Attahadi Medical Journal
2026;3(2):212-217
https://doi.org/10.69667/amj.26215

OPEN ACCESS

Original article

Comparative Analysis of Breast Cancer According to Age, Histological Type, Hormonal Status, and Disease Characteristics

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***Keywords**:*
Breast Cancer, Libyan Women, Invasive Ductal Carcinoma.

A B S T R A C T

Breast cancer (BC) is the most common cancer among women worldwide and a significant public health concern in Libya. The incidence of BC, particularly among younger women in Libya, has been increasing, urging further investigation into the disease's characteristics, early detection, and treatment strategies. This study aimed to compare the clinicopathological and molecular characteristics of breast cancer patients from two datasets of women of different ages. This descriptive retrospective study utilized two datasets containing the medical records of breast cancer patients diagnosed and treated at Tripoli Medical Center. Data were analyzed using descriptive statistics. The variables assessed included age, histological type, molecular subtype, tumor stage, hormone receptor status, lymph node metastasis, and family history of BC. Patients were divided into two age groups to facilitate comparison between young and older women. Frequency distribution and comparative analyses were performed to identify associations with predominant disease patterns. The first group of participants included 524 patients with a mean age of 34.5 years, while the second cohort included 499 patients with a mean age of 43.6 years. Younger women comprised the majority of the first cohort, while the second cohort exhibited a broader age distribution. The results showed that invasive ductal carcinoma (IDC) was the predominant histological pattern in both cohorts. Younger patients were more likely to have aggressive tumor characteristics, higher rates of lymph node metastasis, and more advanced disease stages. Older patients showed a higher prevalence of hormone receptor-positive tumors, particularly luminal molecular patterns, which are generally associated with a better prognosis. In conclusion, this comparative study demonstrates that age significantly influences the distribution of BC subtypes, disease severity, and tumor biology. These findings underscore the importance of increased public awareness about breast cancer causes, especially the effect of nutrition and lifestyle, early BC detection, and individualized treatment strategies to improve BC treatment outcomes.

Introduction

Breast cancer is the most commonly diagnosed cancer among women worldwide and one of the leading causes of cancer-related mortality. According to the World Health Organization (WHO), more than 2.3 million women were diagnosed with breast cancer globally in 2022, accounting for nearly one in four cancers among women (WHO, 2024). The burden of breast cancer continues to rise in low- and middle-income countries due to delayed diagnosis, limited screening programs, restricted access to treatment, and poor nutrition and lifestyle [1-4].

In the Middle East and North Africa region, breast cancer tends to present at a younger age than in Western populations. Studies conducted in Libya have shown that young patients present with advanced- stage disease and aggressive molecular subtypes. In Libya specifically, breast cancer is the most common malignancy among women, with incidence increasing over recent decades. Factors such as family history, hormonal receptor status, age at diagnosis, and molecular subtype play significant roles in determining prognosis and treatment outcomes [5-8].

The present comparative analysis evaluates two datasets containing information on breast cancer patients. The analysis focuses on age distribution, histological type, hormonal receptor status, molecular subtype, tumor stage, and disease characteristics. Comparisons between the datasets provide insight into patterns of breast cancer presentation and possible epidemiological differences between patient groups [9,10].

Methods

***Received**: 27-03-2026 - **Accepted**: 25-05-2026 - **Published**: 01-06-2026*

Attahadi Medical Journal
2026;3(2):212-217
https://doi.org/10.69667/amj.26215

Two datasets of breast cancer patient records were analyzed using descriptive statistics. Variables included age, histological type, molecular subtype, hormonal receptor status, tumor stage, lymph node involvement, and family history. Age groups were categorized to facilitate comparison between younger and older patient populations. Frequency distributions and comparative charts were generated to identify dominant disease patterns.

A descriptive and comparative statistical analysis was conducted to assess whether the two datasets differed significantly by age, histological type, molecular subtype, hormonal receptor profile, tumor category, lymph node status, family history, and metastatic or Stage IV status. Continuous age was compared using Welch's independent samples t-test because the two groups had different variances and age distributions. Categorical variables were compared using Pearson's chi-square test. A p-value was calculated, and results of p-value below 0.05 were considered statistically significant [11-13].

