EGYPTIAN JOURNAL OF CANCER AND BIOMEDICAL RESEARCH (EJCBR)

ORIGINAL ARTICLE

Immunohistochemical Expression of *L1CAM* in Breast Carcinoma: A Clinicopathological Study

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ABSTRACT

Background: Breast carcinoma is a multifactorial disease showing definite molecular subtypes, with specific clinical, pathological, and molecular characteristics. The L1 cell adhesion molecule (L1CAM), one of the immunoglobulin superfamily of cell adhesion molecules, is overexpressed in many carcinomas. Although much research has shown that carcinomas expressing L1CAM have a bad prognosis, the contribution of L1CAM to breast carcinoma has not been completely established. **Aim:** The present study aimed to investigate L1CAM expression in breast carcinoma and its correlation with clinicopathological parameters. **Material and Methods:** This retrospective cohort study was conducted on 100 cases of invasive breast carcinoma retrieved from the archives of the Pathology Laboratory at Mansoura University Oncology Center between 2013 and 2018. Patients' clinical and pathological data were revised. Immunohistochemical staining for L1CAM was performed, and clinicopathological correlation was statistically analyzed. **Results:** L1CAM expression was negative in 10%, weakly positive in 16%, moderately positive in 41%, and strongly positive in 33% of the studied cases. There was no statistically significant relation between L1CAM expression and age, morphological type, tumor grade, tumor size, lymph node status, stage, recurrence, ER, PR, or HER2/neu. However, we found statistically significant relations between strong L1CAM expression and luminal A subtype, as well as between moderate L1CAM expression and luminal B subtype. In contrast, no statistically significant relation was found between L1CAM expression and either HER2-enriched or triple-negative subtypes. **Conclusion:** Our results of L1CAM expression in breast carcinoma call for further attention to its role and prognostic significance in breast cancer.

Keywords: Breast carcinoma, Clinicopathological, Immunohistochemistry, L1CAM

Editor-in-Chief: Prof. M.L. Salem, PhD - Article DOI: 10.21608/jcbr.2025.376670.1399

ARTICLE INFO

Article history
Received: June 05, 2025
Revised: June 28, 2025
Accepted: July 15, 2025

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INTRODUCTION

Breast cancer (BC) is the most common malignant tumor among females all over the world (Kim et al., 2018). It represents 25% of female malignancies worldwide and is regarded as the fifth main cause of death from cancer in females, after lung, colorectal, liver, and stomach cancers (Bray et al., 2024). Breast carcinoma is a multifactorial disease showing definite molecular subtypes, with specific clinical, pathological, and molecular characteristics (Li et al., 2023).

The L1 cell adhesion molecule (L1CAM), one of the immunoglobulin superfamily of cell adhesion molecules, is a transmembrane glycoprotein that has an essential role in terms of nervous system development. L1CAM overexpression was found in several human carcinomas, with accumulating evidence supporting its role in metastasis, pro-angiogenesis, and chemotherapy resistance (Hua et al., 2016; Zhang et al., 2024). It was first reported as a potent prognostic factor for metastases in malignant melanoma (Schrevel et al., 2017).

Although prior and recent studies have shown that carcinomas expressing L1CAM have a poor prognosis (Doberstein et al., 2014; Zhang et al., 2024). The contribution of L1CAM to BC has not been completely established (Moisini et al., 2021). Given that BC morbidity and mortality rates are consistently rising in Egypt (Azim et al., 2023), this retrospective study aimed to assess L1CAM expression in BC and its relationship with different clinicopathological variables.

Material AND METHODS

Study design

This retrospective cohort study was conducted on 100 cases of invasive breast carcinoma retrieved from the archives of the Pathology Laboratory at Mansoura University Oncology Center between 2013 and 2018. The IRB (MFM-IRB) of this study was assessed and approved (Code No. MS.18.07.195) by the Institutional Ethical Committee at the Faculty of Medicine, Mansoura University. The study included patients who underwent a modified radical mastectomy or localized excision.

