer outcomes [29]. Recent clinical studies report that sHER2 tracks treatment efficacy and prognosis, including in advanced disease and in patients receiving HER2-directed agents. Our exploratory analyses showed only modest between-modality differences and no change in the direction of primary findings [29].

Similarly, this study indicated to increase significantly the serum level of Ki-67 in patients with breast cancer compared with controls. One of the most common markers in clinical cancer pathology is Ki-67, a nuclear protein that is present in all growing vertebrate cells [30]. Ki-67 is a marker for cell growth that is mostly used to forecast how well cancer will respond to treatment and how well it will progress. The Ki-67 index is a good way to measure how quickly breast cancer cells are growing [31]. The correlation between Ki-67 and the prognosis of breast cancer has been well investigated, such as [9,32]. Independent prognostic value of Ki-67 has been validated by studies, which have demonstrated that raised Ki-67 levels are associated with worse survival and higher recurrence rates in breast cancer [33]. A study done by [32] suggested that breast cancer has a poor prognosis due to the lack of hormonal therapeutic targets, and Ki-67 may be a biomarker for aggressive, metastatic cancer. Another study suggested that since Ki-67 indications vary by primary and metastatic lesion, they are important for therapy planning and prognosis [34]. Recent studies have begun to investigate circulating Ki-67 as a potential serum biomarker. For example, a study by [9] reported significantly higher serum Ki-67 levels in patients with invasive breast cancer compared to those with benign breast lesions, suggesting its utility in early differentiation. Also, this finding is supported by previous studies which reported that high Ki-67 values in breast cancer patients correlate well with the attainment of complete pathological response, and that Ki-67 may be incorporated into initial clinical assessment to predict chemotherapy effectiveness and response [35]. So, this study suggested the elevated serum Ki-67 levels in breast cancer patients observed in this study are consistent with previous findings and highlight the potential of Ki-67 as a serum-based indicator of tumor activity and this supports the hypothesis that serum Ki-67 reflects tumor proliferation dynamics and may serve as a valuable biomarker for diagnosis and potentially for monitoring therapeutic response.

Ki-67 levels were also significantly higher in lobular carcinoma than in IDC. Ki-67 is a well-established proliferation marker, and its elevated level in lobular type contradicts traditional views that lobular carcinoma is less proliferative than IDC. However, previous studies have shown that some lobular carcinomas can display high Ki-67 indices, especially in pleomorphic variants, indicating a more aggressive phenotype and worse prognosis [36,37]. Notably, aggressive ILC variants show elevated Ki-67 and poorer outcomes, aligning with our signal [38]. That said, some datasets report lower Ki-67 in classic ILC vs IDC, underscoring biological heterogeneity; our finding likely highlights a more proliferative ILC subset and supports closer follow-up and risk stratification, pending confirmation in larger, ILC-enriched cohorts [38].

About the effect of therapy on Ki-67 this study observed elevated or unchanged Ki-67 levels in a subset of patients following prior therapy. Multiple, non-mutually exclusive explanations are plausible such as early non-response or emergent resistance is evidenced by multiple studies indicating that Ki-67 does not consistently decline and may remain elevated or even increase in non-responders, correlating with poorer outcomes [39]. The second reason are sampling window effects related to treatment cycles may capture temporal fluctuations that reflect transient rebounds between cycles [40]. Other reason, tumor heterogeneity and therapy-driven clonal selection may favor the proliferation of more aggressive subclones [41]. Also, differences in assay and matrix (tissue versus circulating measures) introduce further variability [42]. In alignment with existing literature, the increased post-treatment Ki-67 levels in our cohort likely indicate residual proliferative activity rather than an artifact of measurement. Consequently, these findings with caution and highlight the necessity for standardized pre-/post-treatment time points and external validation in subsequent research [43].

In ROC analyses, serum HER2/ERBB2 (sHER2/ECD) and Ki-67 showed very high apparent discrimination. This study reports the exact AUC estimates with 95% confidence intervals, and interpret them cautiously given the limited sample size. The confidence intervals underscore residual uncertainty and do not justify claims of perfect accuracy. This study therefore regards serum HER2/ERBB2 (sHER2/ECD) and Ki-67 as a promising candidate, not a definitive diagnostic test. External validation in an independent cohort—together with calibration and decision-curve analysis is required before clinical adoption or patient stratification.

