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RETRACTED: Kinesin Family Member 2A Serves as a Potential Biomarker Reflecting More Frequent Lymph Node Metastasis and Tumor Recurrence Risk in Basal-Like Breast Cancer Patients

*Hua Yang and Yongjun Liu**

Department of Thyroid and Breast Surgery, The Central Hospital of Wuhan, Tongji Medical College, Huazhong University of Science and Technology, Wuhan, China

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***Correspondence:**
Yongjun Liu
yongque13271@[illegible].com

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Background: Kinesin family member 2A (KIF2A) is reported as an oncogene and a potential biomarker for progression and prognosis in several cancers such as cervical, ovarian, and gastric. However, its clinical value in basal-like breast cancer (BLBC) is unclear. This study aims to evaluate KIF2A expression and its correlation with clinical features and survival rates in BLBC patients.

Methods: KIF2A mRNA and protein expressions in tumor and adjacent tissues from 89 BLBC patients are assessed by reverse transcription-quantitative polymerase chain reaction and immunohistochemistry assays, respectively.

Results: Both KIF2A protein ($p < 0.001$) and mRNA expressions ($p < 0.001$) were higher in tumor than in adjacent tissue. Besides, tumor KIF2A protein expression was positively correlated with N ($p = 0.028$) and TNM ($p = 0.014$) stages; meanwhile, tumor KIF2A mRNA expression was positively correlated with N stage ($p = 0.046$), TNM stage ($p = 0.006$), and tumor size ($p = 0.043$). Additionally, both tumor KIF2A protein ($p = 0.035$) and mRNA ($p = 0.039$) high expressions were correlated with worse disease-free survival (DFS) but not with overall survival (both $p > 0.05$). Moreover, tumor KIF2A protein expression was higher in relapsed patients than in non-relapsed patients within 3 years ($p = 0.015$) and 5 years ($p = 0.031$), whereas no difference was found between the dead and survivors within 3 years ($p = 0.057$) or 5 years ($p = 0.107$). Lastly, after adjustment, tumor KIF2A mRNA high exhibited a trend that correlated with DFS but without statistical significance ($p = 0.051$).

Conclusion: KIF2A correlates with more frequent lymph node metastasis and worse DFS in BLBC patients, shedding light on its potency as a biomarker for BLBC.

Keywords: kinesin family member 2A, basal-like breast cancer, lymph node metastasis, disease-free survival, overall survival

INTRODUCTION

Breast cancer is the most common malignancy in females, with an estimated morbidity of 2 million and a mortality of 0.6 million worldwide in the year 2018 (1–3). As the highest-grade invasive breast cancer, basal-like breast cancer (BLBC) is often incorporated into triple-negative breast cancer, which is featured as the lack of estrogen receptor, progesterone receptor, and human epidermal growth factor 2 receptor expressions, making up for approximately 15% of breast cancers (4–8). The outcomes of BLBC patients are the poorest among all molecular subtypes of breast cancers largely because there are few well-defined treatment methods for BLBC (9, 10). Chemotherapy remains the sole or primary clinical treatment for a majority of BLBC patients due to the absence of favorable surgical conditions or effective therapeutic targets (11). To provide optimized treatment strategies and better survival rates for BLBC patients, finding biomarkers for monitoring the progression and prognosis of BLBC is still an urgent need.

Kinesin family member 2A (KIF2A), an M-type nonmotile microtubule depolymerase of the Kinesin-13 family (12, 13), serves as a tumorigenic gene and a potential biomarker for progression and prognosis in a variety of cancers such as breast, cervical, ovarian, and gastric. (12, 14–20). For example, KIF2A knockdown inhibits the cell proliferation, migration, and invasion of breast cancer (14). KIF2A knockdown also induces the apoptosis of gastric cancer cells by decreasing the membrane type 1 (MT1)-matrix metalloproteinase (MMP) or protein kinase B (AKT) level (16, 21). Besides, KIF2A silencing promotes the apoptosis of tongue squamous cell carcinoma (TSCC) cells by suppressing the phosphatidylinositol-3-kinase (PI3K)/AKT signaling pathway (19). Similar roles of KIF2A are also found in ovarian, lung, glioma, and nasopharyngeal cancers (15, 17, 18, 22). Clinically, a large number of studies reveal that KIF2A shows the potential of a biomarker for several kinds of cancers. A high KIF2A expression is associated with more lymph node metastasis, advanced tumor stage, and/or shortened overall survival (OS) in patients with cervical, colorectal, lung, TSCC, nasopharyngeal cancers, and so on (12, 17, 18, 20, 23). In breast cancer, it is reported that KIF2A is negatively correlated with the survival of breast cancer patients (14). However, the clinical value of KIF2A as a biomarker for BLBC, which is characterized by poor prognosis, has never been investigated before.