Inclusion and exclusion criteria:

The study included cases of breast carcinomas diagnosed between 2013 and 2018 with complete clinical data, available hormonal receptors and HER2/neu status, accessible medical reports, and

corresponding paraffin tissue blocks. Cases with incomplete clinical data, unavailable hormonal receptor status or HER2/neu results, or missing paraffin tissue blocks were excluded from the study .

Clinical parameters and histopathological evaluation:

The pathology reports, hematoxylin and eosin (H&E) stained sections, and immunohistochemical (IHC) stained slides for ER, PR, Ki-67, and HER2/neu of the included cases were systematically reviewed to assess the clinicopathological features, including patient age, tumor laterality, histological type according to the 2019 WHO classification of breast carcinomas, tumor size, lymph node status, hormone receptor profile, HER2/neu expression, and tumor grade based on the Nottingham modification of the Bloom–Richardson grading system. The AJCC system was utilized as a reference for staging. Data on distant metastasis or local recurrence were extracted from electronic medical records. Molecular classification into Luminal A (ER-positive, PR-positive, HER2-negative, Ki67 proliferative index <20%), Luminal B (HER2-negative: ER-positive, PR-negative/low, HER2-negative, Ki67 proliferative index ≥20%, and HER2-positive: ER-positive, PR-positive or negative, HER2-positive, Ki67 proliferative index variable), triple negative (ER-negative, PR-negative, HER2-negative), and HER2-enriched (ERBB2 positive) was done .

Tissue microarray (TMA) Construction:

After reviewing the H&E-stained slides, a representative slide was selected for each case. Well-preserved areas with the highest tumor cellularity were identified, and the corresponding paraffin block was retrieved from the archive. Tissue microarray (TMA) construction was performed manually as described by Shebl et al. (2011). From each donor block, three cores were punched and arranged horizontally in the recipient block (Foda, 2013). Six TMA blocks were constructed.

Immunohistochemical staining procedure:

Tissue sections (4 µm thick) were cut from the constructed microarray blocks. Deparaffinization, rehydration, and antigen retrieval were subsequently performed using the DAKO PT-Link system. IHC staining was performed using the DAKO Autostainer Link 48. The primary antibody employed was a rabbit polyclonal anti-L1CAM (150 kDa subunit; GTX129010, GeneTex, North America, Inc., USA), applied at a dilution of 1:200.

Immunohistochemical analysis:

L1CAM positive expression was defined as brown membranous and, in part, cytoplasmic staining in tumor cells (Wu et al., 2018). High-grade serous carcinoma was used as a positive control to ensure appropriate staining intensity and localization, while the negative control was processed by omitting the primary antibody to confirm specificity. Immunohistochemical assessment of L1CAM was independently conducted by two qualified pathologists blinded to the patients' data. The scoring percentage of positively stained tumor cells was as follows: 0 (0%), 1 (1-10%), 2 (11-50%), and 3 (>50%). The staining intensity was visually scored as follows: zero (negative), I (weak), II (moderate), and III (strong). The final immunoreactive score (IRS) was calculated by multiplying the intensity values by the percentage (Zhang et al., 2015). L1CAM expression was subsequently modified in IRS, and categorized as follows: score 0: negative, scores 1–3: weakly positive, scores 4–6: moderately positive, and scores 7–9: strongly positive.

Statistical analysis

Data were analyzed using SPSS software, version 21 (IBM Corp., Armonk, NY, USA). The Kolmogorov-Smirnov test was applied to assess the normality of data distribution. Qualitative variables were described as frequencies and percentages, while continuous variables were expressed as mean ± standard deviation (SD). A p-value <0.05 was considered statistically significant. Comparisons of categorical variables between groups were performed using the Chi-square test. When more than 25% of cells had an expected count below five, Fisher's exact test and the Monte Carlo test were applied as appropriate corrections. For parametric quantitative data, comparisons between two groups were conducted using the student's t-test, whereas comparisons across more than two groups were performed using analysis of variance (ANOVA).