Results

Age Distribution

The first dataset included 524 patients with a mean age of 34.5 years (Figure 1), while the second dataset included 499 patients with a mean age of 43.6 years. The first dataset represented younger women, whereas the second dataset included a broader age distribution, including older patients, 60 years and older.

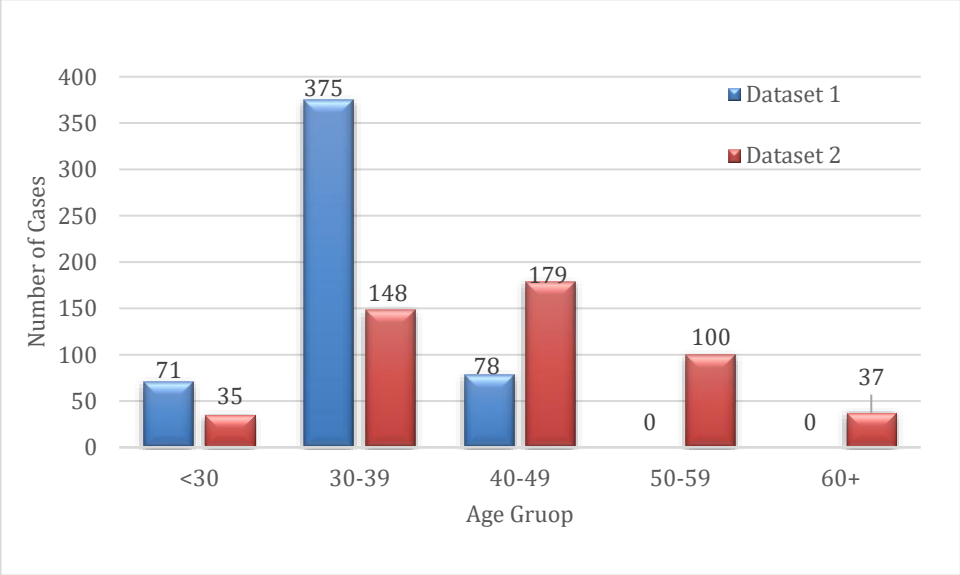

Figure 1. Age group comparison between the two datasets

Results showed that the age-group distribution was significantly variant between the two datasets ($p < 0.001$), with Dataset 1 concentrated mainly in the 30-39 group, while Dataset 2 showed a wider distribution across the 40-49, 50-59, and 60+ groups. Histological type also differed significantly ($p < 0.001$). IDC was the dominant type in both datasets; however, Dataset 1 contained a higher proportion of rare or non-ductal/non-lobular tumors compared with Dataset 2.

Molecular Subtypes and Hormonal Status

Hormonal receptor status and molecular subtype are important predictors of prognosis and therapeutic response in breast cancer. In Dataset 1, Luminal B and Basal-like tumors were among the most frequent subtypes. HER2-positive tumors were also observed in several younger patients. In Figure 2. Dataset 2 demonstrated a predominance of Luminal A tumors, suggesting a larger proportion of hormone receptor-positive disease.

Received*: 27-03-2026 -* ***Accepted****: 25-05-2026 -* ***Published****: 01-06-2026*

