

Activation of EGFL7 within High Grade Ovarian Serous Carcinoma is Associated with Lower Tumor Infiltrating CD4+ and CD8+ Lymphocytes

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Abstract

It has been suggested that Epidermal Growth Factor like domain 7 (EGFL7) promotes tumor cell escape from immunity by downregulating the activation of tumor blood vessels. Aim: to analyze mRNA expression of *EGFL7* within tumor microenvironment of high-grade ovarian serous carcinoma and its association with number of intraepithelial CD4+/CD8 + lymphocytes and expression of molecule involved in diapedesis ICAM-1.

Methods: qPCR analysis of *EGFL7* mRNA in cancer cells and adjacent stromal endothelium microdissected from formalin-fixed paraffin-embedded tumors of 59 high-grade ovarian serous carcinoma patients, was performed. Infiltration of intraepithelial lymphocytes (CD4+/CD8+) and expression of ICAM-1 were evaluated by immunohistochemistry and compared between tumors with different status of *EGFL7* expression. Results: *EGFL7* was expressed in cancer cells (9/59, 15.25%), endothelium (8/59, 13.56%), or both cancer cells and adjacent endothelium (4/59, 6.78%). ICAM-1 was expressed on cancer cells (47/59, 79.66%), stromal endothelium (46/59, 77.97%), or both epithelium and endothelium (40 of 59, 67.8%). *EGFL7*-positivity of cancer cells and endothelium was associated with lower intraepithelial inflow of CD4+ ($p = 0.022$ and $p = 0.029$, respectively) and CD8 + lymphocytes ($p = 0.04$ and $p = 0.031$, respectively) but impact neither epithelial nor endothelial ICAM-1 expression ($p = 0.098$ and $p = 0.119$, respectively). Patients' median follow-up was 23.83 months (range 1.07–78.07). Lack of prognostic significance of *EGFL7*-status and ICAM-1 expression was notified. Conclusion: EGFL7 was independently activated in the cancer epithelium as frequently as in endothelium of human high-grade ovarian serous carcinoma. Activation of *EGFL7* on cancer cells and/or endothelium impairs influx of immune cell effectors into cancer nest.

Background

Ovarian cancer (OvCa) is the leading cause of deaths from gynecological malignancy in the developed world. The overall five-year survival rate for patients with advanced OvCa is only 30–40% [1]. Notwithstanding the good initial response to primary therapy, around 80% of the patients with advanced disease will develop recurrence and finally succumb to the illness [1]. Therefore, more insight in the interaction between OvCa and the immune system is needed to develop more effective anti-tumor immunotherapy to improve the clinical outcome.

Instead of being targeted for immune destruction, OvCa has ability to escape the immune surveillance by creating a highly suppressive environment [2]. Tumor escape from immunity is undoubtedly a promising phenomenon to consider while designing therapeutic tools aimed at preventing cancer progression and metastasis [3, 4].

Blood vessels, which are a part of the tumor microenvironment, constitute a natural physical barrier which regulates the immune response via diapedesis [5]. Activated endothelial cells express high level of cell surface leukocyte adhesion molecules such as E- and P-selectin, intercellular adhesion molecule-1 (ICAM-

1), and vascular cell adhesion molecule-1 (VCAM-1) which participate in the capture of circulating immune cells through the rolling, arrest, firm adhesion, and extravasation of leukocytes into stroma [5, 6]. Thus, immune escape may be achieved by limiting the influx of immune effectors into cancer tissue [7, 8] through down-regulation of endothelial adhesion molecules ICAM-1 and VCAM-1 [9–12].

EGFL7 is an endothelial cell-derived protein that regulates vascular tube formation. Its expression is downregulated in mature vasculature, upregulated in proliferating endothelium [13–15] and deregulated in human cancer [16].

Using experimental approaches, it has been demonstrated that, when expressed by cancer cells, *EGFL7* promotes tumor escape from immunity by downregulating the activation of tumor blood vessels [17]. *EGFL7* in mouse breast and lung carcinoma cells inhibit the endothelial expression of ICAM-1 and VCAM-1, preventing lymphocyte adhesion and transendothelial migration [17]. This observation was additionally confirmed by an analysis of tissue samples derived from large cohort of breast cancer patients, utilizing hybridization in situ as a method to localize a real source of *EGFL7* secretion [18].

Since *EGFL7* is plasma membrane-associated sialidase (lysosomal sialidase) which could accumulate at distant sites from the producing cells [15], it is impossible to answer if elevated expression of *EGFL7* transcripts observed in several human cancer tumors come from activated cancer epithelium or up-regulated endothelial cells of the surrounding stroma.

Laser Capture Microdissection (LCM) technology enables harvesting the cells of interest directly or can isolate specific cells by cutting away unwanted cells to give histologically pure enriched cell populations [19].

The aim of this study was to analyze the expression of *EGFL7* within cancer epithelial nest and the adjacent stroma (tumor microenvironment) of High Grade Ovarian Serous Carcinomas (HGOSCs) and its impact on number of immune cell effectors (CD8+, CD4+) infiltrating cancer epithelial nests as well as correlation with ICAM-1 expression of adjacent blood vessels.