RESULTS

This retrospective study comprised 100 cases of invasive breast carcinoma retrieved from the archives of the Surgical Pathology Laboratory at Mansoura Oncology Center between 2013 and 2018. The clinicopathological characteristics of these cases are summarized in Table 1.

The mean patient age was 56.53 ± 11.98 years. Invasive ductal carcinoma of no special type (IDC-NST) was the predominant histological subtype, accounting for 88% of cases, followed by invasive lobular carcinoma (ILC) (8%). Mucinous carcinoma was identified in three cases, whereas a single case of metaplastic carcinoma was included.

L1CAM immunohistochemical expression was negative in 10% of cases, weak in 16%, moderate in 41%, and strong in 33% (Figures 1–4). Table 2 outlines the association between L1CAM expression and various clinicopathological parameters.

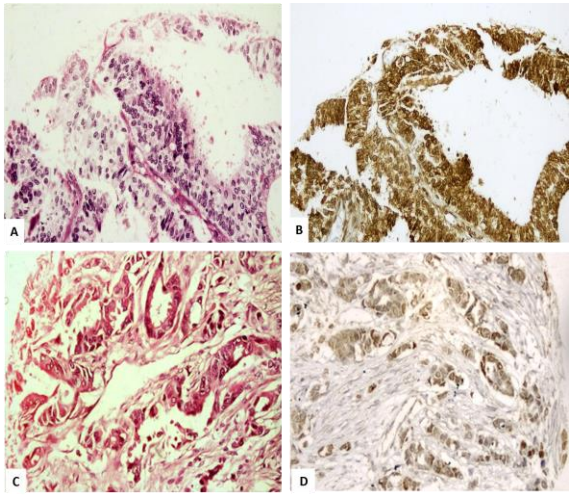

Figure 1: A: Grade I infiltrating ductal carcinoma (H&E x400). **B:** Strong membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score 3x3=9) (L1CAM x400). **C:** Grade I infiltrating ductal carcinoma (H&E x400). **D:** Weak membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score 1x3=3) (L1CAM x400).

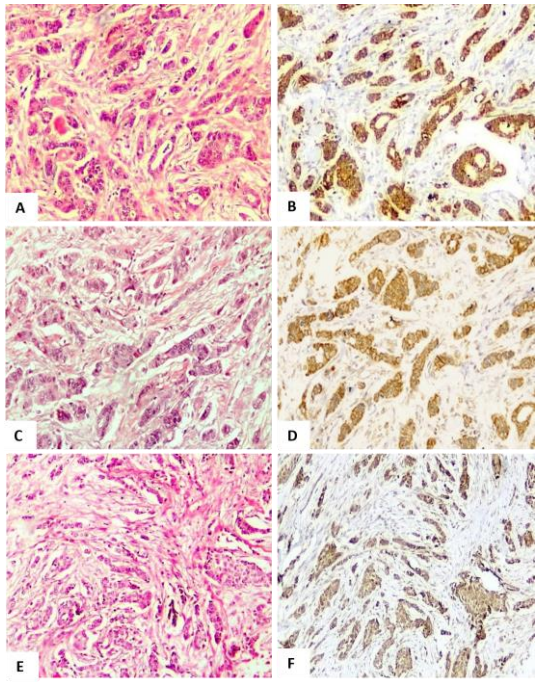

Figure 2: **A**: Grade II infiltrating ductal carcinoma (H&E x400). **B:** Strong membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score 3x3=9) (L1CAM x400). **C:** Grade II infiltrating ductal carcinoma (H&E x400). **D**: Moderate membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score 2x3=6) (L1CAM x400). **E:** Grade II infiltrating ductal carcinoma (H&E x400). **F:** Weak membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score 1x3= 3) (L1CAM x400).

