



ROLE OF miRNA IN THE DIAGNOSIS AND PROGRESSION OF BREAST CANCER AMONG YOUNG AGE FEMALE POPULATION

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Abstract

Introduction: Breast cancer remains a formidable health challenge worldwide, impacting both the older and younger female populations.

Objectives: The main objective of the study is to find the role of miRNA in breast cancer detection at young age female population.

Material and methods: This study employed a retrospective cohort design to investigate the role of miRNA in the diagnosis and progression of breast cancer among young age female populations. Clinical and pathological data were collected from medical records, including patient demographics, tumor characteristics, histological subtypes, and disease stage. Blood samples were collected from each participant to extract miRNA for subsequent analysis.

Results: In the study investigating the role of miRNA-let-7 in the diagnosis and progression of breast cancer among young age female populations, a cohort of 120 participants aged 20 to 40 years was enrolled. Clinical and pathological characteristics were documented, and blood samples were collected for miRNA analysis. The participants' age distribution ranged from 20 to 40 years, with an average age of 32.5 years.

Conclusion: It is concluded that this study underscores the significance of miRNA-let-7 in breast cancer diagnosis and progression among young women. The observed downregulation and its correlation with disease severity suggest its potential utility as a diagnostic and prognostic biomarker.

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Introduction

Breast cancer remains a formidable health challenge worldwide, impacting both the older and younger female populations. The rising incidence of breast cancer cases among young women has prompted extensive research into uncovering the underlying mechanisms, risk factors, and potential diagnostic markers specific to this age group. The limitations of conventional diagnostic methods, such as mammography, in detecting breast cancer in younger women due to

denser breast tissue emphasize the need for novel approaches to early detection [1].

MicroRNAs (miRNAs) have emerged as promising candidates in the field of cancer research, including breast cancer. These small RNA molecules play a pivotal role in post-transcriptional gene regulation, influencing various cellular processes such as proliferation, apoptosis, and migration [2]. In breast cancer, miRNAs have been identified as key players in tumor initiation, progression, and metastasis. Their aberrant expression patterns in breast cancer tissues and



circulation make them attractive candidates for non-invasive diagnostic tools that could bridge the gap in early detection for young female patients. In developing countries, there is a great urge to initiate preventing measurements especially cancer screening [3]. Since 1970 mammography is used as a primary screening method for breast cancer. Due to less availability of mammography equipment, it is not widely available in under developed countries so they used Ultrasonography as an alternative method of screening³. Women having dense breast has a low sensitivity to mammography[4]. These women may have a high risk of breast cancer as compared to less dense breasts. In Denmark and Netherlands, researchers claim that every one of three women suffering from cancer is diagnosed with breast cancer. In recent years supplemental ultrasonography is considered the best screening method to detect more variations of breast cancer as compared to primary mammography [5].

MicroRNAs (miRNAs) are post-transcriptional regulators that bind to complementary sequences on target messenger RNA transcripts (mRNAs), usually resulting in translational repression or target degradation and gene silencing. Deregulation of many of the miRNA's expression has been linked to various types of disease. The expression of several miRNAs has been found to be deregulated in some types of cancer. High levels of some miRNA have been linked to stem cell promotion, while others exhibit a reduced expression of many, promoting loss of differentiation. Both are common traits in tumour development, but many other unknown underlying mechanisms could be affected [6].

Objectives

The main objective of the study is to find the role of miRNA in breast cancer detection at young age female population.

Material and methods

This study employed a retrospective cohort design to investigate the role of miRNA in the diagnosis and progression of breast cancer among young age female populations.

Study Population:

A total of 120 female participants, aged between 20 and 40 years, diagnosed with breast cancer, were included in this study. Ethical approval was obtained from the institutional review board.

Inclusion Criteria:

1. Female participants aged between 20 and 40 years.
2. Participants diagnosed with histologically confirmed breast cancer.
3. Participants with available medical records and complete clinical information.
4. Participants who provided informed consent for the study.

Exclusion Criteria:

1. Participants with incomplete medical records or missing clinical information.
2. Participants with a history of chronic inflammatory conditions or autoimmune disorders that could influence miRNA expression.
3. Participants who were pregnant or breastfeeding during the study period.
4. Participants who underwent neoadjuvant chemotherapy or radiation therapy prior to sample collection, as these treatments could affect miRNA expression profiles.
5. Participants with severe comorbidities or conditions that could confound the analysis or interpretation of results.

Data Collection:

Clinical and pathological data were collected from medical records, including patient demographics, tumor characteristics, histological subtypes, and disease stage. Blood samples were collected from each participant to extract miRNA for subsequent analysis.

miRNA Extraction and Profiling:

Total RNA, including miRNA, was extracted from blood samples using established protocols. The expression levels of specific miRNAs associated with breast cancer were measured using quantitative real-time polymerase chain reaction (qRT-PCR). The selection of miRNAs for analysis was based on previous literature and their known relevance to breast cancer.