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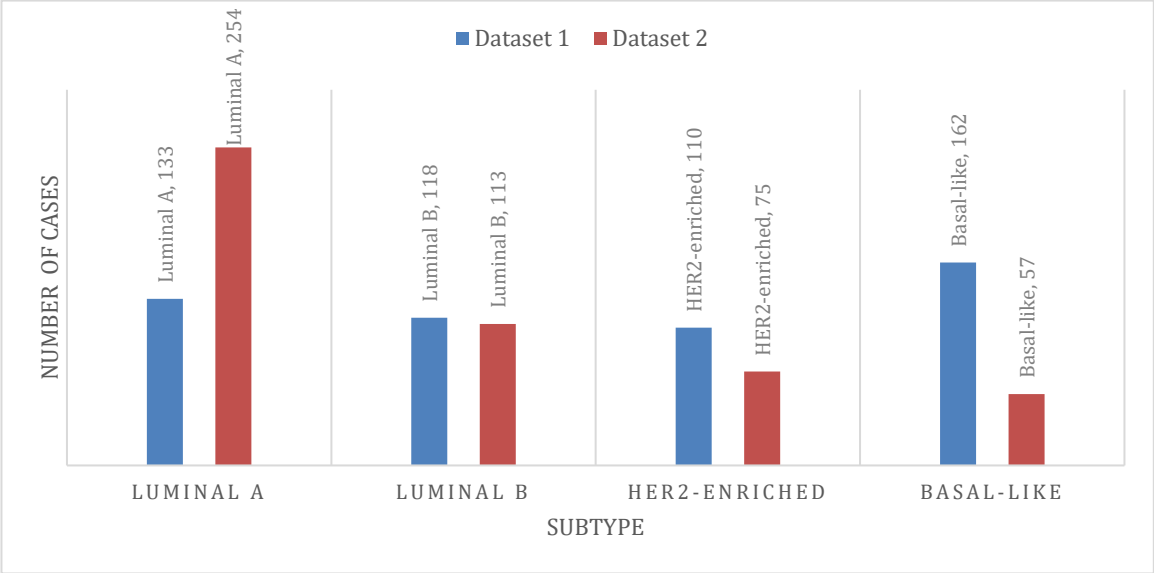

Figure 2. Molecular subtype distribution by dataset

Molecular subtype distribution showed statistically significant differences between the two datasets ($p < 0.001$). Dataset 1 had a higher frequency of Basal-like and HER2-enriched tumors, while Dataset 2 had a higher frequency of Luminal A tumors. This supports the interpretation that Dataset 1 contains a larger proportion of biologically aggressive breast cancer profiles [14-16].

Histological Types

In Table 1, the invasive ductal carcinoma (IDC) represented the dominant histological type in both datasets, consistent with global breast cancer epidemiology. Less common histological variants, such as invasive lobular carcinoma (ILC) and rare sarcomatous tumors, were also identified.

Table 1. Histological type distribution by dataset

Histological type	Dataset 1	Dataset 2
IDC	439	435
ILC	21	53
Other	63	11

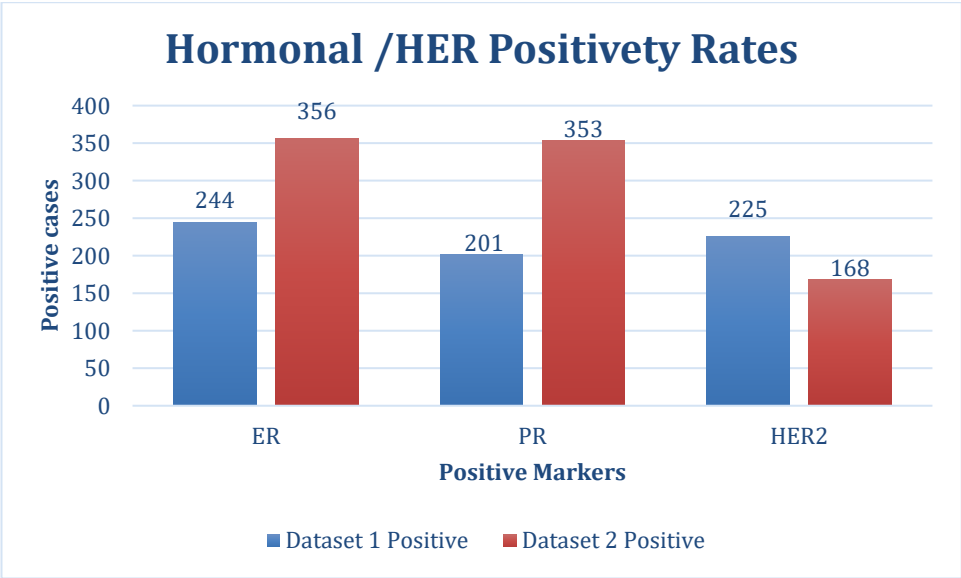

Figure 3. Hormonal Rates

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Table 2. Hormonal and HER2 receptor status by dataset