No significant association was found between L1CAM expression and age, histological type, tumor grade, tumor size, lymph node status, or disease stage. The correlation of L1CAM expression with ER, PR, or HER2/neu status was insignificant. Moreover, no significant relation was observed between L1CAM expression and neoadjuvant therapy or recurrence. With respect to the molecular classification of breast carcinoma, our study revealed a significant association between strong L1CAM expression and the luminal A subtype (p=0.009), as well as between moderate L1CAM expression and the luminal B subtype (p=0.04). Meanwhile, there was insignificant relation between the L1CAM score and HER2-enriched or triple-negative subtypes (P=0.85 and 0.17; respectively).

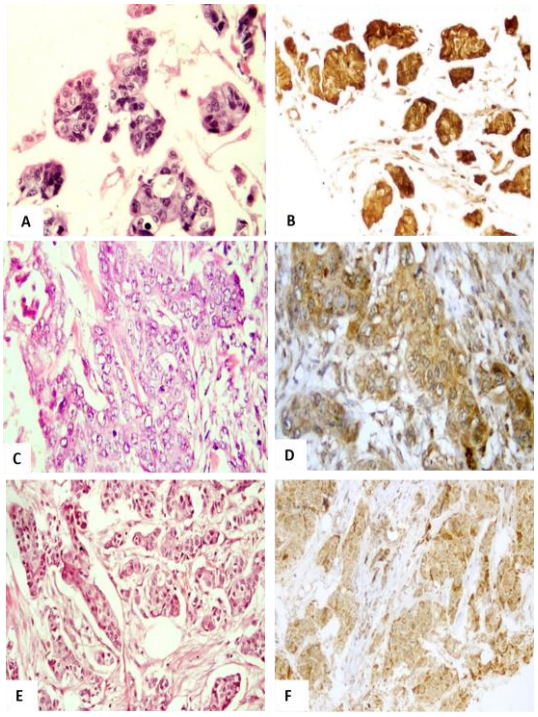

Figure 3: A: Grade III infiltrating ductal carcinoma (H&E x400). **B:** Strong membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score3x3=9) (L1CAM x400). **C:** Grade III infiltrating duct carcinoma (H&E x400). **D:** Moderate membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score 2x3=6) (L1CAM x400). **E:** Grade III infiltrating duct carcinoma (H&E x400). **F:** Weak membranous and cytoplasmic reaction of L1CAM in 10-50% of tumor cells (score2x2=4) (L1CAM x400).

DISCUSSION

Invasive breast carcinoma isn't a single entity but is considered a heterogeneous group with definite pathological and molecular features and highly variable clinical behavior (Provenzano et al., 2018). Advances in molecular technologies have led to the transition from pure morphological to combined histologic and molecular classifications (Pareja and D'Alfonso, 2020).

It has been demonstrated that L1CAM is comprised in every stage of the development of cancer (Tangen et al., 2017). L1CAM may be a talented novel target molecule for antibody-based therapy of malignant tumors (Altevogt et al., 2016). This study aimed to assess the IHC expression of L1CAM in invasive breast carcinomas and to investigate its association with various clinicopathological parameters of the examined cases. Our retrospective cohort study included 100 cases of invasive breast carcinoma, of which 90%

demonstrated positive L1CAM expression, while 10% were negative. Similarly, Abou Gabal et al. (2016) reported L1CAM positivity in 89% of their cases. In contrast, Wu et al. (2018) detected positive L1CAM expression in only 24.1% of cases, while Gwak et al. (2017) reported positivity in just 2.3% of cases.