Material And Methods

Human samples

Cohort of 59 HGOSC patients treated with primary debulking surgery (PDS) at the Department of Gynecologic Oncology, Oncological Center of Gdynia, Polish Red Cross Hospital Gdynia (Poland) between Sep 2013 and Dec 2015.

The patients were informed that surgical specimens would be used for conventional pathological diagnosis and that the remaining tissues would be used for research. No personal patient data was required for this study and the protocols carried no risk, so only verbal informed consent was required from the patients. The protocol was approved by the Ethics Committee of Medical University of Gdansk

(Permit Number: NKBBN/263/2012). Disease staging was defined according to the International Federation of Gynecology and Obstetrics (FIGO) staging system [20].

Tissue samples

We analyzed 59 formalin-fixed paraffin-embedded (FFPE) tissue samples from primary tumors for immunohistochemical (IHC) evaluation of expression of ICAM-1, CD4 and CD8 and for qPCR analysis of Eglf7 mRNA transcripts.

Immunohistochemistry

The immunohistochemical stainings were performed on whole sections of representative FFPE blocks. The staining was performed according to the following protocol (antibody details, suppliers and dilutions are listed in Table 1). Four μm -thick serial sections were cut, deparaffinized and subjected to a heat-induced epitope retrieval step before being incubated with the primary antibodies. Sections were immersed in Target Retrieval Solution (pH 6,0; Dako Cytomation, Denmark) and heated in a pressure cooker. The slides were incubated for 90 minutes with the primary antibodies. The reaction was visualized by the Novolink polymer detection system (Novocastra Laboratories). Appropriate positive (tonsil for both: CD4 and CD8, placenta for ICAM) and negative controls (the primary antibody was replaced with normal mouse IgG at an appropriate dilution) were included for each case. The results of immunohistochemistry were evaluated by two independent pathologists who were blinded for the clinical data.

Table 1
Antibody characteristics.

Antibody	Nr cat	Dilution	Expression	
EGFL7	Santa Cruz	Santa Cruz sc-101349	1:200	Nuclear-cytoplasmic
ICAM	Abcam	[MEM-111] (ab2213)	1:400	Membranous
VCAM	Abcam	[6G9] (ab98954)	1:2000	Membranous
CD4	Millipore	IHCR2110-6	RTU	cytoplasmic
CD8	Millipore	IHCR2114-6	RTU	cytoplasmic

IHC evaluation of ICAM-1

ICAM-1 expression in cancer nests was evaluated with the high-Score method. The score was calculated according to the commonly used formula (the percentage of cells with strong/moderate/weak expression multiplied by 3/2/1, respectively) [21]. Endothelial ICAM-1 expression was scored in each tumor as the proportion of ICAM-1-positive vessels and categorized into 4 subgroups [18].

Evaluation and classification of CD4 + and CD8 + cells

Five areas with the most abundant lymphocyte distribution (hot spots) were selected and micro-photographs were taken. The quantitative analysis was performed with Multiscan 14.2 software. The number of CD4 + and CD8 + cells was counted exclusively within cancer nests. For each case the mean index of CD4 + and CD8 + cells per single high-power field was counted and then statistically analyzed.

qPCR in samples obtained with microdissection

Separate populations of cancer and endothelial cells were harvested using LCM performed as follows. The selected, representative paraffin blocks were cut into 4 um slices and mounted on slides with PEN-membrane (25 × 76 mm) (No. Cat. 11505158, Zeiss). Next, a brief staining protocol was applied, composed of deparaffinization in fresh xylene for 1 min twice followed by 100% ethanol for 1 min, 95% for ethanol 1 min, and 70% ethanol for 1 min. The slides then were transferred into distilled water for 2 min before staining with Hematoxylin for 2 min. Subsequently, slides were rinsed in distilled water until clear before undergoing dehydration in 70% ethanol for 1 min, 95% ethanol for 1 min, 100% ethanol for 1 min, and xylene for 1 min. Areas for microdissection were marked on the original hematoxylin-eosin-stained slide to include two targets, cancer nest and vessels in the surrounding stromal connective tissue. Microdissection was performed within next 2 h with PALM MicroBeam ZEISS Microscopy system. Tissue material was separately collected into AdhesiveCap (Item Number: 415190-9211-000, Zeiss).

Total RNA was extracted from the microdissected FFPE tissues (n = 118, 2 samples for each patient) using RNeasy FFPE Mini Kit (Qiagen) according to the manufacturer's protocol. Quantity and quality of the isolated RNA was determined with NanoDrop 1000 UV Spectrophotometer (Thermo Scientific). Reverse transcription for the 118 microdissected samples was performed with iScript Advanced cDNA Synthesis Kit for RT-qPCR protocol (Bio-Rad).

qPCR to evaluate the expression of *EGF7* was performed using TaqMan Gene Expression Assay (Applied Biosystems) following the manufacturer's protocol using the LightCycler 480 II system (Roche). The samples were analyzed in duplicates.

Statistical analysis

To determine statistically significant differences between the variables, the Mann-Whitney U test was used. The statistical analysis was performed using chi-square test or Fisher's exact probability test. Correlations and differences between variables were assessed using the Spearman's rank correlation coefficient. Overall survival curves were estimated by the Kaplan-Meier method and compared with use of the two-sided log-rank test. P-values of < 0.05 were regarded as significant in each of the analysis. All analyses were performed with the statistical software Statistica 13 (Stat Soft Inc.).