Category	Dataset 1 Positive	Dataset 1 Negative	Dataset 2 Positive	Dataset 2 Negative	P-value
ER	244	280	356	143	<0.001
PR	201	321	353	138	<0.001
HER2	225	297	168	288	0.054

Hormone receptor analysis also showed significant differences for ER and PR expression. In Table 2, ER positivity was significantly different between datasets (p <0.001), and PR positivity was also significantly different (p <0.001). HER2 status approached significance but did not meet the conventional 0.05 threshold (p = 0.054). These results suggest that Dataset 2 contains a higher proportion of hormone receptor-positive tumors, whereas Dataset 1 contains relatively more hormone receptor-negative disease.
Table 3 showed that the tumor size category differed significantly between the datasets (p <0.001), with Dataset 2 showing a high proportion of T2 tumors and Dataset 1 showing relatively more T3 and T4 tumors. Lymph node status was also significantly different (p <0.001), with Dataset 1 having a higher proportion of node-positive cases. Family history differed significantly as well (p <0.001). A crude comparison of metastatic or Stage IV status also showed a significant difference (p <0.001); however, this result should be interpreted carefully because Dataset 1 records metastasis using the M category, while Dataset 2 records Stage IV status via overall staging.

Table 3. Tumor category, lymph node status, family history, and metastatic/Stage IV comparison

Category	Dataset 1	Dataset 2	P-value
Tumor category	T1: 137, T2: 170, T3: 156, T4: 61	T1: 71, T2: 289, T3: 129, T4: 10	<0.001
Lymph node status	Positive: 423, Negative: 98	Positive: 316, Negative: 183	<0.001
Family history	Yes: 120, No: 404	Yes: 171, No: 328	<0.001
Metastatic/Stage IV	Metastatic/Stage IV: 84, Non-metastatic: 430	Metastatic/Stage IV: 20, Non-metastatic: 476	<0.001

Overall, the p-value analysis confirms that the two datasets are not statistically similar in several key clinical dimensions. Among the most important differences observed between different ages are molecular subtype, estrogen/progesterone receptor status, tumor class, tumor spread to lymph nodes, and metastatic tumor status or stage IV (Table 3). These differences are clinically relevant because younger age, Basal-like subtype, HER2-enriched subtype, hormone receptor negativity, lymph node involvement, and higher tumor category are usually associated with more aggressive disease behavior and may influence treatment planning and prognosis.

Table 4. Statistical comparison between Dataset 1 and Dataset 2

Category	Variable	Statistical test	Comparison	P-value	Interpretation
1	Age	Welch's independent samples t-test	34.5 vs 43.6 years	<0.001	Significant
2	Age group	Chi-square test	Age-category distribution	<0.001	Significant
3	Histological type	Chi-square test	IDC / ILC / Other	<0.001	Significant
4	Molecular subtype	Chi-square test	Luminal A / Luminal B / HER2-enriched / Basal-like	<0.001	Significant
5	ER status	Chi-square test	Positive vs Negative	<0.001	Significant
6	PR status	Chi-square test	Positive vs Negative	<0.001	Significant
7	HER2 status	Chi-square test	Positive vs Negative	0.054	Not significant at 0.05
8	Tumor size category	Chi-square test	T1 / T2 / T3 / T4	<0.001	Significant
9	Lymph node status	Chi-square test	Positive vs Negative	<0.001	Significant

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10	Family history	Chi-square test	Yes vs No	<0.001	Significant
11	Metastatic / Stage IV status	Chi-square test	Dataset 1 M1 vs Dataset 2 Stage IV	<0.001	Significant

Dataset 1 included 524 records, and Dataset 2 included 499 records. The mean age in Dataset 1 was 34.5 years compared with 43.6 years in Dataset 2. This difference was statistically significant (p <0.001) in Table 4, indicating that Dataset 1 represents a substantially younger patient group.