This study aims to detect KIF2A protein and mRNA expressions in the BLBC tissue and its adjacent non-cancerous tissue by immunohistochemistry (IHC) and reverse transcription-quantitative polymerase chain reaction (RT-qPCR), respectively, so as to evaluate the correlation of KIF2A with clinical characteristics, disease-free survival (DFS), and OS in BLBC patients.

METHODS

Patients

After the approval of the Ethics Committee of The Central Hospital of Wuhan, Tongji Medical College, Huazhong University of Science and Technology, this study retrospectively collected the clinical data and the fresh-frozen specimens of 89 BLBC patients who underwent surgery in the hospital between January 2016 and December 2019. The patients were screened from the database according to the following criteria: (i) histopathological diagnosis of BLBC; (ii) resection; (iii) fresh-frozen tumor and adjacent tissues; (iv) the availability of clinicopathologic data and survival data. However, patients with the following conditions were not included in the study: (i) due to improper preservation, the specimens of patients were unable to be used for IHC assay and RT-qPCR assay; (ii) those who had a history of other primary tumors or malignant disease at diagnosis. Signed informed consents were obtained from patients or their relatives.

Acquisition of Data and Specimens

We reviewed the database of the hospital and collected the relevant clinicopathological data and treatment information of patients. For survival analysis, follow-up data of patients were collected for the calculation of DFS and OS. Meanwhile, the tumor and adjacent tissues of patients were obtained from the specimen library, all of which were stored in liquid nitrogen and made available for RT-qPCR assay and IHC assay.

Reverse Transcription-Quantitative Polymerase Chain Reaction Assay

The KIF2A mRNA expression in the specimens was assessed by RT-qPCR assay. Briefly, total RNA was extracted from the tumor and adjacent tissues of patients by TRIzol™ Reagent (Thermo Fisher Scientific, Waltham, MA, USA), followed by reverse transcription into cDNA using the ReverTra Ace qPCR RT Kit (Toyobo, Osaka, Kansai, Japan). Subsequently, qPCR was conducted by SYBR Green Realtime PCR Master Mix (Toyobo, Osaka, Kansai, Japan) to quantify the KIF2A mRNA expression, which was calculated by the $2^{-\Delta\Delta Ct}$ method with β-actin as an internal reference. The forward primer for KIF2A was 5′-GCCTTTGATGACTCAGCTCC-3′, and the reverse primer for KIF2A was 5′-TTCCTGAAAAGT CACCACCC-3′. The primers used in qPCR were designed in accordance with the previous study (14). The high and low expressions of KIF2A mRNA were classified on the basis of its median value in the tumor specimens.

Immunohistochemistry Assay

The KIF2A protein expression in the specimens was examined by IHC assay. The IHC staining procedures were implemented as in previous studies (24, 25). KIF2A Polyclonal Antibody (5 μg/ml, Invitrogen, Carlsbad, CA, USA) was applied as the primary antibody, and the F(ab′)2-Goat anti-Rat IgG (H + L) (1:20,000, Invitrogen, Carlsbad, CA, USA) was used as the secondary antibody. Diaminobenzidine and hematoxylin were used for staining and counterstaining. A photograph was obtained and analysis performed with a light microscope. The expression of KIF2A protein based on the IHC staining was quantified by a widely used methodology (24, 25). According to the methodology, an IHC score was generated on the basis of staining intensity and the percentage of positively stained

cells in the visual field. IHC scores >3 and ≤3 were identified as high expression and low expression, respectively (25). Two pathologists assessed the IHC score independently. If inconsistent IHC scores were marked by the pathologists for the same sample, then the mean value of the IHC scores was calculated.