Results

Patient population

The median age of the patients was 59 years (range 39–86), the median duration of follow-up was 23.83 months (range 1.07–78.07). The 5-year disease free survival (DFS) rate was 20.35%. The clinicopathological HGOSC data are presented in Table 2.

Table 2
The clinicopathological characteristics of HGOSC patients (n = 59)

feature	value
Age (years)	median 59 (range 39–86)
Preoperative CA125 (U/ml)	median 849 (range 6.8-25000)
Ascites Yes/No (number)	38/21
Preoperative peripheral blood neutrocytes (G/l)	median 6.15 (range 3.27–10.99)
Preoperative peripheral blood lymphocytes (G/l)	median 1.5 (range 0.43–3.02)
FIGO I (number/percentage)	8 / 13.6%
FIGO II (number/percentage)	1 / 1,7%
FIGO III (number/percentage)	48 / 81.4%
FIGO IV (number/percentage)	2 / 3.3%
Residual disease: 0 cm (number/percentage)	8 / 13.6%
Residual disease: <1 cm (number/percentage)	22 / 37.3%
Residual disease: >1 cm (number/percentage)	29 / 49.1%
OS (months).	median 26.99 (range 1.07–78.07)

EGFL7 expression at mRNA level

Expression of *EGFL7* within tumor microenvironment (epithelium and/or adjacent endothelium) was detected in 13 of 59 (22.03%) HGOSCs.

We noted the increase in the PCR product only in a low proportion of samples, therefore, the initially planned quantitative analysis was not possible and the qualitative scoring had to be applied. In details, activation of *EGFL7* was detected in cancer epithelium (9/59, 15.25%), endothelium (8/59, 13.56%) or in both: cancer epithelium and adjacent endothelium (4/59, 6.78%). Presence or lack of expression of *EGFL7* had no impact on progression free survival (PFS) and overall survival (OS) of the patients ($p = 0.175$ and $p = 0.912$ respectively).

Correlation of clinicopathological HGOSC population data and *EGFL7* expression of cancer cells and endothelium are presented in Table 3 and Table 4, respectively.

Table 3

The clinicopathological characteristics of HGOSCs population related to Egfl7 and ICAM-1 status of cancer cells

feature	Cancer Egfl7(+)	Cancer Egfl7(-)	p	Cancer ICAM-1(+)	Cancer ICAM-1(-)	p
Age (years) median (range)	60 (40–84)	58.5 (39–86)	0.626	58 (39–84)	62 (43–86)	0.309
Preoperative CA125 (U/ml) median (range)	660 (6.8–3000)	1000.8 (19.56–25000)	0.204	837 (6.8–25000)	1304 (174–8910)	0.337
Ascites Y/N number	6/3	32/18	1	32/15	6/6	0.315
Preoperative neutrocytes (G/l) median (range)	7.17 (5.38–8.19)	6.02 (3.27–10.99)	0.446	6.15 (3.27–10.99)	5.64 (4.99–8.55)	0.929
Preoperative lymphocytes (G/l) median (range)	1.465 (1.28–2.99)	1.5 (0.43–3.02)	0.732	1.49 (0.43–3.02)	1.8 (1.12–2.55)	0.244
FIGO I	1	7	0.882	6	2	0.830
FIGO II	0	1		1	0	
FIGO III	8	40		38	10	
FIGO IV	0	2		2	0	
Residual disease: 0 cm	1	7	0.962	7	1	0.311
Residual disease: <1 cm	4	18		19	3	
Residual disease: >1 cm	4	25		21	8	
Platin sensitive	7	27	0.081	16	2	0.462
Platin refractor / resistance	0	18		26	8	

Table 4

The clinicopathological characteristics HGOSCs population related to Egfl7 and ICAM-1 status of endothelial cells

feature	Endothelium	Endothelium	p	Endothelium	Endothelium	p
	Egfl7 (+)	Egfl7 (-)		ICAM-1 (+)	ICAM-1 (-)	
Age (years) median (range)	59 (40–80)	59 (39–68)	0.625	59.5 (39–86)	57 (43–80)	0.752
Preoperative CA125 (U/ml) median (range)	1026 (19.56–3012)	837 (6.8-25000)	0.795	900 (6.8-25000)	570 (88-9935)	0.605
Ascites Y/N number	3/5	36/16	0.119	29/17	9/4	0.754
Preoperative neutrocytes (G/l) median (range)	7.665 (3.69–8.51)	6.02 (3.27–10.99)	0.502	5.925 (3.27–10.99)	6.15 (5.3–8.89)	0.221
Preoperative lymphocytes (G/l) median (range)	1.63 (1.18–2.11)	1.43 (0.43–3.02)	0.394	1.5 (0.43–3.02)	1.4 (0.64–2.27)	0.991
FIGO I	1	7	0.914	5	3	0.456
FIGO II	0	1		1	0	
FIGO III	7	41		39	9	
FIGO IV	0	2		1	1	
Residual disease: 0 cm	1	2	0.705	6	2	0.659
Residual disease: <1 cm	2	20		19	3	
Residual disease: >1 cm	5	24		21	8	
Platin sensitive	6	28	0.081	15	3	1.000
Platin refractor / resistance	0	18		27	7	

No matter *EGFL7* was expressed in cancer epithelium, endothelium or in both it had no impact on OS ($p = 0.761$, $p = 0.849$, $p = 0.995$, respectively).