Statistical Analysis:

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Descriptive statistics were used to summarize patient demographics and clinical characteristics. The expression levels of miRNAs were compared between different groups using appropriate statistical tests, such as t-tests or Mann-Whitney U tests.

Results

In the study investigating the role of miRNA-let-7 in the diagnosis and progression of breast cancer among young age female populations, a cohort of 120 participants aged 20 to 40 years was enrolled. Clinical and

pathological characteristics were documented, and blood samples were collected for miRNA analysis. The participants' age distribution ranged from 20 to 40 years, with an average age of 32.5 years. Histological subtypes of breast cancer included invasive ductal carcinoma, invasive lobular carcinoma, and others. Most participants were diagnosed at stages II and III, with varying tumor sizes and lymph node involvement. Hormone receptor status was also recorded.

Table 01: Demographic profile of patients

Characteristics	Mean Age	Histological Subtypes (%)	Disease Stage (%)
Age (years)	32.5	Invasive Ductal Carcinoma: 60% Invasive Lobular Carcinoma: 25% Others: 15%	Stage II: 45% Stage III: 40% Stage IV: 15%
Hormone Receptor Status (%)		Positive: 70% Negative: 30%	

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Table 02: Expression analysis of miRNA

Group	Expression Levels (qRT-PCR)	p-value
Breast Cancer	Downregulated	<0.05
Healthy Controls	Normal	

The expression levels of miRNA-let-7 were measured using qRT-PCR. Comparative analysis between breast cancer cases and healthy controls revealed significant downregulation of miRNA-let-7 in breast cancer patients ($p < 0.05$). ROC curve analysis indicated that miRNA-let-7 had an area under

the curve (AUC) of 0.80, signifying its potential diagnostic accuracy in distinguishing breast cancer cases from healthy controls among young women. Multivariate logistic regression analysis was performed to assess the relationship between miRNA-let-7 expression and disease progression.

Table 03: Diagnostic accuracy

Diagnostic Parameter	Area Under the Curve (AUC)
ROC Curve Analysis	0.80

Adjusting for potential confounders, the study found a significant negative association between miRNA-let-7 expression and disease progression (odds ratio = 0.43, 95% confidence interval: 0.21 - 0.89, $p = 0.022$).

Table 04: Association with diseases progression

Association Parameter	Odds Ratio	95% CI	p-value
miRNA-let-7 Expression	0.43	0.21 - 0.89	0.022

Discussion

The present study explored the role of miRNA-let-7 in the diagnosis and progression of breast cancer among young age female populations. The findings shed light on the potential diagnostic and prognostic value of miRNA-let-7 in identifying and monitoring breast cancer in this specific demographic. The discussion revolves around the

implications of the study's results, their alignment with existing literature, and the significance of miRNA-let-7 as a potential biomarker [7]. The downregulation of miRNA-let-7 in breast cancer cases observed in this study is consistent with previous research that has highlighted miRNA dysregulation as a common occurrence in cancer. Downregulated miRNAs are known to play a role in



tumorigenesis by regulating key genes involved in cell cycle control, apoptosis, and metastasis. In this context, the diminished expression of miRNA-let-7 is likely to contribute to the development and progression of breast cancer among young women. The study's results suggest that miRNA-let-7 holds promise as a diagnostic marker [8]. The ROC curve analysis demonstrated a reasonable AUC value, indicating that miRNA-let-7 could potentially discriminate between breast cancer cases and healthy controls with a satisfactory level of accuracy. This finding supports the notion that miRNAs can serve as non-invasive and easily detectable biomarkers for early cancer detection, particularly in young age populations where early diagnosis is crucial for improved outcomes [9]. The association between miRNA-let-7 expression and disease progression adds another layer of significance to its role. The observed negative association between miRNA-let-7 expression and disease progression suggests that lower miRNA-let-7 expression may be linked to a more aggressive disease course. This aligns with the hypothesis that miRNA-let-7 acts as a tumor suppressor, and its downregulation contributes to cancer progression. Importantly, the study contributes to the growing body of research addressing breast cancer among young women, a population that has distinct clinical characteristics and prognostic factors compared to older individuals [10]. The identification of miRNA-let-7 as a potential biomarker opens avenues for targeted interventions and personalized treatment strategies. Furthermore, the study underscores the value of miRNA analysis in understanding the molecular mechanisms underlying breast cancer in this demographic [11-13].

Conclusion

It is concluded that this study underscores the significance of miRNA-let-7 in breast cancer diagnosis and progression among young women. The observed downregulation and its correlation with disease severity suggest its potential utility as a diagnostic and prognostic biomarker. Further research is warranted to validate these findings and unravel the

underlying molecular mechanisms, with implications for improved breast cancer management.

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