Statistical Analysis

The difference comparison was checked by using the paired *t*-test, Wilcoxon signed-rank test, independent sample *t*-test, or Wilcoxon rank-sum test. Association analysis was determined by using Spearman's rank correlation test. DFS and OS were analyzed using the Kaplan–Meier method and the log-rank test. Cox's proportional hazards model method regression was performed to analyze the factors affecting DFS and OS. Data analysis was carried out with SPSS 26.0 (IBM Corp., Armonk, NYk, USA). Graphs were constructed by using GraphPad Prism 7.01 (GraphPad Software Inc., San Diego, CA, USA). A value $p < 0.05$ indicated statistical significance.

RESULTS

Clinical Characteristics

The mean age of the BLBC patients was 56.3 ± 11.1 years. Besides, the number of BLBC patients with good differentiation, intermediate differentiation, and poor differentiation was 17 (19.1%), 38 (42.7%), and 34 (38.2%), respectively, and the median [interquartile range (IQR)] value of tumor size was 2.5 (1.5–3.5) cm in the BLBC patients. In terms of T stage, the number of BLBC patients with T1, T2, and T3 was 35 (39.3%), 45 (50.6%), and 9 (10.1%), respectively. In regard to the N stage, there were 37 (41.6%), 22 (24.7%), and 30 (33.7%) BLBC patients with N0, N1, and N2 stages, respectively. With respect to the TNM stage, the number of BLBC patients with stage I, IIA, IIB, and IIIA was 17 (19.1%), 33 (37.1%), 7 (7.9%), and 32 (36.0%), respectively. Furthermore, the number of BLBC patients receiving neoadjuvant chemotherapy and adjuvant chemotherapy was 50 (56.2%) and 71 (79.8%), respectively (**Table 1**).

TABLE 1 | Characteristics of BLBC patients.

Items	BLBC patients (*N* = 89)
Age (years), mean ± SD	56.3 ± 11.1
Pathological differentiation, *n* (%)	
Well	17 (19.1)
Intermediate	38 (42.7)
Poor	34 (38.2)
Tumor size (cm), median (IQR)	2.5 (1.5–3.5)
T stage, *n* (%)	
T1	35 (39.3)
T2	45 (50.6)
T3	9 (10.1)
N stage, *n* (%)	
N0	37 (41.6)
N1	22 (24.7)
N2	30 (33.7)
TNM stage, *n* (%)	
I	17 (19.1)
IIA	33 (37.1)
IIB	7 (7.9)
IIIA	32 (36.0)
Neoadjuvant chemotherapy, *n* (%)	
No	39 (43.8)
Yes	50 (56.2)
Adjuvant chemotherapy, *n* (%)	
No	18 (20.2)
Yes	71 (79.8)

BLBC, basal-like breast cancer; SD, standard deviation; IQR, interquartile range.

KIF2A Protein and mRNA Expression in Tumor and Adjacent Tissues

The stained photographs of KIF2A protein expression in tumor and adjacent tissues of BLBC patients are shown in **Figure 1A**. In BLBC patients, both KIF2A IHC score (mean value: 5.5 ± 3.0 vs. 2.7 ± 1.6) ($p < 0.001$) and KIF2A mRNA expression [median (IQR) value: 2.521 (2.004–3.769) vs. 1.031 (0.716–1.263)] ($p < 0.001$) were higher in tumor than in adjacent tissue (**Figures 1B, C**).

Correlation of Tumor KIF2A Expression with Clinical Characteristics

In BLBC patients, tumor KIF2A IHC score was positively correlated with both N stage ($p = 0.028$) and TNM stage ($p = 0.014$). Also, tumor KIF2A mRNA expression was positively correlated with N stage ($p = 0.046$), TNM stage ($p = 0.006$), and tumor size ($p = 0.043$). However, no correlation of tumor KIF2A IHC score or tumor KIF2A mRNA expression with other clinical characteristics was observed (**Table 2**).

Correlation of Tumor KIF2A Protein Expression with Survival

In BLBC patients, a high tumor KIF2A protein expression was correlated with worse accumulating DFS ($p = 0.035$) (**Figure 2A**), and a tumor KIF2A IHC score was higher in patients who relapsed within 3 years ($p = 0.015$) or 5 years ($p = 0.031$) than in those who did not relapse within 3 years or 5 years, respectively (**Figures 2B, C**). However, no correlation of tumor KIF2A protein expression with accumulating OS was found in BLBC patients ($p = 0.105$) (**Figure 2D**). Also, no difference in the tumor KIF2A IHC score between BLBC deaths and the survival rate within 3 years ($p = 0.057$) or 5 years ($p = 0.107$) was found (**Figures 2E, F**).