ICAM-1 expression

We observed that ICAM-1 was expressed by both cancer and endothelial cells (Fig. 1C). ICAM-1 expression in cancer cells was noted in 47 cases (79.66%) and in endothelial cells in 46 cases (77.97%); in 40 cases (67.8%) the expression was observed in both compartments. ICAM-1 expression in cancer cells was score with High-score method [21] with the median expression level of 20 (range 0 to 200). Endothelial ICAM-1 expression was calculated as the proportion of positive vessels (median 18.75%, range 0%-94.12%) and then scored semi-quantitatively with a 4-tier system using the thresholds of 1%, 30% and 60% [18]. Thus, 13 cases (22.03%) were scored as 0, 25 (42.37%) as 1+, 12 (20.34%) as 2 + and 9 (15.25%) as 3+. We observed no correlation (Spearman's rho) between ICAM-1 expression in either compartment and the analyzed clinicopathological features ($p > 0.05$).

Based on the median ICAM-1 score in cancer cells (20), we dichotomized the group into high expressing subgroup (22 cases, 37.29%) and low expressing subgroup (37 cases, 62.71%). Similarly, the median proportion of ICAM-1-positive vessels (18.75%) was used to divide the high expressing subgroup (30 cases, 50.85%) and low expressing subgroup (29 cases, 49.15%). The clinicopathological characteristics related to ICAM-1 status of cancer and endothelial cells are depicted in Table 2 and Table 3, respectively. We observed no differences in OS or PFS between high and low ICAM-1 expression in either compartment ($p > 0.05$).

We observed no significant association between *EGFL7* and ICAM-1 expression in either compartment ($p > 0.05$). *EGFL7* expression in cancer cells was observed in 6/47 (12.77%) ICAM-1-positive and in 3/12 (25.00%) ICAM-1-negative tumors; ICAM-1 scores were also similar whether *EGFL7* was expressed or not. Analogously, *EGFL7* expression in endothelia was observed in 7/46 (15.21%) ICAM-1-positive and in 1/13 (7.69%) ICAM-1-negative cases; the proportions of ICAM-1 expressing vessels were also similar in both groups (Fig. 2).

Immunohistochemistry for CD4 + and CD8 + cells

Both, CD4 + and CD8 + T cells were detected within cancer cell nests and sporadically in the mesenchymal stroma (Fig. 1A, Fig. 1B). For purpose of this study intraepithelial (IE) CD4 + and CD8 + infiltrates were further evaluated. The median number of (IE)CD4 + and (IE)CD8 + cells was 5 (range 0.33–26.33) and 12.33 (range 1.00–53) per single (HPF), respectively.

Association of mRNA Egfl7 status with (IE)CD4 + and (IE)CD8 + cells.

Further, we compared the number of (IE)CD4 + and (IE)CD8 + infiltrates between tumor with different *EGFL7*-status of cancer epithelium and endothelium.

Tumors with *EGFL7*-positive cancer cells ($n = 9$) were less infiltrated with (IE)CD4 + and (IE)CD8 + lymphocytes compared to negative ones ($n = 50$) (median 1.67, range 0.33–12.33 vs. median 6.00, range 0.67–26.33, $p = 0.022$ and median 5.00 range 1.0 to 12.67 vs. 13.17 range 1 to 53, $p = 0.04$, respectively).

Tumors with *EGFL7*-positive endothelial cells ($n = 8$) were less infiltrated with (IE)CD4 + and (IE)CD8 + lymphocytes compared to negative ones ($n = 51$) (median 2.0, range 0.33-10.00 vs. median 6.00, range

0.33–26.33, $p = 0.029$ and median 5.00 range 1.0 to 18.0 vs. 12.67 range 1 to 53, $p = 0.031$, respectively).

Tumors having simultaneously *EGFL7*-positive cancer and endothelial cells ($n = 4$) were less infiltrated with (IE)CD4+ and (IE)CD8+ lymphocytes compared to the negative ones ($n = 55$) (median 1.00 range 0.33–3.00 vs. median 5.67, range 0.33–26.33, $p = 0.007$ and median 1.83 range 1.0 to 12.67 vs. 12.67 range 1 to 53, $p = 0.013$, respectively).

Discussion

EGFL7 expression has been previously analyzed in one study on human ovarian cancer tissue samples derived from 177 patients [22]. In that study immunohistochemical staining for *EGFL7* was performed using formalin fixed paraffin-embedded tissue microarrays. 72 of 177 analyzed cases (40.7%) had tumors with serous histology, but information about grading was not specified [22]. High levels of *EGFL7* expression were noted in 23 of 72 (31.9%) serous cancers. Survival analysis performed for the entire cohort showed that the epithelial ovarian cancer patients having tumors with high *EGFL7* expression had a poorer DFS but similar OS to those with low *EGFL7* expression [22].

Here, we analyzed *EGFL7* mRNA transcripts in HGOSC using different methodology, thus, the results of both studies are difficult to compare.