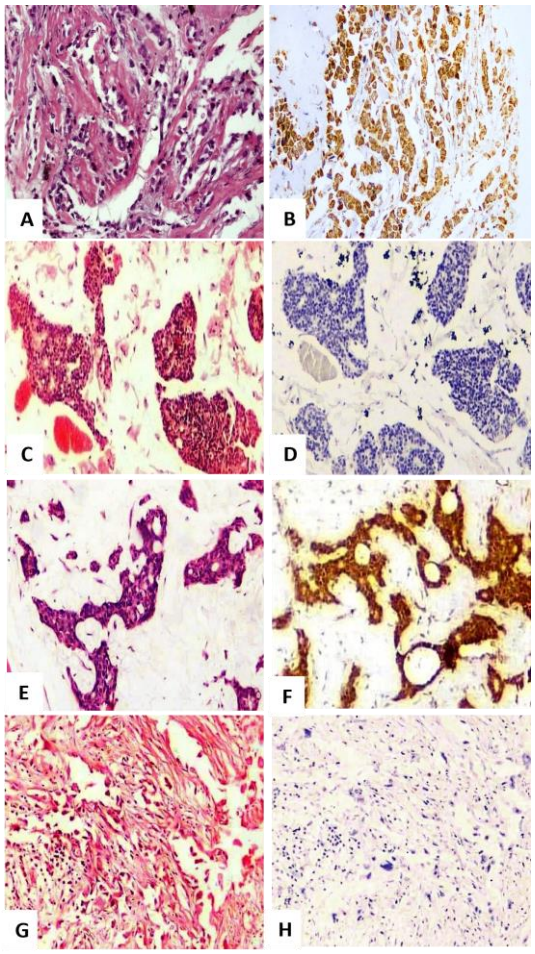

Figure 4. A: Invasive lobular carcinoma showing Indian file pattern (H&E x400). **B:** Moderate membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score 2x3= 6) (L1CAM x400). **C:** Mucinous carcinoma (H&E x400). **D:** Negative reaction of L1CAM score 0 (L1CAM x400). **E:** Mucinous carcinoma (H&E x400). **F:** Strong membranous and cytoplasmic reaction of L1CAM in >50% of tumor cells (score 3x3= 9) (L1CAM x400). **G:** Metaplastic carcinoma showing glandular and spindle cell components (H&E x400). **H:** Negative reaction of L1CAM score 0 (IHC x400).

Our retrospective cohort study included 100 cases of invasive breast carcinoma, of which 90% demonstrated positive L1CAM expression, while 10% were negative. Similarly, Abou Gabal et al. (2016) reported L1CAM positivity in 89% of their cases. In contrast, Wu et al. (2018) detected positive L1CAM expression in only 24.1% of cases, while Gwak et al. (2017) reported positivity in just 2.3% of cases. The discrepancy in the percentage of L1CAM expression may be justified by several reasons, including differences in detection techniques, e.g., IHC, western blot analysis, protein extraction, and cell culture.

Table 1: Clinicopathological features of the studied cases

Clinicopathological features	The study group (n=100)
Histopathological Type	
IDC-NST	88 (88%)
ILC	8 (8%)
Mucinous	3 (3%)
Metaplastic	1 (1%)
***Grade (n=88)**	
G1	4 (4.5%)
G2	65 (73.9%)
G3	19 (21.6%)
Tumor size	
T1	17 (17%)
T2	59 (59%)
T3	21 (21%)
T4	3 (3%)
LN status	23(23%)
Negative	77 (77%)
Positive	
TNM staging	
I	8 (8%)
II	46(46%)
III	45(45%)
IV	1 (1%)
ER	
Positive	77 (77%)
Negative	23 (23%)
PR	
Positive	70 (70%)
Negative	30 (30%)
HER2neu	
Positive	32 (32%)
Negative	58 (58%)
Equivocal	10 (10%)
Molecular classification	
Luminal A	57 (57%)
Luminal B	20 (20%)
Her2 positive	15 (15%)
Triple-negative	8 (8%)
Neoadjuvant therapy	
Positive	70 (70%)
Negative	30 (30%)
Recurrence/metastasis	24 (24%)
Positive	76 (76%)
Negative	

IDC-NST: Invasive ductal carcinoma-No special type, ILC: Invasive lobular carcinoma, G: Grade; T: Tumor; LN: Lymph node; TNM: Tumor, node and metastasis; ER: Estrogen receptors; PR: Progesterone receptors; HER2neu: Human epidermal growth factor receptor 2. *Grading was applied only to IDC-NST cases (n=88), as established grading systems are not applicable to special histological subtypes such as lobular, mucinous, or metaplastic carcinoma.

