# **VEGF-A Is Associated With the Degree of TILs and PD-L1 Expression in Primary Breast Cancer**

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Abstract. Background/Aim: Vascular endothelial growth factor-A (VEGF-A), an important angiogenic factor, has been reported to effect cancer growth and development. Recent reports indicated that anti-VEGF therapy has an important effect of enhancing anti-tumor immunity in various cancers. In the current study, we investigated the relationship between VEGF-A expression and immunological factors, including programmed cell death ligand 1 (PD-L1) and the degrees of stromal tumor-infiltrating lymphocytes (TILs) in breast cancer. Patients and Methods: This study enrolled 97 cases with invasive breast cancer who had undergone surgery without preoperative therapy. The grades of stromal-TILs were evaluated using the criteria of the International Working Group for TILs in breast cancer: low, intermediate, and high. VEGF-A and PD-L1 positivity were evaluated by immunohistochemistry. The relationship between VEGF-A expression and the expression of PD-L1 and TILs was investigated. Results: Among the 97 cases, 37 (38.1%) had positive VEGF-A expression in the breast tumor. We divided the cases in two groups based on the VEGF-A expression levels. The analysis revealed that PD-L1 positivity was significantly associated with VEGF-A expression in the breast tumor (29.7% vs. 10.0%, p=0.014). Among the cases with positive PD-L1, 36.7% of VEGF-positive cases and none of VEGF-negative cases had low TILs in the breast tumor. Conclusion: VEGF-A expression in breast cancer may reflect PD-L1 expression in the tumor. VEGF-A may act as

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a negative biomarker of TILs in PD-L1-positive breast cancer. Our results suggest that VEGF-A may be predictive of immunological features and may serve as a useful biomarker for immuno-targeting therapy in patients with breast cancer.

Vascular endothelial growth factor-A (VEGF-A), one of the most important angiogenic factors (1-3), has been reported to effect cancer growth and development (3-6). VEGF-A is also involved in the regulation of immune response in various cancers (3, 7-14). Recent reports have indicated that anti-VEGF therapy has the important effect of enhancing anti-tumor immunity in various cancers (3, 7-14). The immune system affects tumor progression and dissemination, and treatment response (15-18). Immune cell infiltration has been observed in breast cancer tissue (15-18) and tumorinfiltrating lymphocytes (TILs) has been reported to reflect immunological characteristics in cancer tissue. Several studies have also aimed to elucidate the functions of TILs in cancer tissue and the immune response in cancer has been driven by the specific functions of TILs (19). Several recent clinical studies, including our study, revealed that TILs were a prognostic factor and predictor of the response to chemotherapy in patients with breast cancer (15-22). Anti-VEGF targeting therapy has been reported to be involved in the regulation of immune responses and to increase the intratumoral infiltration of lymphocytes (7). Anti-VEGF therapy also enhanced the efficacy of immune checkpoint inhibitors in several cancer therapy (8, 9, 12). We reported that programmed death-ligand 1 (PD-L1) expression was associated with the response to chemotherapy in cases with HER2-positive breast cancer (23). PD-L1 and PD-1 (programmed cell death protein-1) are considered immune checkpoint factors that eliminate T-cell activation and inhibit the immune reaction to cancer cells in a lot of cancers including breast cancer (23, 24). These factors have attracted attention as novel therapeutic targets in various types of cancers. However, it is unknown whether VEGF-A is related

to these immunological features in breast cancer. In the current study, we investigated the relationships between VEGF-A expression and immunological factors, including PD-L1 and degrees of stromal TILs in breast cancer, which have been suggested to be prognostic factors or which may reflect immunological features in breast cancer.

## **Patients and Methods**

We retrospectively investigated the ninety-seven cases with primary breast cancer (T1-4, N0-2, M0) at the Division of Breast and Endocrine Surgery, Graduate School of Medicine, Gunma University between June 2009 and February 2015. All 97 patients had undergone radical breast surgery. None of the patients had received preoperative chemotherapy. The exclusion criteria were as follows: bilateral breast cancer, previous treatment for breast cancer, presence of distant metastases, pregnancy or breastfeeding at the time of diagnosis, other current malignancies, diabetes mellitus, or severe cardiac, hematological, renal, pulmonary, or hepatic abnormalities. Patients with incomplete clinical information and male patients were excluded. All patients included in this study gave their informed consent at the time of surgery for inclusion in future analyses. All procedures performed in studies involving human participants were in accordance with the ethical standards of the Clinical Ethics Committee of Gunma University and with the Helsinki declaration.