Interestingly, our study supports the suggestion that *EGFL7* expression is frequent in epithelial ovarian cancers as we detected *EGFL7* mRNA transcripts in 13 of 59 (22.03%) HGOSC cases. Unfortunately, we did not manage to perform quantitative analyses of mRNA in microdissected tissue samples, thus, the impact of intensity of expression of *EGFL7* mRNA on OS and PFS was not assessable. However, *EGFL7*-status of tumor microenvironment (cancer epithelium and adjacent endothelium) had no predictive and prognostic value in analyzed cohort of HGOSC patients.

EGFL7-expression levels were found to correlate with a higher tumor grade in gliomas [23] and colon cancer [24], not influencing the prognosis. However, it conferred poorer prognosis and higher metastatic score in hepatocellular carcinoma [25], but better prognosis and absence of lymph node invasion in human breast cancer [26]. These ambiguous results indicate that *EGFL7* expression in human cancer needs to be carefully analyzed as *EGFL7* may play a

complex role in cancer biology depending on cancer origin [23–26] and the source of *EGFL7* secretion: cancer cells, endothelium or both.

Since it had been proven that *EGFL7* is plasma membrane-associated sialidase, which could accumulate in distant tissues from the producing cells [15], it is impossible to answer if expression of *EGFL7* observed in OvCas [22] comes from activated cancer epithelium or up-regulated endothelial cells in the surrounding stroma. Therefore, we had decided to analyze the impact of *EGFL7* on diapedesis using LCM technology, which enables to harvest the epithelial and endothelial cells directly to give histologically enriched cell populations for separate qPCR analyses [19].

We expected to detect *EGFL7* mRNA at least in endothelial cells as these reflect upregulation of *EGFL7* gene in activated cancer vessels due to neoangiogenesis and/or inflammatory process. Presence of *EGFL7* mRNA transcripts found in microdissected cancer cells indicates the endogenous activation of *EGFL7* gene in human HGOSCs. To the best of our knowledge this is the first study documenting activation of *EGFL7* in human HGOSC. Interestingly the frequency of epithelial and endothelial activation of *EGFL7* was comparable. Further, ICAM-1 was also found to be expressed both on cancer epithelium and endothelium of adjacent stromal vessels thus we decided to assess the correlation between *EGFL7* and ICAM-1 matched according the source of origin.

Although it was suggested that *EGFL7* negatively regulates the expression of ICAM-1 in endothelial cells [27] we did not find the difference in the intensity of ICAM-1 expression between endothelium with different *EGFL7*-status. Similarly lack of difference of ICAM-1 expression was observed for cancer ICAM-1 expressing cells with different *Egfl7*-statuses.

Our understanding of the role of ICAM-1 in ovarian cancer development remains limited. The elevated expression of ICAM-1 in freshly isolated ovarian cancer cells [28] suggest that ICAM-1 expression may promote the malignant progression of ovarian cancer. Findings of studies on other malignant tumors suggest that ICAM-1 contributes to carcinogenesis by at least two mechanisms. It mediates the accumulation of inflammatory cells, which facilitates the instability of the tumor environment, triggers tumorigenesis, and maintains the release of trophic factors to enhance cancer cell survival [29, 30]. Second, ICAM-1 partially mediates the invasive and metastatic potential of cancer cells [29–33]. These observations were not confirmed for our cohort of HGOSC patients as we found that cancer-ICAM-1 expression was not correlated with FIGO stage and lacked prognostic significance.

To assess the potential impact of *EGFL7* on diapedesis we decided to compare intraepithelial immune infiltrates between tumors having *EGFL7* activated in cancer nests and/or adjacent vessels and those without *EGFL7* activation.

Presence of *EGFL7* mRNA transcripts in epithelium and/or endothelium of tumor microenvironment was associated with a lower influx of adaptive immune effectors (CD4 + and CD8 + lymphocytes) into cancer nests. This provides direct information that in some part, immune escape is achieved by limiting the influx of immune effectors into cancer tissue by activation of *EGFL7*. The role of epithelial and endothelial *EGFL7* should be further evaluated in HGOSCs.

The weakness of the current study is the lack of quantitative assessment of *EGFL7*, the retrospective design and the small size of cohort involved. Its strength lies of separate analyses of *EGFL7* transcripts in epithelium and adjacent endothelium of histologically homogenic group HGOSC tissue samples and consistency of the treatment of patients under uniform standards enabling the assessment of the prognostic significance of all the analyzed biomarkers.

Conclusion: Endogenous *EGFL7* activation in cancer cells and its upregulation in endothelium are frequent in HGOSCs and could negatively impact diapedesis. *EGFL7* associated down-regulation of ICAM-1 was

not observed. Function and predictive value of *EGFL7* mRNA transcripts should be evaluated in larger cohorts.

List Of Abbreviations

Egfl7 - Epidermal Growth Factor like domain 7

OvCa - Ovarian cancer

ICAM-1 - intercellular adhesion molecule-1

VCAM-1 - vascular cell adhesion molecule-1

LCM - Laser Capture Microdissection

HGSOC - High Grade Ovarian Serous Carcinoma

PDS - primary debulking surgery

FIGO - The International Federation of Gynecology and Obstetrics

FFPE - formalin-fixed paraffin-embedded

IHC - immunohistochemical

DFS - disease free survival

PFS - progression free survival

OS - overall survival

HPF - high-power field

IE - intraepithelial

Declarations

Ethics approval and consent to participate: The patients were informed that surgical specimens would be used for conventional pathological diagnosis and that the remaining tissues would be used for research. No personal patient data was required for this study and the protocols carried no risk, so only verbal informed consent was required from the patients. The protocol was approved by the Ethics Committee of Medical University of Gdansk (Permit Number: NKBBN/263/2012).