The discrepancy in the percentage of L1CAM expression may be justified by several reasons, including differences in detection techniques, e.g., IHC, western blot analysis, protein extraction, and cell culture. In addition, various technical factors such as differences in IHC protocols, microarray analysis, and positivity cut-off of L1CAM expression may also contribute. Moisini et al. (2021) in their study considered L1CAM positive when ten percent or more of tumor cells exhibit membranous staining, while Zhang et al. (2015), Wu et al. (2018), and our study considered L1CAM expressed on the cell membrane and partly in the cytoplasm as a

positive feature. Moreover, inter-observer variability in interpretation, differences in sample sizes, and variations in hormonal and HER2/neu status among the cases contribute to the difficulty in comparing L1CAM expression results across various research studies .

With respect to patient age, our study demonstrated no significant association between L1CAM expression and age. This finding is consistent with the results of Schröder et al. (2009), who also reported the absence of a significant correlation. Conversely, Moisini et al. (2021) documented a significant association, noting higher L1CAM expression in patients diagnosed at a younger age.

In our study, no significant association was observed between L1CAM expression and the histopathological type of invasive breast carcinoma, consistent with the findings reported by Abou Gabal et al. (2016), Wu et al. (2018), and Moisini et al. (2021).

Our findings showed no significant association between L1CAM expression and tumor grade. This contrasts with the results of Abou Gabal et al. (2016) and Wu et al. (2018), who reported a significant positive correlation between L1CAM expression and higher tumor grades. Such discrepancies may be explained, at least in part, by inter-observer variability in the microscopic grading of invasive ductal carcinoma.

With respect to tumor size, our study demonstrated no significant association between L1CAM expression and tumor size. This finding is consistent with the results of Abou Gabal et al. (2016), Wu et al. (2018), and Moisini et al. (2021), who also reported a lack of significant correlation between these parameters.

Regarding nodal involvement, our study did not identify any significant association between L1CAM expression and lymph node status. This finding is in line with the results of Moisini et al. (2021). In contrast, Abou Gabal et al. (2016) reported a significant association between L1CAM expression and lymph node metastasis. Such discrepancies may be explained by differences in sample size as well as variations in the categorization of lymph node involvement across studies.

Our study demonstrated no significant association between L1CAM expression and TNM stage. This finding is consistent with the results of Moisini et al. (2021), yet contrasts with the studies of Zhang et al. (2015) and Wu et al. (2018), which reported a significant correlation between L1CAM expression and TNM stage. Such discrepancies may be attributed to differences in sample size and the heterogeneity in the nature of the studied cohorts.

Our study displayed no significant association between L1CAM expression and ER, PR, or HER2/neu status. Consistently, Wu et al. (2018) also reported the absence of a statistically significant relationship between L1CAM expression and these receptors. As regards the molecular classification of the studied cases, our results revealed a significant correlation between strong L1CAM expression and the luminal A subtype, as well as between moderate L1CAM expression and the luminal B subtype.

The significant association between L1CAM expression and the luminal B subtype, which is characterized by more aggressive biological behavior and poorer clinical outcomes compared to luminal A, supports the proposed role of L1CAM in tumor progression. These findings are consistent with those of Moisini et al. (2021), who reported that all L1CAM-positive recurrent or metastatic cases belonged to the luminal B subtype.

Interestingly, the presence of strong L1CAM expression in some Luminal A cases, which are typically considered low risk, may suggest the existence of a more aggressive subset within this group, despite otherwise favorable profile.

