

ORIGINAL ARTICLE

Mechanisms of AEG-1 and CXCR4 gene expression regulating the epithelial-mesenchymal transition pathway involved in brain metastases of breast cancer

YanJun Chen¹, XinJun Wang²

¹Department of General Surgery; ²Department of Neurosurgery, the Fifth Affiliated Hospital of Zhengzhou University, Zhengzhou, Henan, 450052 China

Summary

Purpose: To study the astrocyte elevated gene (AEG)-1 in breast cancer and the mechanism of the chemokine receptor CXCR4 regulating the epithelial-mesenchymal transition (EMT) involved in brain metastases of breast cancer.

Methods: A total of 20 breast cancer patients with and 40 without brain metastases were recruited. The expressions of AEG-1, CXCR4, E-cadherin, N-cadherin and α -SMA were detected by immunohistochemical staining, real-time (RT) quantitative (q) PCR and Western blot respectively in cancer and adjacent normal tissues.

Results: The expressions detected in the adjacent normal

tissues from both groups showed no significant difference ($p>0.05$). In the group with brain metastases, AEG-1, CXCR4, N-cadherin, α -SMA, mRNA and the relative expression level of protein were higher than those of patients without brain metastases, while E-cadherin showed the opposite trend.

Conclusion: AEG-1 and CXCR4 activate and regulate the EMT pathway to participate in brain metastases.

Key words: AEG-1, brain metastases, breast cancer, CXCR4, EMT

Introduction

The incidence of breast cancer ranks second among all malignant tumors in females, the first being cervical cancer. Comprehensive application of surgery, radiotherapy and chemotherapy, endocrine and targeted therapy can significantly prolong survival of patients [1]. However, the incidence of distant metastases increases at the same time and approximately 30-60% of the patients eventually die of brain metastases [2]. The EMT pathway participates in the local invasion and distant metastases of cancer cells as well as locating the target organ. It therefore plays an important role in the occurrence and development of breast cancer, cervical cancer, gastric cancer and colorectal cancer [3,4]. Its degree of activation is controlled by a variety of genes such as AEG-1 and

chemokine receptor CXCR4 [5,6]. As shown by Brown et al. [7], AEG-1 as a proto-oncogene participates in the genesis, progression, invasion and metastases of breast cancer. AEG-1 is found with elevated expression and increased activity in multiple malignant tumors but low to no expression in normal and benign cells. The overexpression of AEG-1 can increase the metastases and invasion of tumors while silencing the gene can lower its malignant biological ability [8], which suggests that AEG-1 may participate in regulating the location of transfer sites. CXCR4 is a member of the G-protein-coupled receptor superfamily and plays an important role in the process of tumor proliferation, infiltration, angiogenesis and metastases and is closely related to the homing and transmis-

sion of immune cells [9,10]. Therefore, this study focused on the mechanisms of AEG-1 and CXCR4 regulating EMT pathway in brain metastases of breast cancer, providing a new target for early diagnosis and intervention.

Methods

Subject information

A total of 20 patients with brain metastases from breast cancer and 40 breast cancer patients without brain metastases were recruited from June 2014 to June 2016. Breast cancer tissues and adjacent normal tissues (at least 3cm away from the tumor) were obtained. The mean age of patients with brain metastases was 66.6 ± 12.3 years with 5 cases with triple-negative cancer. The mean diameter of the primary tumor was 3.6 ± 0.7 cm. The mean age of patients without brain metastases was 66.5 ± 14.7 years with 11 cases of triple-negative cancer and the mean diameter of primary tumor was 3.7 ± 0.9 cm. The baseline data of two groups were comparable.

Methods

Immunohistochemical staining, RTqPCR and Western blot were used to detect the expressions of AEG-1, CXCR4, E-cadherin, N-cadherin and α -SMA in the tumor tissues and adjacent normal tissues from both groups of patients. Tissue paraffin sections with thickness of about $4\mu\text{m}$ were made and preserved under -80°C . Three samples were randomly generated using each patient's cancer tissue and adjacent normal tissue.