Consent for publication: not applicable

Availability of data and materials: The datasets used and/or analysed during the current study are available from the corresponding author on reasonable request. **Competing interested:** The authors declare that they have no competing interests.

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Authors' contributions

Study concepts and design: JJSz, Data acquisition: AZ, NK, JJSz. Quality control of data and algorithms: AZ, NK, BW. Data analysis and interpretation: JJSz, AZ, WB. Statistical analysis: AZ, JJSz, MB. Manuscript preparation: JJSz. Manuscript editing: JJSz, MB, WB. Manuscript review: WB, JJSz, AZ, NK, BW, MB. All authors read and approved the final manuscript.

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References

1. Jemal A, Bray F, Center MM, Ferlay J, Ward E, Forman D. Global cancer statistics. *Ca Cancer J Clin.* 2011;61:69–90. doi:.
2. Yigit R, Massuger L, Figdor CG, Torensma R. Ovarian cancer creates a suppressive microenvironment to escape immune elimination. *Gynecol Oncol.* 2010;117:366–72. doi:.
3. Ogino S, Galon J, Fuchs CS, Dranoff G. Cancer immunology—analysis of host and tumor factors for personalized medicine. *Nat Rev Clin Oncol.* 2011;8:711–9. doi:.
4. Quesnel B. Tumor dormancy and immune escape. *APMIS.* 2008;116:685–94. doi:.
5. Muller WA. Mechanisms of transendothelial migration of leukocytes. *Circ Res.* 2009;105:223–30. doi:.
6. Wu NZ, Klitzman B, Dodge R, Dewhirst MW. Diminished leukocyte-endothelium interaction in tumor microvessels. *Cancer Res.* 1992;52:4265–8.
7. Castermans K, Griffioen AW. Tumor blood vessels, a difficult hurdle for infiltrating leukocytes. *Biochim Biophys Acta.* 2007;1776:160–74. .
8. Liu Z, Guo B, Lopez RD. Expression of intercellular adhesion molecule (ICAM)-1 or ICAM-2 is critical in determining sensitivity of pancreatic cancer cells to cytotoxicity by human gamma delta-T cells: implications in the design of gamma delta-T-cell based immunotherapies for pancreatic cancer. *J Gastroenterol Hepatol.* 2009;24:900–11. doi:.
9. Piali L, Fichtel A, Terpe HJ, Imhof BA, Gisler RH. Endothelial vascular cell adhesion molecule 1 expression is suppressed by melanoma and carcinoma. *J Exp Med.* 1995;181:811–6. doi:.

10. Kuzu I, Bicknell R, Fletcher CD, Gatter KC. Expression of adhesion molecules on the endothelium of normal tissue vessels and vascular tumors. *Lab Invest.* 1993;69:322–8.
11. Griffioen AW, Damen CA, Martinotti S, Blijham GH, Groenewegen G. Endothelial intercellular adhesion molecule-1 expression is suppressed in human malignancies: the role of angiogenic factors. *Cancer Res.* 1996;56:1111–17.
12. Dirkx AE, Oude Egbrink MG, Kuijpers MJ, van der Niet ST, Heijnen VV, Bouma-ter Steege JC, et al. Tumor angiogenesis modulates leukocyte-vessel wall interactions in vivo by reducing endothelial adhesion molecule expression. *Cancer Res.* 2003;63:2322–9.
13. Parker LH, Schmidt M, Jin SW, Gray AM, Beis D, et al. The endothelial cell-derived secreted factor Egr1 regulates vascular tube formation. *Nature.* 2004;428:754–8. .
14. Soncin F, Mattot V, Lionneton F, Spruyt N, Lepretre F, Begue A, et al. VE-cadherin, an endothelial repressor of smooth muscle cell migration. *Embo J.* 2003;22:5700–11. doi:.
15. Lelièvre E, Hinek A, Lupu F, Buquet C, Soncin F, Mattot V. VE-cadherin/egr1 regulates vascular elastogenesis by interacting with lysyl oxidases. *Embo J.* 2008;27:1658–70. doi:.
16. 10.5301/JBM.2013.10568
Fan C, Yang LY, Wu F, Tao YM, Liu LS, Zhang JF, He YN, Tang LL, Chen GD, Guo L. The expression of Egr1 in human normal tissues and epithelial tumors. *Int J Biol Markers.* 2013 Apr 23;28(1):71–83. doi: .
17. Delfortrie S, Pinte S, Mattot V, et al. Egr1 promotes tumor escape from immunity by repressing endothelial cell activation. Published Online First on October 28, 2011; doi:.
18. Pannier D, Philippin-Lauridant G, Baranzelli MC, Bertin D, Bogart E, Delprat V, Villain G, Mattot V, Bonnetterre J, Soncin F. High expression levels of egr1 correlate with low endothelial cell activation in peritumoral vessels of human breast cancer. *Oncol Lett.* 2016 Aug;12(2):1422–8. doi:.
19. Espina V, Wulfkuhle JD, Calvert VS, VanMeter A, Zhou W, Coukos G, Geho DH, Petricoin EF 3rd, Liotta LA. Laser-capture microdissection. *Nat Protoc.* 2006;1(2):586–603. .
20. Prat J, FIGO Committee on Gynecologic Oncology. Staging classification for cancer of the ovary, fallopian tube, and peritoneum. *Int J Gynaecol Obstet.* 2014;124:1–5. doi:.
21. Lipponen PK, Colon Y. Simple quantitation of immunohistochemical staining positive in microscopy for histopathology routine. *Acta Sterol* 1992; 11/1:125–132. URL: .
22. Oh J, Park SH, Lee TS, Oh HK, Choi JH, Choi YS. High expression of epidermal growth factor-like domain 7 is correlated with poor differentiation and poor prognosis in patients with epithelial ovarian cancer. *J Gynecol Oncol.* 2014 Oct;25(4):334–41. doi: .
23. Huang CH, Li XJ, Zhou YZ, Luo Y, Li C, Yuan XR. Expression and clinical significance of EGFL7 in malignant glioma. *J Cancer Res Clin Oncol.* 2010;136:1737–43. doi:.
24. Diaz R, Silva J, Garcia JM, Lorenzo Y, Garcia V, Pena C, et al. Deregulated expression of miR-106a predicts survival in human colon cancer patients. *Genes Chromosomes Cancer.* 2008;47:794–802. doi:.