MiRNAs, naturally occurring RNA molecules, regulate cell cycle, proliferation, apoptosis, and migration [44]. In this study, *miR-17* was significantly downregulated in patients with breast cancer compared to controls. There have been reports in several studies that *miR-17* promotes cancer cell invasion and migration and is dysregulated in many malignancies [45,46]. Many tumorigenic mechanisms involve *miR-17*, including the *miR-17–19* family. This topic, related to cancer cell proliferation and apoptosis, has been studied extensively recently [12]. Previous studies showed that breast cancer tissues have higher *miR-17* levels than normal breast tissues. High *miR-17* expression may indicate a poor breast cancer outcome [47]. Overexpression of *miR-17* increased cell proliferation and tumour growth, and it was critically involved in the development of breast cancer; and showed promise as a biomarker for predicting the prognosis of breast cancer [48]. Also, a study by [49] has shown that *miR-17* promotes breast cancer cell migration by directly targeting and downregulating Netrin-4 (NTN4), a protein known to suppress tumor cell motility and invasion. There may be a connection between the biology of breast cancers that promotes progression and metastasis and dysregulated microRNAs [50]. Beyond treatment exposure, patient mix and biospecimen likely explain the discrepancy with tissue-based reports. Studies that

found higher *miR-17-5p* mostly analyzed tumor tissue collected pre-therapy [49], whereas we measured circulating miRNAs (serum/plasma) during/after therapy. miRNA profiles can differ by matrix (tissue vs circulating) and by subtype (ER/PR/HER2) [51]. Our cohort comprised unselected breast-cancer patients, and the sample size did not allow adequately powered, subtype-stratified testing. Pre-analytical/analytical factors (timing of sampling relative to treatment, hemolysis control, normalization) may also contribute [52]. Taken together, these contextual differences plausibly account for the lower circulating *miR-17-5p* observed here and warrant confirmation in pre-treatment, matrix-matched, subtype-stratified cohorts.

This study aligns with several previous studies, such as a study in a cell line, which found miR-17 was significantly downregulated in breast cancer patients compared to healthy controls and suggests that *miR-17* works as a tumor suppressor and oncogene by affecting cell proliferation in a cell-type-specific manner dependent on the cellular environment and target mRNAs [53]. Also, according to [54], *miR-17* was significantly downregulated in triple-negative breast cancer (TNBC) cell lines, suggesting that *miR-17* acts as a tumor suppressor in TNBC by targeting ETS variant transcription factor 1 (ETV1), and its low abundance may contribute to the pathogenesis of TNBC, indicating that *miR-17* may serve as a therapeutic target for TNBC. Another study reported that *miR-17* expression was decreased in breast cancer tissues, particularly in younger patients, and that elevating *miR-17* in vitro suppressed oncogenic mediators and enhanced immune recognition via UL16 Binding Protein 2 (ULBP2) induction [13]. So, this study suggested that the downregulation of *miR-17* from treated breast cancer patients may be attributed not only to the biological characteristics of the tumor but also to the effects of anticancer therapy.

In the current study, *miR-1307* exhibited a significant downregulation in patients with breast cancer compared to healthy controls. *miR-1307*, recently identified as a cancer-associated miRNA, is regarded as a risk factor for the progression of metastatic malignancies [14]. This marked decrease suggests a potential regulatory role for *miR-1307* in breast cancer pathogenesis. This downregulation was observed by a study that found the downregulation of *miR-1307* indicates a loss of tumor-suppressive function, contributing to drug resistance in breast cancer cells [55]. Under normal conditions, *miR-1307* negatively regulates the expression of Murine Double Minute 4 (MDM4), a key inhibitor of the tumor suppressor protein p53 [56]. Reduced levels of *miR-1307* lead to overexpression of MDM4, which in turn impairs apoptosis and allows cancer cells to survive despite chemotherapy treatment. Consequently, the downregulation of *miR-1307* is pivotal in chemoresistance and may function as a prospective diagnostic and therapeutic target in metastatic breast cancer [55]. Further research suggests that *miR-1307* may boost ovarian cancer chemoresistance by altering ING5 expression. Thus, miRNAs largely contribute to cancer treatment resistance [57].