Discussion

The comparison of the two datasets reveals important differences in breast cancer presentation by age and tumor biology. Younger patients in Dataset 1 had a higher frequency of aggressive molecular subtypes, including HER2-enriched and Basal-like cancers, which are generally associated with poorer prognosis. In contrast, Dataset 2 included older patients with a higher proportion of Luminal A tumors, typically associated with better prognosis and responsiveness to hormonal therapy. This aligns with the latest scientific information on breast cancer in young women, highlighting the heterogeneity and complexity of this type of cancer [5, 17,18, 24, 25]. The findings are consistent with published literature indicating that younger women are more likely to present with aggressive disease characteristics and advanced stages at diagnosis. The predominance of IDC in both datasets also aligns with international breast cancer trends.

The statistically significant p-values identified in the present analysis have strengthened the reliability of the observed correlation between age, hormonal status, tumor subtype, and disease characteristics. These findings support the hypothesis that biological and molecular differences in breast cancer are strongly influenced by patient age and hormonal receptor expression patterns.

Compared with international data, the present study suggests that Libyan breast cancer patients may present at younger ages and with more aggressive molecular characteristics. Similar observations have been reported in some other Arab and African countries. Such findings highlight the necessity of providing earlier detection programs, improved screening strategies, and enhanced public awareness campaigns focusing on breast cancer risk factors and early symptoms in these countries [19, 23]. The findings of the present study are particularly important within the Libyan context, where breast cancer remains the most common malignancy among women and where tardy diagnosis continues to be a major healthcare challenge. Previous Libyan studies have shown that many patients present at advanced stages and with larger tumor sizes compared with patients in developed countries. Delayed medical consultation, restricted screening programs, and limited awareness regarding breast cancer symptoms may contribute to these observations.

Hormone receptor analysis revealed significant differences between the datasets. Hormone receptor-positive tumors were more common among older women, while hormone receptor-negative tumors were relatively more prevalent among younger patients. This pattern has important therapeutic implications, as hormone receptor-positive tumors are generally associated with a better response to hormone therapy and higher survival rates [26, 27].

The current analysis also revealed statistically significant associations between age group and molecular subtype distribution ($p<0.05$). Younger patients were more likely to have HER2-positive and basal cell-like tumors, while Luminal A tumors were more common among older patients. These findings are consistent with studies by Carey et al. (2006) and Foulks et al. (2010), who reported that triple-negative and HER2-rich breast cancers are more common in younger women and are associated with a more aggressive clinical presentation [20, 21, 25]. Invasive ductal carcinoma was the predominant histological pattern in both datasets, consistent with global breast cancer epidemiology. Previous studies by Sung et al. (2021) and Harbeck et al. (2019) have indicated that invasive ductal carcinoma is the most common breast cancer subtype worldwide. The significant prevalence of invasive ductal carcinoma in this study corroborates previous regional findings from North Africa and the Middle East [3, 9, 22, 28, 29].

Conclusion

This comparative analysis highlights the influence of age on breast cancer subtype distribution, hormonal receptor status, and disease aggressiveness. Younger patients demonstrated more aggressive tumor biology, whereas older patients showed higher rates of hormone receptor-positive disease. These findings emphasize the importance of early detection, individualized treatment strategies, and improved screening programs in Libya. Overall, the results of this study contribute important preliminary epidemiological information regarding breast cancer characteristics among Libyan patients. Further studies with larger multisource datasets and survival analysis are recommended to better understand prognostic outcomes and optimize individual treatment strategies.

Received*: 27-03-2026 -* ***Accepted****: 25-05-2026 -* ***Published****: 01-06-2026*

Acknowledgments
The authors wish to express their sincere gratitude to Tripoli Hospital for their cooperation and commitment to this research.

Conflicts of Interest
The authors declare no conflicts of interest.

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Received*: 27-03-2026 -* ***Accepted****: 25-05-2026 -* ***Published****: 01-06-2026*