25. Wu F, Yang LY, Li YF, Ou DP, Chen DP, Fan C. Novel role for epidermal growth factor like domain 7 in metastasis of human hepatocellular carcinoma. *Hepatology*. 2009;50:1839–50. doi:.
26. Philippin-Lauridant G, Baranzelli MC, Samson C, Fournier C, Pinte S, Mattot V, Bonnetterre J, Soncin F. Expression of Eglf7 correlates with low-grade invasive lesions in human breast cancer. *Int J Oncol*. 2013;42(4):1367–75. doi:.
27. Delfortrie S, Pinte S, Mattot V, Samson C, Villain G, Caetano B, LauridantPhilippin G, Baranzelli MC, Bonnetterre J, Trottein F, et al. Eglf7 promotes tumor escape from immunity by repressing endothelial cell activation. *Cancer Res*. 2011;71:7176–86. doi:.
28. Santin, AD, Rose GS, Hiserodt JC, Fruehauf J, Eck LM, Garcia RI, Schranz V, Disaia PJ, Pecorelli S, Granger GA. Effects of cytokines combined with high-dose gamma irradiation on the expression of major histocompatibility complex molecules and intercellular adhesion molecule-1 in human ovarian cancers. *Int. J. Cancer* 1996;65:688–694. .
29. Lin YC, Shun CT, Wu MS, Chen CC. A novel anticancer effect of thalidomide: inhibition of intercellular adhesion molecule-1-mediated cell invasion and metastasis through suppression of nuclear factor-kappaB. *Clin Cancer Res*. 2006;12:7165–73. DOI:.
30. Roland CL, Harken AH, Sarr MG, Barnett CC Jr. ICAM-1 expression determines malignant potential of cancer. *Surgery*. 2007;6:705–7. DOI:.
31. Brooks KJ, Coleman EJ, Vitetta ES. The antitumor activity of an anti-CD54 antibody in SCID mice xenografted with human breast, prostate, non-small cell lung, and pancreatic tumor cell lines. *Int J Cancer*. 2008;123:2438–45. doi:.
32. Miele, M.E., Bennett, C.F., Miller, B.E., Welch, D.R. Enhanced metastatic ability of TNF-alfa-treated malignant melanoma cells is reduced by intercellular adhesion molecule-1 (ICAM-1, CD54) antisense oligonucleotides. *Exp Cell Res*. 1994;1:231–41. .
33. Wang S, Coleman EJ, Pop LM, Brooks KJ, Vitetta ES, Niederkorn JY. Effect of an anti-CD54 (ICAM-1) monoclonal antibody (UV3) on the growth of human uveal melanoma cells transplanted heterotopically and orthotopically in SCID mice. *Int J Cancer*. 2006;118:932–41. .