Immunohistochemical staining

The sections were deparaffinized with xylene and hydrated by gradient ethanol. After incubation for 20 min at 37°C with 3% H_2O_2 normal goat serum was added dropwise and incubated at 27°C for 30 min. Monoclonal primary antibodies of mouse-anti-human AEG-1, CXCR4, E-cadherin, N-cadherin and α -SMA were added dropwise (Jiangsu Biyuntian Technology Co., Ltd, Nanjing, China; working concentration 1:2000). The

sections were then incubated in the wet box at 4°C overnight. The normal mouse IgG served as negative control. Then, polyclonal secondary antibodies of rabbit-anti-mouse IgG were added (Beijing Zhongshan-Golden Bridge Biological Technology Co., Ltd, China working concentration 1:500). The sections were incubated at 27°C for 20 min. Enzyme horseradish peroxidase (HRP)-labeled-streptavidin (Sigma, St. Louis, Mo, USA) was then added dropwise and the sections were incubated at 27°C for 20 min. The sections were washed with PBS buffer 5 min for 3 times. After treatments including DAB color development, hematoxylin stain, hydrochloric acid alcohol differentiation, gradient ethanol dehydration and xylene transparentization, the sections were sealed with neutral balsam, dried at room temperature and observed under light microscope. The results were determined using the semi-quantitative method according to the staining intensity and the proportion of stained cells. If the cytoplasm or nucleus were stained to dark brown, it was determined as positive. Zero point meant no positive staining, 1 weak staining, 2 medium staining and 3 strong staining. Positive cells ratio of $\leq 5\%$ was characterized as 0 points, 6-25% as 1 point, 26-50% as 2 points, 51-75% as 3 points and $> 75\%$ as 4 points. The two numbers were multiplied with a product of 0-3 categorized as negative and 4-12 categorized as positive.

RT-qPCR

Total RNA was extracted from cells by the conventional Trizol reagent. The concentration and purity were determined by ultraviolet spectrophotometer and cDNA was synthesized using the reverse transcription kit. Shanghai Biological Engineering Co., Ltd. synthesized primers according to the Gene bank sequence (Table 1). The reaction ingredients included 2 μl of cDNA and 3 μl of each of the forward and reverse primers + 0.5 μl of Taq polymerase + 1 μl of dNTPs + 3 μl of MgCl_2 + 10 \times 5 μl of buffer + 2.5 μl of ddH_2O . The reaction conditions were 95°C for 5min 95°C for 30s, 58°C for 30s and 72°C for 60s for a total of 30 cycles and ended with 72°C for 10min. The 2% agarose gel electrophoresis was used for identification of PCR products. The gel was then analyzed under ultraviolet spectrophotometry

Table 1. Target gene primer sequence

Target gene	Primer Sequence	bp
AEG-1	5'-AAATAGCCAGCCTATCAAGACTC-3' 5'-TTCAGACTTGGTCTGTGAAGGAG-3'	325
CXCR4	5'- GAACTTCCTATGCAAGGCAGTCC-3' 5'- CCATGATGTGCTGAAACTGGAAC-3'	246
E-cadherin	5'-ATCAAAGGTATCACGGCAAACG-3' 5'-CGGAGAGCTCGTCCACGTAT-3'	479
N-cadherin	5'- GTGCCATTAGCCAAGGGAATTCAGC-3' 5'- GCGTTCCTGTTCCACTCATAGGAG-3'	337
α -SMA	5'-CCGAGATCTCACCGACTACCTCA-3' 5'-GCAGTGGCCATCTCATTCTCAA-3'	144
GAPDH	5'- CGCGAGAAGATGACCCAGAT-3' 5'-GCACTGTGTTGGCGTACAGG-3'	128

with a digital gray line value analysis. The results were recorded using the $2^{-\Delta\Delta Ct}$ method.