Correlation of Tumor KIF2A mRNA Expression with Survival Rates

In BLBC patients, a high tumor KIF2A mRNA expression was correlated with worse accumulating DFS ($p = 0.039$)

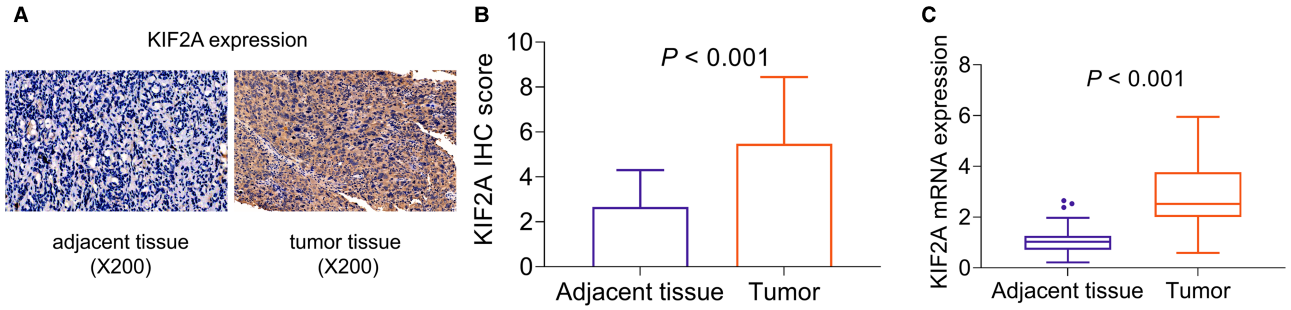

FIGURE 1 | Comparison of KIF2A expression between tumor and adjacent tissue. Stained photographs of KIF2A protein expression (**A**). KIF2A IHC score (**B**) and KIF2A mRNA expression (**C**) in tumor and adjacent tissue of BLBC patients. KIF2A, kinesin family member 2A; IHC, immunohistochemistry; BLBC, basal-like breast cancer.

(**Figure 3A**). Besides, tumor KIF2A mRNA expression was higher in patients who relapsed within 3 years than in those who did not relapse within 3 years ($p = 0.050$), while no difference of tumor KIF2A mRNA expression was found between patients who relapsed within 5 years and those who did not relapse within 5 years ($p = 0.117$) (**Figures 3B, C**). In addition, there was no correlation of tumor KIF2A mRNA expression with accumulating OS in BLBC patients ($p = 0.136$) (**Figure 3D**). Besides, there was no difference of tumor KIF2A mRNA expression between BLBC deaths and survivors within 3 years ($p = 0.122$) or 5 years ($p = 0.100$) (**Figures 3E, F**).

Factors Affecting Survival

Cox's proportional hazards regression analyses were performed to evaluate factors affecting DFS and OS, and the findings are displayed in **Tables 3 and 4**, respectively. Tumor KIF2A protein high [$p = 0.042$, hazard ratio (HR) [95% confidential interval (CI): 2.347 (1.033–5.336)], tumor KIF2A mRNA high [$p = 0.045$, HR (95% CI): 2.[illegible] (1.018–4.[illegible])], T stage [$p = 0.027$, HR (95% CI): 1.858 (1.071–3.223)], and N stage [$p = 0.047$, HR (95% CI): [illegible]540 (1.005–2.361)] were factors related to 0020 worse DFS. From the forward stepwise multivariate Cox's regression analysis, T stage was an independent factor for a shortened DFS [$p = 0.032$, HR (95% CI): 1.892 (1.056–3.[illegible]9)], while tumor KIF2A mRNA high showed a similar trend but without statistical significance [$p = 0.051$, HR (95% CI): 2.141 (0.997–4.600)] (**Table 3**).