Figures

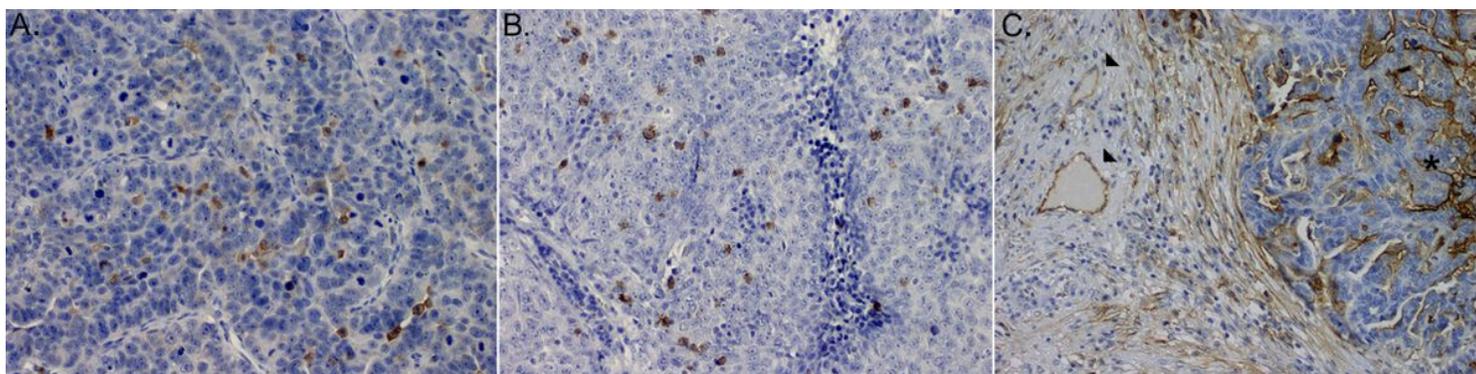


Figure 1

Microphotograph of immunohistochemical staining for: A) (IE)CD4+ lymphocytes, B) (IE)CD8+ lymphocytes, C) ICAM-1 within primary HGSOCs: (stars) expression on cancer cells, (arrows) expression on immune cells.

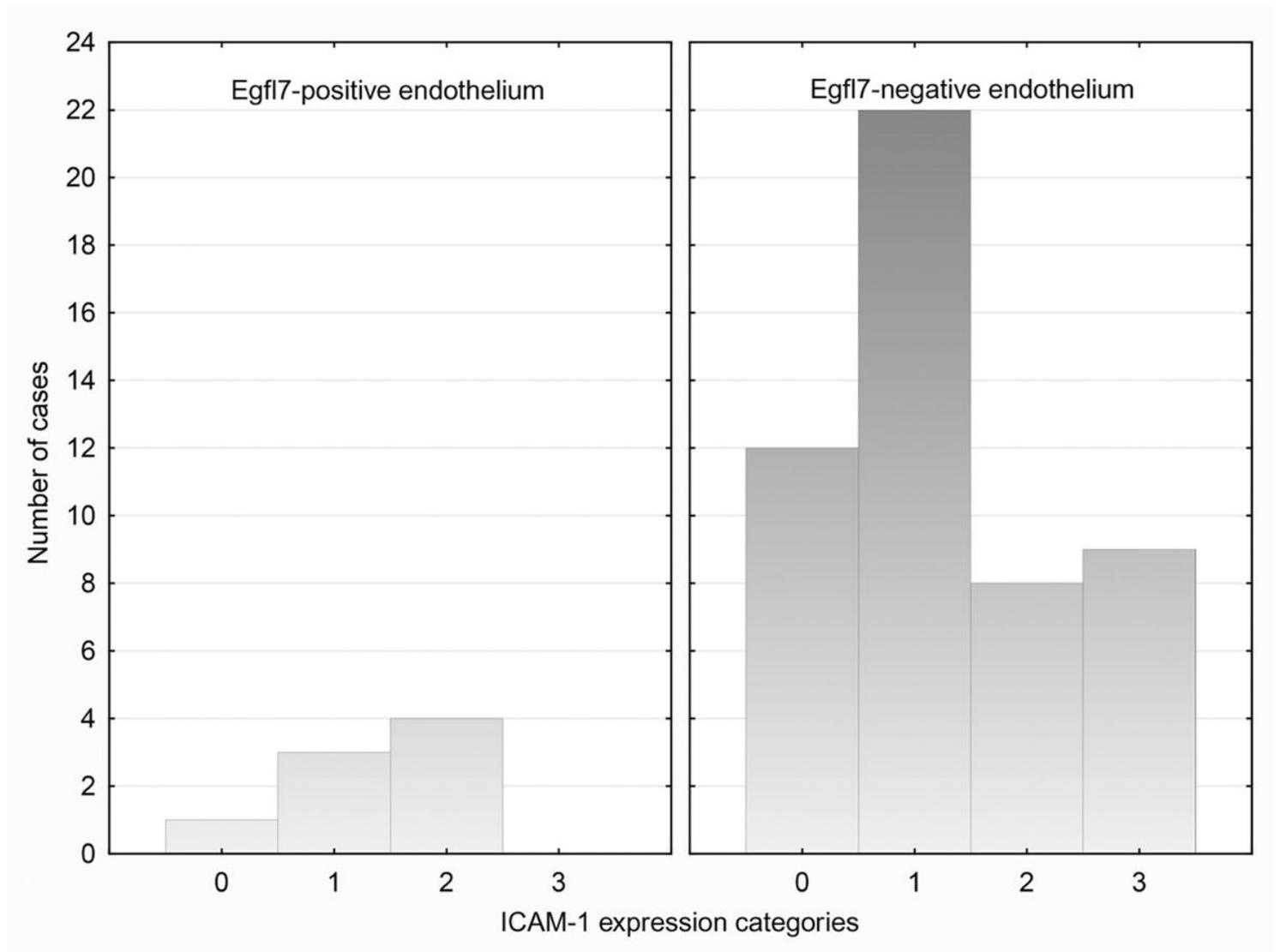


Figure 2

Categories of endothelial-ICAM-1 expression in relation to Egfl7 status of endothelial cells

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