The following clinical data were obtained: the patient's age, tumor TNM stage, and estrogen receptor (ER) expression status, progesterone receptor (PgR) expression status, and the HER2 score of the primary tumor, nuclear grade (NG) and lymphovascular invasion. The ER and PgR statuses were assessed by the Allred score  $\geq 3$  indicating positive of ER and PgR (25, 26). HER2 overexpression was determined by immunohistochemistry analysis and a fluorescence in-situ hybridization (FISH) analysis with IHC 3+ or IHC 2+/FISH+ indicating positive of HER2 (27). VEGF expression was assessed according to the percentage of immunoreactive cells in a total of 1,000 neoplastic cells using quantitative analysis. The cutoff between high and low VEGF-A expression was 25% of positive cancer cells using a polyclonal antibody against VEGF-A protein (A-20; 1/200 dilution; Santa Cruz Biotechnology, Dallas, TX, USA) (28). The proportional grades of stromal (Str)-TILs in surgical specimens were determined by pathologist as low (0-10%), intermediate (20-40%), and high (50-90%), using an immunohistochemistry method and the criteria of the International Working Group for TILs 2014 in breast cancer (29). PD-L1 (Abcam, ab208572, 1:200 dilution) was considered positive if expressed on at least 1% of tumor cells (i.e., a tumor proportion score  $\geq 1\%$ ) (30). Anti-CD8 antibodies (Abcam, ab4055, 1:1,000 dilution) were counted manually in 15 to 20 high-power fields. Intratumoral lymphocytes were graded by T-cells per highpower field as low ( $\leq$ 5), intermediate (6 to 19), or high ( $\geq$ 20) (31).

Statistical analysis. The cases with breast cancer were divided into two groups: those with high expression of VEGF-A and those with low expression of VEGF-A in the breast cancer tissue. We conducted a univariate statistical analysis using the Fisher's exact test or the  $c^2$  test with Yates' correction. To compare the two groups, Student's *t*-test was used. The analyses were carried out using the SPSS version 25 software (IBM, Chicago, IL, USA). RecurrenceTable I. Patient clinicopathological characteristics depend on VEGF expression.

	VEGF expression		<i>p</i> -Value
	negative (n=60)	positive (n=37)	
Age (years) (median)	56.5 (40-86)	58.0 (36-83)	0.281
Т			
1	29	26	0.106
2	28	10	
3/4	3	1	
Lymph node	24	7	0.025
involvement (n)			
ER positive (n)	52	33	0.488
PgR positive (n)	49	29	0.442
HER2 positive (n)	11	4	0.243
NG			
1	11	8	0.347
2	30	13	
3	19	16	
ly positive (n)	29	15	0.590
v positive (n)	11	7	0.638
TILs			
Low	38	18	0.360
Intermediate	17	15	
High	5	4	
PD-L1 positive (n)	6	11	0.014

n, Number; NG, nuclear grade; TILs, tumor infiltrating lymphocytes, PD-L1, programmed death ligand.

free survival (RFS) was calculated using the Kaplan-Meier method. The log-rank test was used to evaluate differences between the recurrence-free intervals. Differences were considered significant when p<0.05.

### Results

In this study, 97 patients with breast cancer were included in the analysis. Among all patients, 37 (38.1%) had positive VEGF-A expression in the breast tumor. We divided the patients into two groups based on VEGF-A expression (Table I). All patients with high degrees of TILs showed high expression of CD8. The analysis revealed that positive expression of PD-L1 was significantly associated with VEGF-A expression (29.7% vs. 10.0%, p=0.014) in primary tumors. Expression of PD-L1 is used as companion diagnosis for immune checkpoint inhibitors in cancer therapy (32, 33). The degrees of TILs among patients with both PD-L1positive and VEGF-A-positive expression were low grade 36.7%, intermediate grade 36.7%, and high grade 27.3%. On the other hand, those of TILs among patient with PD-L1positive and VEGF-A-negative expression were low grade 0%, intermediate grade 50%, and high grade 50%. Among the cases positive for PD-L1, 36.7% of VEGF-A-positive cases and none of the VEGF-A-negative cases had low TILs

in the primary tumor. The RFS curves did not significantly differ between patients with high and low VEGF-A expression (data not shown).