In regard to OS, T stage [$p = 0.011$, HR (95% CI): 2.684 (1.253–5.752)], N stage [$p = 0.003$, HR (95% CI): 2.927 (1.454–5.893)], TNM stage [$p = 0.008$, HR (95% CI): 3.216 (1.360–7.605)], and neoadjuvant chemotherapy [$p = 0.034$, HR (95% CI): 3.908 (1.111–13.747)] were factors for worse OS, but neither tumor KIF2A protein high ($p = 0.117$) nor tumor KIF2A mRNA high ($p = 0.145$) were factors. From the forward stepwise multivariate Cox's regression analysis, N stage was an independent factor for a shortened OS [$p = 0.004$, HR (95% CI): 8.199 (1.933–34.776)], whereas adjuvant chemotherapy was an independent factor

TABLE 2 | Correlation of tumor KIF2A expression with clinical characteristics.

Items	KIF2A IHC score		KIF2A mRNA expression	
	Mean ± SD	*p*-value	Median (IQR)	*p*-value
Age		0.700		0.804
≤60 years	5.4 ± 2.8		2.526 (1.928–3.874)	
>60 years	5.6 ± 3.3		2.446 (2.091–3.357)	
Pathological differentiation		0.140		0.370
[illegible]	4.4 ± 3.0		2.154 (1.433–2.764)	
Intermediate	5.8 ± 3.1		2.947 (2.016–3.956)	
[illegible]r	5.7 ± 2.8		2.556 (2.008–3.606)	
Tumor size		0.084		0.043
<3 cm	5.1 ± 2.8		2.283 (1.705–3.602)	
≥3 cm	6.2 ± 3.2		2.784 (2.057–4.360)	
T stage		0.130		0.272
T1	5.0 ± 3.2		2.154 (1.553–3.545)	
T2	5.6 ± 2.8		2.689 (2.128–3.856)	
T3	6.6 ± 3.2		2.134 (1.928–3.753)	
N stage		0.028		0.046
N0	4.9 ± 2.8		2.512 (2.030–3.266)	
N1	4.8 ± 2.9		2.115 (1.475–3.255)	
N2	6.7 ± 2.9		3.474 (2.087–4.346)	
TNM stage		0.014		0.006
I	5.0 ± 3.0		2.264 (1.348–2.858)	
II	4.7 ± 2.8		2.296 (1.688–3.329)	
III	6.7 ± 2.8		3.408 (2.109–4.283)	
Neoadjuvant chemotherapy		0.249		0.487
No	5.0 ± 2.9		2.512 (2.032–3.384)	
Yes	5.8 ± 3.0		2.609 (1.933–3.956)	
Adjuvant chemotherapy		0.373		0.798
No	4.9 ± 3.2		2.475 (1.952–3.611)	
Yes	5.6 ± 2.9		2.521 (1.981–3.788)	

IHC score, immunohistochemistry score; KIF2A mRNA, Kinesin family protein 2A microRNA; SD, standard deviation; IQR, interquartile range.

