Concurrent Down-regulation of the EAF1 and the EAF2 Genes in the Invasive Ductal Carcinoma Type of Breast Cancer

Sogand Heydaran\textsuperscript{1*}; Sirous Naeimi\textsuperscript{2}; Hamid Galehdari\textsuperscript{3}
\textsuperscript{1}Islamic Azad University, Branch Kazerun, Province Fars, Iran.
\textsuperscript{1}\textsuperscript{*}sogandheydaran@yahoo.com
\textsuperscript{2}Islamic Azad University, Branch Kazerun, Province Fars, Iran.
\textsuperscript{3}Department of Genetics, Faculty of Science, Shahid Chamran University of Ahvaz, Ahvaz, Iran.

Abstract
In mammals, the EAF1 and EAF2 genes build an active transcription module with other components. These genes code for factors acting as potent inhibitor of the Wnt-β catenin pathway, which might be due to their function as tumor suppressor gene. Recently, the involvement of both above-mentioned factors was described in some human tumors, but not yet in breast cancer. Breast cancer is one of the most cancer cases in Iran after colon and stomach carcinoma. We aimed therefore to investigate for the first time a possible correlation between breast cancer and the EAF1 and the EAF2 gene expression.

We collected invasive ductal carcinoma tumor grading (grade 1 to 3) with marginal normal tissue from forty women diagnosed with breast cancer with the average age of 50 years old. All patients underwent triple marker test (ER/PR and Her2/neu), indeed the most of them were triple positive with few triple negative individuals. After RNA extraction, cDNA was synthesized for subsequent real-time polymerase chain reaction. The humanRPL27 gene was used as endogenous control.

Analysis of real-time PCR results showed a significant down-regulation of EAF1 (p-value: 0.028), and of EAF2 (p-value: 0.0134) in tumor tissue samples in comparison to normal one. There was no correlation between clinical parameters and the target genes.

We could find significant connection between both tumor suppressor genes in triple positive and triple negative breast cancer patients, which deserves more attention.

Key-words: Breast Cancer, Invasive Ductal Carcinoma, Elongation Factor, EAF1, EAF2.

1. Introduction

The Elongation Factor for RNA Polymerase II (ELL) is a protein coding gene identified firstly in myeloid leukemia as a fusion partner gene in the 11;19 chromosome translocation (1). The
ELL also plays an early role before its assembly into the Elongation factor component of the super elongation complex (SEC) by stabilizing RNA polymerase II recruitment/initiation and entry into the pause site (2). In addition to ELL, researchers have identified several other factors as regulator of mRNA synthesis during the elongation phase (3). The function of a group of these factors including Elongin, TFIIF, and ELL, is to facilitate the processivity of transcription by suppressing transient pausing by Pol II (4).

Investigation by yeast two hybrid screen using ELL as the bait resulted in discovery of two ELL associated partners named as EAF1 & EAF2, respectively (5).

The EAF1 (ELL Associated Factor 1) is a protein coding gene that is associated with Eosinophilic angiocentric fibrosis (EAF) disease, also known as the IgG4-related systemic disease of unknown etiology (6).

EAF2 as the paralog gene to the EAF1 gene (ELL Associated Factor 2) is associated with prostate cancer (7). Both human EAF1 and EAF2 genes are strongly homologue to the vertebrates with evolutionary conserved domains (8). Recently, Jing-Xia et al. postulated a novel role for the EAF1 and the EAF2 factors as potent repressor of β-catenin in the Wnt signaling pathway. They also suggested the two EAF1 and EAF2 factors as tumor suppressor genes (8) that in this aspect might have distinct impact on the cell surveillance and/or apoptosis. As we know, the dysregulation of the Wnt signaling pathway, with accumulation of β-catenin in the cytosol as the consequence, is the main highlight in the pathogenicity of colon cancer in human. In this context, the dysfunction of upstream regulation factors including the EAF1 and the EAF2 would dramatically change the balance between oncogenes and tumor suppressor genes in the cell.

Based on the novel suggested function of the EAF1 and the EAF2, and because of unknown role of these factors in breast cancer (BC), their expression profile would provide useful information for better prognosis.

In the present study we aimed for the first time to analyze the EAF1 and the EAF2 gene expression in the invasive ductal carcinoma (IDC), as the most common aggressive type of BC in Iranian women (9,10). After colon and stomach cancer, BC is the most common type of cancers with higher mortality rate in Iran (11,12).

2. Methods

Sample collection: we selected forty patients with BC diagnosis for this study after informed consent. All samples have been collected from the Saadie's specialized Oncology hospital in Shiraz.
city locating in south Iran. Their age ranged between 38-60 years old with negative history of BC in family members. All patients underwent triple test for ER-PR-HER2 (hormone receptor for Estrogen, Progesterone, and Her2/neu). Fresh tumor and marginal normal tissue biopsies obtained from each patient that split in two parts: one part covered immediately with RNA-later (GeneAll ® Company, South Korea) and the other part used for pathologic diagnosis of breast carcinoma and grading of tumor. Ethical research committee of Medical university of Shiraz has approved the project under the resisted number 15230503971998.