This may explain the variability in clinical outcomes observed within the same molecular subtype. Furthermore, these findings could have important clinical implications for refining risk stratification, optimizing follow-up protocols, and potentially guiding the development of targeted therapies in hormone receptor-positive breast cancer.

Meanwhile, our study demonstrated no significant association between the L1CAM expression and either the HER2-enriched or triple-negative subtypes. Similarly, Wu et al. (2018) reported no significant correlation between L1CAM expression and molecular subtypes. However, they observed a significant relationship between soluble L1CAM (sL1) and both the HER2-enriched and triple-negative subtypes. This discrepancy may be explained by differences in the assessment methods of hormonal receptor IHC expression.

Wu et al. (2018) defined ER and PR positivity as immunostaining in ≥10% of tumor cells, whereas in our study, ER and PR status were determined using the Allred scoring system, with scores of 0–2 regarded as negative and scores of 3–8 as positive. Furthermore, variation in the applied techniques could also contribute to this divergence, as Wu et al. (2018) employed enzyme-linked immunosorbent assay (ELISA) on fasting peripheral venous blood samples to quantify sL1, while our study relied exclusively on immunohistochemistry (IHC) to assess L1CAM protein expression in breast carcinoma tissue.

Table 2: Correlation between L1CAM expression and clinicopathological features of the studied cases

	Total number	L1CAM Negative (N=10)	L1CAM positive (N=90)			Test of significance (P-value)
			Weak positive (N=16)	Moderate positive (N=41)	Strong positive (N=33)	
Age (years) Mean ± SD	100	56.53 ± 11.98	58.43 ± 12.20	55.71 ± 10.37	57.91 ± 12.52	F= 0.325 P= 0.808
Histological type						
IDC-NST	88	8 (9.1%)	14 (15.9%)	37 (42%)	29 (32.9%)	MC=0.806 P= 0.848
Other types	12	2 (16.7%)	2 (16.7%)	4 (33.3%)	4 (33.3%)	
***Grade (n=88)**						
G1	4	0 (0%)	0 (0%)	3 (75%)	1 (25%)	MC=3.29 P= 0.772
G2	65	6 (9.2%)	11 (16.9%)	28 (43.1%)	20 (30.8%)	
G3	19	2 (10.5%)	3 (15.8%)	6 (31.6%)	8 (42.1%)	
Tumor size						
T1 & T2	76	8 (10.5%)	11 (14.5%)	32 (42.1%)	25 (32.9%)	χ2= 0.644 P=0.886
T3 & T4	24	2 (8.3%)	5 (20.8%)	9 (37.5%)	8 (33.3%)	
LN status						
Negative	23	2 (8.7%)	4 (17.3%)	10 (43.5%)	7 (30.4%)	χ2= 0.191 P= 0.97
Positive	77	8 (10.4 %)	12 (15.6%)	31 (40.3%)	26 (33.8%)	
TNM Stage						
I & II	54	4 (7.4%)	10 (18.5%)	24 (44.4%)	16 (29.6%)	χ2= 1.99 P= 0.572
III & IV	46	6(13%)	6 (13%)	17 (36.9%)	17 (36.9%)	
ER						
Positive	77	7 (9.1%)	15 (19.5%)	30 (38.9%)	25 (32.5%)	MC=3.18 P= 0.364
Negative	23	3 (13.0%)	1 (4.3%)	11 (47.8%)	8 (34.8%)	
PR						
Positive	70	5 (7.1%)	13 (18.6%)	28 (40%)	24 (34.3%)	MC=3.04 P= 0.385
Negative	30	5 (16.7%)	3 (10.0%)	13 (43.3%)	9 (30.0%)	
HER2neu						
Positive	32	6 (18.8%)	2 (6.3%)	14 (43.8%)	10 (31.1%)	MC=7.14 P=0.308
Negative	58	3 (5.2%)	12 (20.7%)	24 (41.4%)	19 (32.8%)	
Equivocal	10	1 (10.0%)	2 (20%)	3 (30%)	4 (40%)	
Molecular classification						
Luminal A	57	3 (5.3%)	14 (24.6%)	19 (33.3%)	21 (36.8%)	χ2= 11.54 **P= 0.009***
Luminal B	20	4 (20.0%)	0 (0%)	11 (55%)	5 (25%)	MC=8.18 **P= 0.04***
Her2-enriched	15	2 (13.3%)	2 (13.3%)	5 (33.3%)	6 (40%)	MC=0.79 P=0.85
Triple-negative	8	1 (12.5%)	0 (0%)	6 (75%)	1 (12.5%)	MC=5.01 P=0.17
Neoadjuvant therapy						
Positive	30	4 (13.3%)	5 (16.7%)	9 (30%)	12 (40%)	χ2=2.39 P=0.495
Negative	70	6 (8.6%)	11 (15.7%)	32 (45.7%)	21 (30%)	
Recurrence/metastasis						
Positive	24	2 (8.3%)	4 (16.7%)	8 (33.3%)	10 (41.7%)	MC=1.56 P=0.667
Negative	76	8 (10.5%)	12 (15.8%)	33 (43.4%)	23 (30.2%)	