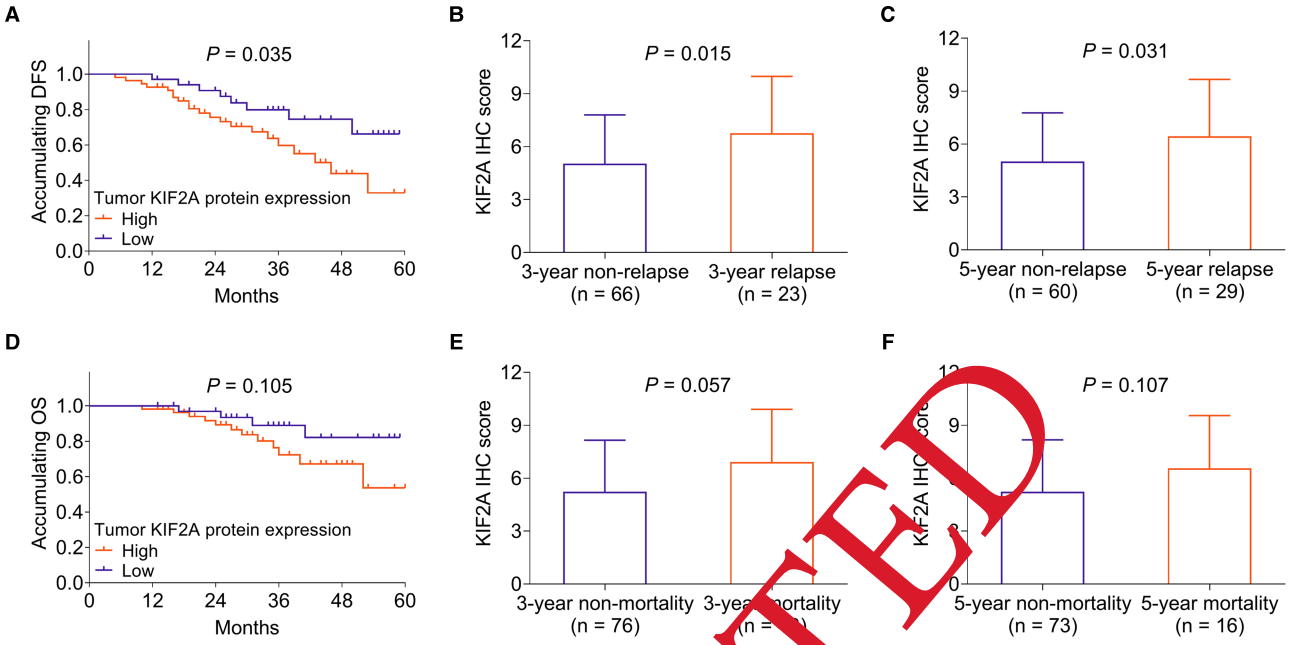

FIGURE 2 | Association of tumor KIF2A protein expression with DFS and OS. The association of tumor KIF2A protein expression with accumulating DFS in BLBC patients (**A**); the difference of KIF2A IHC score between relapsed BLBC patients and non-relapsed patients within 3 years (**B**) and 5 years (**C**). The association of tumor KIF2A protein expression with accumulating OS in BLBC patients (**D**); the difference in KIF2A IHC score between BLBC deaths and survivors within 3 years (**E**) and 5 years (**F**). KIF2A, kinesin family member 2A; IHC, immunohistochemistry; BLBC, basal-like breast cancer; DFS, disease-free survival; OS, overall survival.