After taking biopsy, immunohistochemically-staining assay performed as routine procedures for ER/PR/HER2 testing in the patient's specimens. The positive HER2 samples were definite as plus three, and other scoring (plus one and plus two) marked as negative.

RNA Extraction and cDNA Synthesis

RNA was extracted using Trizol ® (Invitrogen Company, Germany). Subsequently, DNase treatment and cDNA synthesis were done by Ampliqon ® (Denmark) as described by Company instructions.

Quantitative Expression Analysis of EAF1 and EAF2 Genes

We used here the RPL27 housekeeper gene as internal normalizer for SYBR-Green based real-time-PCR. We designed three Primer pairs by primer3® for EAF1, EAF2, and RPL27, respectively. Primer sequences and corresponding product size are shown in the table 1. All q-PCR reactions were triplicated for more accuracy.

Statistical analysis: Graph Pad Prism8®was used to analyze Mann–Whitney $t$- test and Anova one way, and correlation coefficient of target genes.

<table>
<thead>
<tr>
<th>Primer</th>
<th>Sequence</th>
<th>Accession number</th>
<th>Size</th>
</tr>
</thead>
<tbody>
<tr>
<td>EAF1-F</td>
<td>5-CAAGTTGGCAAGGAGATGAAG-3</td>
<td>NM_033083.7</td>
<td>105bp</td>
</tr>
<tr>
<td>EAF1-R</td>
<td>5-GTCTTTCTGGTAAAGCCGTTTG-3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>EAF2-F</td>
<td>5-GAAGGCAGAAGCTAGTCTAATGG-3</td>
<td>NM_018456.6</td>
<td>160bp</td>
</tr>
<tr>
<td>EAF2-R</td>
<td>5-ATGTCCTGAGACACACATATCC-3</td>
<td></td>
<td></td>
</tr>
<tr>
<td>RPL27-F</td>
<td>5-ATCGCCAAGAGATCAAAGAT-3</td>
<td>NM_000988.5</td>
<td>123bp</td>
</tr>
<tr>
<td>RPL27-R</td>
<td>5-TCTGAAGACATCCTATGGACG-3</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
3. Results

We had to exclude 16 from 40 samples because of inappropriate RNA concentration, or failure of clinical data of patients. From these samples, six patients were negative for ER and PR, and 14 samples positive for HER2/neu. In total, 10 samples were positive for triple marker. Four samples under 40 years old were positive for HER2/neu, but negative for PR/ER. The mentioned results were summarized in the figure 2.

The fold change calculation ($2^{\Delta\Delta Ct}$) revealed that the expression of both the $EAF1$ and the $EAF2$ genes in the tumor tissue compared to the normal tissue is significantly decreased ($p$-value for the $EAF1$ gene: 0.028, and for the $EAF2$ gene: 0.0134), respectively (figure 3).

Statically, there is no significant correlation between the $EAF1$ and the $EAF2$ genes in tumor tissue, regardless of demographic and clinical parameters (Tables 2 and 3).
Figure 2- Statically Analysis has shown significant down regulation of the *EAF1* and the *EAF2* genes (*p*-value for the *EAF1* gene: 0.028, and for the *EAF2* gene: 0.0134) in tumor tissue compared to normal tissue of BC patients.

Table 2- Correlation of the *EAF1* Gene Expression and Clinic-pathological Characteristics

<table>
<thead>
<tr>
<th></th>
<th>Patient (T) vs. ER</th>
<th>Patient (T) vs. PR</th>
<th>Patient (T) vs. HER2</th>
<th>Patient (T) vs. Grade</th>
<th>Patient (T) vs. age</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spearman r</td>
<td>0/1447</td>
<td>0/1447</td>
<td>-0/1641</td>
<td>-0/02323</td>
<td>-0/1503</td>
</tr>
<tr>
<td>95% confidence interval</td>
<td>-0/3441 to 0/5718</td>
<td>-0/3441 to 0/5718</td>
<td>-0/5850 to 0/3265</td>
<td>-0/4836 to 0/4472</td>
<td>-0/5756 to 0/3391</td>
</tr>
<tr>
<td>P value</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>P (two-tailed)</td>
<td>0/5545</td>
<td>0/5545</td>
<td>0/5020</td>
<td>0/9248</td>
<td>0/5392</td>
</tr>
<tr>
<td>P value summary</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>Exact or approximate P value?</td>
<td>Approximate</td>
<td>Approximate</td>
<td>Approximate</td>
<td>Approximate</td>
<td>Approximate</td>
</tr>
<tr>
<td>Significant? (alpha = 0.05)</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Number of XY Pairs</td>
<td>19</td>
<td>19</td>
<td>19</td>
<td>19</td>
<td>19</td>
</tr>
</tbody>
</table>

Table 3- Correlation of the *EAF2* gene expression and clinic-pathological characteristics