IDC-NST: Invasive ductal carcinoma-No special type, **G**: Grade; **T**: Tumor; **LN**: Lymph node; **TNM**: Tumor, node and metastasis; **ER**: Estrogen receptors; **PR**: Progesterone receptors; **HER2neu:** Human epidermal growth factor receptor 2; **F:** F test; **MC:** Monte Carlo test; **P**: P value; **χ2:** Chi-square test. *Grading was applied only to IDC-NST cases (n=88), as established grading systems are not applicable to special histological subtypes such as lobular, mucinous, or metaplastic carcinoma.

Doberstein et al. (2014) reported that L1CAM mRNA expression was higher in triple-negative breast carcinomas compared to non–triple-negative cases. Additionally, Zhang et al. (2024) demonstrated that in triple-negative breast carcinoma, L1CAM is co-regulated with the transcription factor forkhead box C1 (FOXC1), thereby contributing to tumor progression and aggressiveness. The discrepancy between our findings and these studies may be attributed to methodological differences, as these studies evaluated L1CAM at both the protein and mRNA levels, employing techniques such as western blot analysis and chromatin immunoprecipitation, whereas our study relied solely on immunohistochemistry.

With regard to recurrence, our study demonstrated no significant association between L1CAM expression and tumor recurrence. This was in contrast with Moisini et al. (2021). This discrepancy may be explained by differences in study design, particularly the sample size and proportion of recurrent cases, as recurrent tumors constituted 50% of the cases in Moisini et al. (2021), compared to only 24% in our cohort. Furthermore, their study was restricted to ER-positive, HER2/neu-negative breast carcinomas, whereas our study included all molecular subtypes without stratification by hormonal or HER2/neu status.

Our findings suggest a potential role of L1CAM as a prognostic marker in breast carcinoma, particularly within hormone receptor-positive tumors. However, this study has limitations that should be acknowledged. The retrospective design limits the ability to establish causal relationships and is dependent on the availability of existing medical records. In addition, the study was conducted in a single center, which may restrict the generalizability of the findings to other populations with different clinical or demographic characteristics. Moreover, while L1CAM expression was assessed using a standardized internal scoring approach, there is currently no universally accepted evaluation method for this marker in breast cancer, which could affect the comparability of results across studies.

Despite these limitations, the study provides valuable insights into L1CAM expression in breast carcinoma and highlights its potential prognostic value, particularly in hormone receptor-positive subtypes.

In conclusion, the observed L1CAM expression pattern suggests a possible role in identifying biologically aggressive tumors within hormone receptor-positive categories, offering a potential complement to traditional molecular subtyping. Our results of L1CAM expression in breast carcinoma call for further attention to its role and prognostic significance in breast cancer.

Conflict of interest

None.

Fund

None.

Data Availability statements

Data supporting this study are available upon reasonable request.

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