Western blot

RIPA lysate was added to the tissue homogenate to extract the total protein of cells, which was quantified using the Coomassie brilliant blue method. The amount of protein in each sample were normalized using a β -actin antibody before each protein assay. Ten μ g of total protein were separated by 8% SDS-PAGE. The protein with a negative charge was transferred to the PVDF membrane with the addition of mouse-anti-human AEG-1, CXCR4, E-cadherin, N-cadherin and α -SMA monoclonal antibodies (1:2000, Invitrogen, Carlsbad, California, USA) and left overnight. The rabbit-anti-mouse polyclonal antibodies (1:500, Applied Biosystems, City Foster, California, USA) were then added and incubated at room temperature for 4hrs. The protein was then washed with PBS and applied with electrochemiluminescence (ECL) for protein detection. The results were scanned and analyzed semi-quantitatively using Lab Works 4.5 gel imaging system (Invitrogen, Carlsbad, California, USA) and recorded using Integrated Optical Density (IOD).

Statistics

SPSS20.0 software was used for the statistical analysis. The measurement was expressed as mean \pm standard deviation. Independent samples t test was used for inter-group comparisons. The number of count was recorded using the number of cases or their percents. Chi-square test was used for comparisons be-

tween groups. A p value less than 0.05 was considered to be statistically significant.

Results

Immunohistochemical staining results analysis

In cancer tissues, the positive expression rates of AEG-1, CXCR4, N-cadherin and α -SMA in patients with brain metastases were significantly higher than in patients without brain metastases ($p < 0.05$). There was no significant difference between the two groups in the adjacent normal tissues ($p > 0.05$) (Table 2).

RT-qPCT results analysis

The expressions of AEG-1, CXCR4, N-cadherin and α -SMA mRNA were significantly higher in patients with brain metastases than in patients without brain metastases ($p < 0.05$). There was no significant difference between the two groups in the adjacent normal tissues ($p > 0.05$) (Table 3).

Western blot results analysis

The expressions of AEG-1, CXCR4, N-cadherin and α -SMA mRNA were significantly higher in patients with brain metastases than in patients without brain metastases ($p < 0.05$). There was no significant difference between the two groups in the adjacent normal tissues ($p > 0.05$) (Table 4).

Table 2. Immunohistochemical staining analysis

Group	Cases, n	AEG-1 n (%)	CXCR4 n (%)	N-cadherin n (%)	α -SMA n (%)	E-cadherin n (%)
Cancer tissues with brain metastases	60	31 (51.7)*	33 (55.0)*	28 (46.7)*	25 (41.7)*	10 (16.7)*
Normal tissues with brain metastases	60	6 (10.0)#	8 (13.3)#	5 (8.3)#	3 (5.0)#	4 (6.7)#
Cancer tissues without brain metastases	120	40 (33.3)	45 (37.5)	32 (26.7)	33 (27.5)	47 (39.2)
Normal tissues without brain metastases	120	15 (12.5)	17 (14.2)	13 (10.8)	11 (9.2)	12 (10.0)

*brain metastases vs no brain metastases in cancer tissues, $p < 0.05$; #brain metastases vs no brain metastases in adjacent normal tissue, $p > 0.05$.

Table 3. RT-PCR results analysis

Group	AEG-1	CXCR4	N-cadherin	α -SMA	E-cadherin
Cancer tissues with brain metastases	0.4658 \pm 0.1235*	0.5526 \pm 0.1624*	0.6123 \pm 0.2132*	0.4869 \pm 0.2025*	0.1026 \pm 0.0652*
Normal tissues with brain metastases	0.1232 \pm 0.0564#	0.1625 \pm 0.0523#	0.2132 \pm 0.0629#	0.0659 \pm 0.0057#	0.0595 \pm 0.0062#
Cancer tissues without brain metastases	0.3262 \pm 0.1023	0.3524 \pm 0.1124	0.4215 \pm 0.1659	0.2659 \pm 0.1024	0.4568 \pm 0.1857
Normal tissues without brain metastases	0.1128 \pm 0.0629	0.1241 \pm 0.0427	0.2025 \pm 0.0852	0.0754 \pm 0.0052	0.0659 \pm 0.0033