## Discussion

The immune system affects not only tumor growth, but also treatment response (15-18). PD-L1 expression is associated with immunological features of tumor and immune biomarkers. The key observations of the current study in cases with breast cancer are the following: (1) among various clinicopathological characteristics, VEGF-A expression was significantly associated with positive PD-L1 expression; (2) among the PD-L1-positive cases, 36.7% of VEGF-A-positive cases had low TILs in the breast tumor, while none of the VEGF-A-negative cases had low TILs in the breast tumor. Our results suggest that VEGF-A expression is associated with PD-L1 and may be predictive of immunological features and biomarkers of immune checkpoint inhibitors in cases with breast cancer.

VEGF-A is one of the most important angiogenic factors that is strongly associated with the tumor immune microenvironment. There is a small but clear body of evidence associating VEGF-A or hypoxia-inducible factors with PD-L1 (8, 13, 34). PD-L1 expression was associated with VEGF-A expression in clear cell renal carcinoma, and VEGF-A signaling is needed for PD-L1 up-regulation in tumor cells or M2 macrophages (35, 36). Furthermore, positive VEGF-A expression around the vessels was observed significantly more frequently in PD-L1-positive groups of patients with high-grade glioma and Hodgkin lymphoma (13, 37). These findings are consistent with our results that VEGF-A expression was significantly associated with PD-L1 positivity.

PD-L1 expression and the degree of TIL expression reflect the status of tumor immunological features (15-18). Lymphocytes are often observed around cancer tissue. These immune-related lymphocytes are associated with the proliferation and elimination of cancer cells, reflecting immunological reactions between cancer cells and lymphocytes. The state of TILs has been identified as a useful predictive marker for prognosis or response to cancer therapies in various types of cancers. TILs are composed of various types of immuno-related cells, and PD-1/PD-L1 immune check point pathway involves the tumor microenvironment (15-18). Expression of PD-L1 is used as a companion diagnostic tool for immune checkpoint inhibitors in cancer therapy (32, 33). Prospective trials to evaluate the efficacy of PD-1 and PD-L1 antibodies are ongoing in cases with several cancers, including breast cancer (38-40). PD-L1 is now a companion diagnostic tool of a PD-L1 inhibitor, atezolizumab, for the treatment of triple-negative breast cancer (33). In the present study, among the patients with positive PD-L1, some of the VEGF-A-positive patients, but none of the VEGF-A-negative patients had low-grade TILs in the breast tumor. Higher levels of TILs present at diagnosis were associated with chemotherapy responsiveness (15, 17, 41). Together, these past and present results imply the possibility that VEGF-A may reflect the status of PD-L1 expression and functions of TILs in breast cancer. These findings may provide evidence that VEGF-A is a potent predictor for determining adaptation for immune checkpoint therapy in cases with breast cancer.

Patients positive for both PD-L1 and VEGF-A have relatively higher rates of low TILs: although immune checkpoint inhibitors are not effective in such patients, and anti-VEGF therapy may be effective. As explained in the introduction section, anti-VEGF targeting therapy has been reported to be involved in the regulation of immune responses and in increased intratumoral infiltration of lymphocytes (7). Anti-VEGF therapy also enhanced the efficacy of immune checkpoint inhibitors in cancer therapy (8, 9, 12). In cases with lung cancer, a combination of anti-PD-1 and PD-L1 therapies and anti-VEGF therapies has been an effective treatment strategy (3, 7). Consistent with our findings, in those studies both VEGF-A and PD-L1 signaling blockade in cancer therapy was a successful strategy.

This preliminary study has potential limitations, including its retrospective design and the relatively small number of included patients (n=97). However, to the best of our knowledge, this is the first report to describe the relationship between the expression of VEGF-A and the expression of PD-L1 in breast cancer. Additional studies are necessary to elucidate whether VEGF-A predict the immunological status in breast cancer tissue and VEGF-A is useful as a biomarker of immune checkpoint inhibitors in cases with breast cancer.

In conclusion, we demonstrated that VEGF-A expression in primary breast tumor reflected PD-L1 expression in the tumor. VEGF-A may act as a negative biomarker of TILs in PD-L1-positive breast cancer. In light of our results, VEGF-A may reflect immunological features and is a useful biomarker for immunotargeting therapy in cases with breast cancer. Additional studies are needed to determine whether VEGF-A is a biomarker for immune checkpoint inhibitors in cases with breast cancer.

#### **Conflicts of Interest**

The Authors declare that they have no competing financial interests related to this study.

## **Authors' Contributions**

TH analyzed data and TF wrote the initial draft of the manuscript. TF, TH, SK, ST, YN, SK, and RY collected data and were involved in the initial study conception and design. TF and KS interpreted the results and were involved in drafting the work and revising it critically for important intellectual content. TF approved the final version to be published. All Authors have read and approved the final manuscript.

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