<table>
<thead>
<tr>
<th></th>
<th>patient(T) vs. ER</th>
<th>patient(T) vs. PR</th>
<th>patient(T) vs. HER2</th>
<th>patient(T) vs. Grade</th>
<th>patient(T) vs. age</th>
</tr>
</thead>
<tbody>
<tr>
<td>Spearman r</td>
<td>-0/1315</td>
<td>-0/1315</td>
<td>0/02332</td>
<td>0/1767</td>
<td>-0/1128</td>
</tr>
<tr>
<td>95% confidence interval</td>
<td>-0/5739 to 0/3703</td>
<td>-0/5739 to 0/3703</td>
<td>-0/4603 to 0/4963</td>
<td>-0/3297 to 0/6041</td>
<td>-0/5610 to 0/3865</td>
</tr>
<tr>
<td>P value (two-tailed)</td>
<td>0/6030</td>
<td>0/6030</td>
<td>0/9268</td>
<td>0/4831</td>
<td>0/6558</td>
</tr>
<tr>
<td>P value summary</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
<td>ns</td>
</tr>
<tr>
<td>Exact or approximate P value?</td>
<td>Approximate</td>
<td>Approximate</td>
<td>Approximate</td>
<td>Approximate</td>
<td>Approximate</td>
</tr>
<tr>
<td>Significant? (alpha = 0.05)</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
<td>No</td>
</tr>
<tr>
<td>Number of XY Pairs</td>
<td>18</td>
<td>18</td>
<td>18</td>
<td>18</td>
<td>18</td>
</tr>
</tbody>
</table>
4. Discussion

Knowingly, about eighty percent of BC patients are positive for ER/PR, and other twenty percent are positive for HER2/neu oncogene, which makes the tumor more aggressive (13). Usually, the age of onset in HER2/neu positive patients is lower (14). Frequently, HER2/neu negative younger women with BC have pathogenic mutations in the BRCA1 gene. Here, we calculated the average age of ten BC patients negative for HER1/neu as 40.6 years old. It is to mention that the average age of onset for BC in Iran is about 46 to 49 years (15), which is reflecting in our total samples, but the average age of our patients negative for HER2/neu oncogene is much lower as general BC population in Iran. However, we recommend the BRCA1 gene mutation screening for at least these ten cases. On the other hand, the mutation frequency in the BRCA1 gene in BC affected women in Iran is much lower as reported for general BC patients, worldwide (16).

In the present study, we assessed for the first time the relative expression changes of the two tumor suppressor genes in Iranian women with the ductal type of breast cancer. Data showed that regardless of the age, triple marker condition, and tumor grading, the expression of the EAF1 and the EAF2 is significantly decreased. It could be possible that the significant down-regulation of both tumor suppressor genes promote tumorigenesis, at least in Iranian BC patients.

Recently, researchers have reported the significant down-regulation of both mentioned genes in prostate cancer in the mice model (17). They suggested that the cooperative working of the EAF1 and the EAF2 factors might be important for prostate epithelial hemostasis, and the failure of them would lead to malignancy in prostate tissue (17,18).

First evidence that the EAF1 and EAF2 factors might be a potent inhibitor of the canonical Wnt/β-catenin signaling reported by Liu and colleagues (18). They hypothesized that this ability might be a consequent of the TSG activity of both factors. Furthermore, the EAF family have conserved biological activities across diverse species (19). Previously, Nandini et al. suggested that the dysregulation of the Wnt-signaling pathway would be associated with metastasis in Triple negative BC (20), in despite of our study contain only few patients with triple negative BC. In addition, none of our patients was in metastasis stage. In this context, we can assume a higher risk of metastasis for such individuals, who eventually need more intensive care and therapy.

Recent report presumed a link between the Wnt/β-catenin signaling and the TNBC tumorigenesis by regulating the key tumor-associated characteristics, including migration, stemness, proliferation, and chemo resistance in TNBC cells and Cancer stem cells (CSCs) (21). Although, most of the participants in this study were triple positive, according to the gene expression results, it
can be assumed that the Wnt/β-catenin signaling might also be involved of yet unknown reasons in triple positive BC (TPBC) patients.

Our quantitative PCR data of these factors showed for the first time their significant downregulation in concurrent TNBC and TPBC, at least in Iranian women. Unfortunately, we could not access to a larger sample size to strengthen our data. Because of the importance of the possible novel involvement of the two TSG factors EAF1 and EAF2 in the breast tumorigenesis, and to increase the accuracy, we recommend to replicate the study with more BC samples.

Conflict of Interest

The authors declare that they have no conflict of interests.

Acknowledgments

The authors have special thanks to all the patients participating in this study.

Author Contributions

- **Conceptualization:** Hamid Galehdari
- **Funding acquisition:** Hamid Galehdari, Sogand Heydaran
- **Supervision:** Hamid Galehdari, Sirus Naeimi
- **Writing - original draft:** Sogand Heydaran
- **Writing - review & editing:** Sogand Heydaran, Hamid Galehdari

References