* brain metastases vs no brain metastases in cancer tissues, $p < 0.05$; #brain metastases vs no brain metastases in adjacent normal tissue, $p > 0.05$

Table 4. Western blot results analysis

Group	AEG-1	CXCR4	N-cadherin	α -SMA	E-cadherin
Cancer tissues with brain metastases	0.45±0.13*	0.59±0.15*	0.63±0.21*	0.47±0.18*	0.12±0.05*
Normal tissues with brain metastases	0.11±0.05#	0.13±0.04#	0.20±0.07#	0.07±0.02#	0.05±0.01#
Cancer tissues without brain metastases	0.33±0.11	0.36±0.12	0.41±0.18	0.27±0.09	0.48±0.21
Normal tissues without brain metastases	0.12±0.04	0.13±0.05	0.23±0.13	0.08±0.02	0.07±0.02

* brain metastases vs no brain metastases in cancer tissues, $p < 0.05$; #brain metastases vs no brain metastases in adjacent normal tissue, $p > 0.05$

Discussion

This study showed that the expressions of AEG-1, CXCR4, N-cadherin and α -SMA mRNA were all significantly higher in patients with brain metastases than in those without brain metastases, while the expression of E-cadherin showed the opposite trend. There was no significant difference between the two groups in the adjacent normal tissues. This suggests that AEG-1 and CXCR4 are highly expressed in breast cancer tissues, activating and regulating the EMT pathway to participate in brain metastases.

Previous studies [11,12] suggest that the expression of AEG-1 is also closely related to TNM stage, pathological grade, therapeutic effect and survival. AEG-1 can be used as an early predictor of distant metastasis such as the brain and lung [13]. AEG-1 targeted inhibition can reduce the incidence of tumor recurrence and metastasis [14]. CXCL12 is the only natural chemokine known to bind and activate CXCR4. The CXCL12/CXCR4 signaling axis is involved in the development and progression of many tumors [15]. Using specific antibodies, selective peptides and siRNA to block the CXCL12/CXCR4 signal axis activation expression can significantly inhibit breast cancer metastasis to the lymph nodes and lung [16]. CXCR4 is involved in the metastasis of tumor cells to the target organ [17]. At the same time, CXCR4 is often highly expressed in common metastatic sites such as lymph nodes, lung, liver, brain and bone

marrow, while its expression is low in the kidney [18,19]. E-cadherin is a marker of epithelial phenotype while N-cadherin, α -SMA and vimentin are markers of mesenchymal phenotype. The decreased expression of epithelial phenotypic markers and increased expression of mesenchymal phenotypic markers are consistent with the EMT pathway and tumor metastasis [20]. EMT plays a major role in tumor recurrence and metastasis in malignant tumors of epithelial origin [21].

This study used multiple detection methods to detect the expressions of AEG-1, CXCR4 and multiple EMT markers in cancer tissues and adjacent tissues from breast cancer patients with brain metastases. It was suggested that AEG-1, CXCR4 and EMT markers could offer an early prediction of tumor recurrence and metastasis and provide important targets for early intervention. Next, overexpression or silencing of target can be used to confirm the value of regulating the biological behavior of tumor and provide a theoretical basis for clinical application. Then we can investigate the specific regulation mechanism of AEG-1, CXCR4 and EMT. Finally, the sensitivity and specificity curves of AEG-1, CXCR4 and EMT marker molecules can be established in early detection and used to improve the value of clinical application.

Conflict of interests

The authors declare no conflict of interests.

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