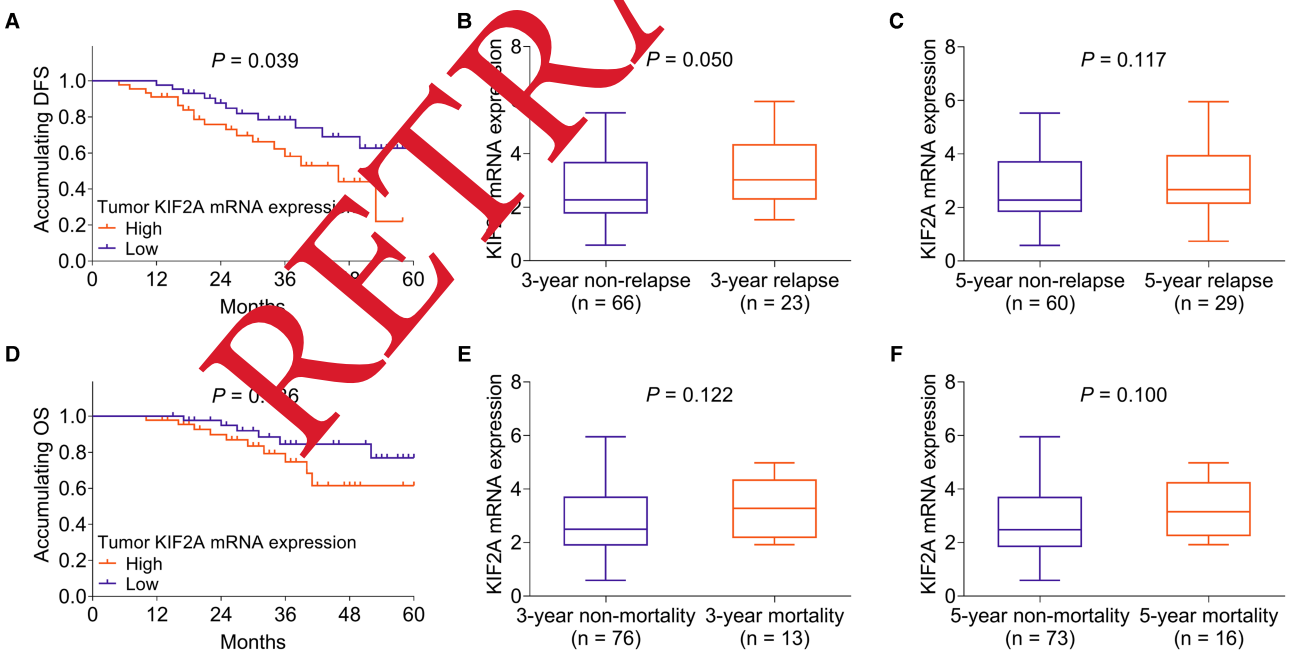

FIGURE 3 | Association of tumor KIF2A mRNA expression with DFS and OS. The association of tumor KIF2A mRNA expression with accumulating DFS in BLBC patients (**A**); the difference of tumor KIF2A mRNA expression between relapsed BLBC patients and non-relapsed patients within 3 years (**B**) and 5 years (**C**). The association of tumor KIF2A mRNA expression with accumulating OS in BLBC patients (**D**); the difference of tumor KIF2A mRNA expression between BLBC deaths and survivors within 3 years (**E**) and 5 years (**F**). KIF2A, kinesin family member 2A; BLBC, basal-like breast cancer; DFS, disease-free survival; OS, overall survival.

TABLE 3 | Factors affecting DFS by Cox's proportional hazards regression analysis.

Items	*p*-value	HR	95% CI	
			Lower	Upper
Univariate Cox's regression analysis				
Tumor KIF2A protein high	0.042	2.347	1.033	5.336
Tumor KIF2A mRNA high	0.045	2.181	1.018	4.672
Age >60 years	0.751	0.883	0.410	1.903
Pathological grade	0.120	1.521	0.897	2.578
Tumor size ≥3 cm	0.201	1.610	0.776	3.342
T stage	0.027	1.858	1.071	3.223
N stage	0.047	1.540	1.005	2.361
TNM stage	0.056	1.674	0.986	2.842
Neoadjuvant chemotherapy	0.280	1.513	0.713	3.209
Adjuvant chemotherapy	0.641	1.240	0.503	3.054
Forward stepwise multivariate Cox's regression analysis				
Tumor KIF2A mRNA high	0.051	2.141	0.997	4.600
T stage	0.032	1.892	1.056	3.389

DFS, disease-free survival; HR, hazard ratio; CI, confidence interval; KIF2A, kinesin family member 2A; TNM, tumor, node, and metastasis.

TABLE 4 | Factors affecting OS by Cox's proportional hazards regression analysis.

Items	*p*-value	HR	95% CI	
			Lower	Upper
Univariate Cox's regression analysis				
Tumor KIF2A protein high	0.117	2.484	0.796	7.750
Tumor KIF2A mRNA high	0.145	2.152	0.7[illegible]	6.033
Age >60 years	0.505	0.6[illegible]7	0.241	2.013
Pathological grade	0.217	1.552	0.773	3.119
Tumor size ≥3 cm	0.294	1.690	.634	4.505
T stage	0.01[illegible]	2.684	1.[illegible]53	5.752
N stage	0.00[illegible]	2.927	1.454	5.893
TNM stage	0.008	3.216	1.360	7.605
Neoadjuvant chemotherapy	0.[illegible]34	3.[illegible]08	1.111	13.747
Adjuvant chemotherapy	0.[illegible]	1.324	0.376	4.667
Forward stepwise multivariate Cox's regression analysis				
N stage	0.0[illegible]	8.199	1.933	34.776
Adjuvant chemotherapy	0.041	0.053	0.003	0.891

OS, overall survival; HR, hazard ratio; CI, confidence interval; KIF2A, kinesin family member 2A; TNM, tumor, node, and metastasis.

for a prolonged OS [$p = 0.041$, HR (95% CI): 0.053 (0.003–0.891)].

DISCUSSION

The major findings are outlined as follows: (1) KIF2A was overexpressed in tumor than in the adjacent tissue of BLBC patients. (2) Tumor KIF2A expression was correlated with advanced N and TNM stages in BLBC patients. (3) Tumor KIF2A high expression was correlated with worse DFS but not with OS in BLBC patients.