On the other hand, this study disagreed with several studies reported overexpression of *miR-1307* in breast cancer, such as a study done by [15] has shown that overexpression of *miR-1307* in breast cancer can promote tumor cell proliferation, migration, invasion, and angiogenesis, indicating its oncogenic potential. These biological effects suggest that *miR-1307* contributes to tumor aggressiveness and progression by identifying Protamine 2 (PRM2) as a novel direct target of *miR-1307* in breast cancer, providing further insight into the molecular mechanisms through which this microRNA exerts its tumor-promoting effects. Other studies indicate *miR-1307* overexpression exerts its effects by directly targeting tumor suppressor genes such as SMYD4 and MDM4 [58]. While *miR-1307* overexpression has been associated with tumor progression and drug resistance, emerging data suggest that *miR-1307* exerts anti-angiogenic and tumor-suppressive functions. So, these opposing roles underscore the significance of miRNA arm selection and suggest that targeting the regulatory balance between *miR-1307* arms may offer novel therapeutic opportunities in breast cancer management [59]. Discrepancies likely reflect treatment exposure and sampling: studies reporting higher *miR-17-5p* sampled pre-therapy, whereas ours were during/after treatment; biospecimen type (tissue vs serum/plasma) and timing may also contribute.

The observed downregulation of *miR-1307* in serum supports its potential as a non-invasive biomarker for breast cancer detection or monitoring. Further validation studies are warranted to explore its subtype-specific behavior and predictive value in treatment response.

Despite prior therapy, circulating miRNA levels decreased in our cohort (including *miR-17-5p* and *miR-1307-3p*). The reduced tumor burden lowers tumor-derived miRNA release (free and vesicle-bound) [60], therapy can suppress transcription/processing programs that govern miRNA biogenesis and secretion [52]. Exosomal output may decline under cytotoxic or endocrine treatment, and systemic clearance (immune phagocytosis) may improve [61]. Sampling timing relative to treatment cycles can also capture transient dips. Future work with standardized pre/post-treatment time points is warranted to confirm trajectories and predictive utility.

The statistical analysis in grades and stages shows that there were no statistically significant differences in the serum levels of EGFR2 and Ki-67, or the expression levels of *miR-17* and *miR-1307*, across different tumour grades (I–III) and stages (I–IV) in breast cancer patients. This lack of significance shows that the levels of these biomarkers may not be directly linked to the grade or stage of the tumor's growth. This could be because of the effects of treatment, differences across patients, or the fact that these markers show the presence of cancer rather than its severity. Also, because the number of cases within each stratum was very small. Therefore, the non-significant results should be considered inconclusive, not evidence of no association. Future work should use larger, stratified cohorts with pre-specified power to reliably test grade/stage trends.

Positive correlation was observed between EGFR2 and Ki-67, indicating that elevated EGFR2 levels are closely linked to increased proliferative activity in breast cancer cells. This is consistent with previous studies reporting that HER2/EGFR2 overexpression is associated with high Ki-67 indices, aggressive tumor phenotypes, and poor clinical outcomes [62].

In contrast, both *miR-17* and *miR-1307* exhibited significant negative correlations with EGFR2 and Ki-67, suggesting that lower expression of these miRNAs is associated with increased oncogenic and proliferative activity of EGFR2 and Ki-67. This supports literature showing that *miR-17* may function as a tumor suppressor in certain breast cancer subtypes, particularly triple-negative cases, by targeting oncogenes such as ETS Variant Transcription Factor 1 ETV1 and inhibiting cell proliferation and migration [13,63].

Moreover, a perfect positive correlation between *miR-17* and *miR-1307* suggests that their expression levels are tightly co-regulated, possibly reflecting a shared upstream regulatory mechanism or involvement in common biological pathways. Co-regulation of miRNAs has been observed in cancer as a coordinated mechanism to modulate multiple targets simultaneously [64].

Conclusion.

This study demonstrated a significant increase in serum EGFR2 and Ki-67 levels among breast cancer patients, indicating enhanced tumor aggressiveness and proliferation. In contrast, the notable downregulation of *miR-17* and *miR-1307* suggests a loss of tumor-suppressive regulation. The strong inverse correlation between these miRNAs and the elevated protein markers highlights their potential as biomarkers for diagnosis and treatment monitoring in breast cancer.

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Data availability statement.

Underlying data

10.5281/zenodo.16952715[51] Maysoon RAWDATA 2025.xlsx contain raw data for the article.

Ethical Approval.

The study was carried out in line with the Declaration of Helsinki. The Ethics Committee of the University of Wasit, College of Science – Health Directorate (approval UW.Sci.2025.0723, July 23, 2025). All participants provided informed consent before enrollment.

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