Kinesin superfamily proteins (KIFs) are microtubule-dependent motor proteins that provide strength to the intracellular transportation of membranous organelles and macromolecules, as well as cell division (26, 27). KIF2A, as a member of KIFs, possesses microtubule-depolymerizing activities and regulates the activities of multiple cancer cells (14, 17, 19, 23, 26, 28). For example, KIF2A facilitates the proliferation, invasion, and migration of breast, cervical, ovarian, lung, and gastric cancer cells *in vitro*; furthermore, it is upregulated in tumor tissues of patients with these cancers (14, 15, 17, 20, 21). In line with these previous studies, the current study disclosed that KIF2A was overexpressed in tumor than in adjacent tissue of BLBC patients. It could be explained by the fact that upregulated KIF2A enhanced the capacity of cancer cells to proliferate, invade, and migrate by increasing MT1-MMP or the AKT level (16, 21), as well as repressed their apoptosis by activating the PI3K/Akt signaling pathway (19), leading to its high expression in tumor tissues compared with adjacent tissues in BLBC patients.

KIF2A is clinically correlated with poor clinicopathological features in multiple cancers (12, 14, 18, 20, 28, 29). For example, a study shows that KIF2A expression is positively correlated with the severity of lymph node metastasis in patients with breast and cervical cancers (14, 20). Another study reveals that the overexpression of KIF2A is associated with advanced T and TNM stages in colorectal cancer patients (12). Partly in consistent with these findings, the present study demonstrates that tumor KIF2A expression (protein and mRNA) was correlated with higher N and TNM stages. In addition, tumor KIF2A mRNA expression was correlated with a larger tumor size in BLBC patients. The possible reasons for these are as follows: (1) KIF2A aggravates the invasion and migration of cancer cells by downregulating the polo-like kinase 4 (PLK4)/miR-129-5p axis, thus activating the PI3K/AKT/vascular endothelial growth factor signaling pathway (30, 31), leading to more frequent lymph node metastasis in BLBC patients. (2) KIF2A also exacerbates the proliferation and reduces the apoptosis of cancer cells by inhibiting the PLK4/miR-129-5p axis or the PI3K/Akt signaling pathway (30, 32), resulting in the larger tumor size in BLBC patients. (3) By accelerating proliferation and metastasis of cancer cells, KIF2A might cause higher TNM stage in BLBC patients.

In terms of survival, KIF2A is associated with poor DFS or OS in patients with hepatocellular, cervical, lung, and colorectal cancers (12, 17, 20, 29). This study also showed that tumor KIF2A high expression (protein and mRNA) was correlated with worse DFS. However, no correlation of KIF2A with OS was found in BLBC patients. The reasons might be as follows: (1) As mentioned above, tumor KIF2A was associated with a larger tumor size, more frequent tumor metastasis, and advanced TNM stage, thus shortening DFS in

BLBC patients. (2) For patients who received further treatment after relapse, the treatment efficacy was uncertain, which resulted in estimable mortality. Thus, no correlation between KIF2A and OS was found in BLBC patients. In the present study, it was worth noting that tumor KIF2A mRNA high expression presented a trend of being an independent risk factor related to DFS but without statistical significance from the Cox's proportional hazards regression analysis, which was attributed to its correlation with N stage, and the tumor size weakened its effect in multivariate analysis. Meanwhile, the characteristics of the tumor were the main contributor to the prognosis of the patients.

It could not be denied that there were a few limitations in this study. Firstly, the small sample size led to low statistical power, and a further study with a larger sample size is now proposed to be conducted. Secondly, the potential mechanisms underlying the oncogenic effects of KIF2A in BLBC are required to be clarified in the future. Thirdly, there might exist several confounding factors such as treatment after relapse, which influenced the findings in this study. Fourthly, the clinical value of KIF2A in other types of breast cancer could be investigated in the future.

Conclusively, KIF2A is highly expressed in tumor than in adjacent tissue; also, tumor KIF2A high expression correlates with more frequent lymph node metastasis and worse DFS in BLBC patients. The above discoveries shed light on the potency of KIF2A as a biomarker for BLBC.

DATA AVAILABILITY STATEMENT

The original contributions presented in the study are included in the article; further inquiries can be directed to the corresponding author/s.

ETHICS STATEMENT

The studies involving human participants were reviewed and approved by The Central Hospital of Wuhan, Tongji Medical College, Huazhong University of Science and Technology. The patients/participants provided their written informed consent to participate in this study.

AUTHOR CONTRIBUTIONS

YL contributed to the conception and design of the study. HY contributed to performing the experiments, data acquisition, and analysis. YL contributed to the preparation of the manuscript. All authors contributed to the article and approved the submitted version.

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