

Identification of genes involved in breast cancer and breast cancer stem cells

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Abstract: Breast cancer is the most frequent type of cancer in women. Great progress has been made in its treatment but relapse is common. One hypothesis to account for the high recurrence rates is the presence of cancer stem cells (CSCs), which have the ability to self-renew and differentiate into multiple malignant cell types. This study aimed to determine genes that are expressed in breast cancer and breast CSCs and to investigate their correlation with stemness. RNA was extracted from established breast cancer cell lines and from CSCs derived from five different breast cancer patients. DNA microarray analysis was performed and any upregulated genes were also studied in other cancer types, including colorectal and lung cancer. For genes that were expressed only in breast cancer, knockdown-based experiments were performed. Finally, the gene expression levels of stemness transcription factors were measured. The outcome of the analysis indicated a group of genes that were aberrantly expressed mainly in breast cancer cells with stemness properties. Knockdown experiments confirmed the impact of several of these on *NANOG*, *OCT3/4*, and *SOX2* transcription factors. It seems that several genes that are not directly related with hormone metabolism and basic signal transduction pathways might have an important role in relapse and disease progression and, thus, can be targeted for new treatment approaches for breast cancer.

Keywords: breast cancer, cancer stem cells, stemness, DNA microarray

Introduction

Breast cancer is the most frequent type of cancer among women, with more than 230,000 new cases diagnosed in the US in 2013. It is the leading cause of death in women worldwide, and the second highest cause in the US among all cancer types.^{1,2} The treatment of breast carcinoma mainly involves conserving surgery or mastectomy, depending on the localization of the tumor and the stage.^{3,4} Chemotherapy and/or radiation therapy, as well as hormone-dependent therapies, is also used, depending on stage, histology, and biomarkers.⁵

One of the major problems in cancer treatment is multidrug resistance, as many breast tumors either possess or develop resistance to chemotherapeutic drugs.⁶ The recurrence of breast cancer is also an important issue in the treatment, and the ability to predict a pattern for breast cancer recurrence is of high priority for many researchers.⁷ According to previously published literature and experimental data, resistance and recurrence of breast cancer could be due to the existence of cancer stem cells (CSCs), the epithelial–mesenchymal transition, and the signaling transduction pathways as well as microRNAs.^{8–11}

CSCs have the ability to self-renew and initiate differentiation into heterogenic cancer cells, which may cause metastasis and relapse.¹² In breast cancer, it has been

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demonstrated that there is a linear relationship between the gene expression of stemness markers and the stage of the disease.¹³

Because these cells are correlated with the progression of the disease, as well as with resistance and recurrence of breast cancer, it is essential to investigate and identify new markers or new targets correlated with them. The present study aims to identify genes that are overexpressed in breast CSCs using samples from different patients and to ascertain any associations with stemness transcription factors.

The experimental data indicated a group of genes with high gene expression in breast CSCs, but not in breast, colon, and lung cancer cells. A possible relationship between these genes and stemness was ultimately demonstrated.

Materials and methods

Cell lines

Human breast CSCs (36102-29P; Celprogen, CA, USA), colon CSCs (36112-39P; Celprogen), and lung CSCs (36107-34P; Celprogen) were cultured in appropriate growth medium provided by the manufacturer (M36102-29E, M36112-39E, M36107-34E; Celprogen) in 25 cm² flasks (E36102-29-T25, E36112-39-T25, E36107-34-T25; Celprogen). The human carcinoma cell lines used were obtained from the European Collection of Cell Cultures – Health Protective Agency (ECACC-HPA, Salisbury, UK): MDA-MB 231, T47D, and MCF-7 are human breast cancer lines, COLO699N is a nonsmall-cell lung carcinoma line (NSCLC), and HCT-116 is a colorectal cancer line. Cells were cultured in 75 cm² flasks (5520200; Orange Scientific, Braine-l'Alleud, Belgium) in the recommended media supplemented with the appropriate amount of heat-inactivated fetal bovine serum (10106-169; Thermo Fisher Scientific, Waltham, MA, USA) and 2 mM L-glutamine (G5792; Sigma-Aldrich, Munich, Germany). The cells were incubated at 37°C in a 5% CO₂ environment.

Peripheral blood mononuclear cells were obtained from five breast cancer patients as well as from a healthy 30-year-old male. The blood samples were collected, placed in tubes with Ethylenediaminetetraacetic acid (EDTA) as an anticoagulant (Vacutainer K3E 7.2mg, Fisher Scientific, Pittsburgh, PA, USA), and rotated for 30 minutes to prevent coagulation. To isolate peripheral blood mononuclear cells, whole blood cells were centrifuged with polysucrose solution (Biocoll separating solution 1077; Biochrom, Germany). Mononuclear cells, lymphocytes, platelets, and granulocytes were collected after centrifugation and washed twice with phosphate-buffered saline (P3813; Sigma-Aldrich,

Munich, Germany). Cells from the healthy donor were then incubated at 4°C for 30 minutes with EpCAM magnetic beads (39-EPC-50; Gentaur, Belgium), while those from patients were incubated with pan-cytokeratin (39-CUST; Gentaur) at 4°C for 30 minutes. EpCAM is an epithelial cell adhesion molecule-associated antigen that is expressed in the vast majority of carcinomas.¹⁴ Following incubation, the samples were placed in a magnetic field, selected, and then washed with phosphate-buffered saline. The EpCAM-negative selected cells (noncancerous) and the pan-cytokeratin-positive cells were isolated and cultured in 25-cm² flasks with RPMI-1640 medium (R6504; Sigma). The endothelial cells were removed with CD31 beads (CD31-50; Gentaur).

After a few passages, spheres were observed in patient samples. They were collected and cultured in STEMPRO human embryonic stem cells (hESC) serum-free media (SFM) (A10007-01; Thermo Fisher Scientific), which contained Dulbecco's modified Eagle's medium (DMEM)/F12 supplemented with glutamax, mercaptoethanol, bovine serum albumin 25%, and STEMPRO hESC supplement. According to the recommended protocol, fibroblast growth factor (10 µg/mL) was added to the culture. The cells were then incubated at 37°C in a 5% CO₂ environment.

Patients

The first patient was a 67-year-old woman with early diagnosed breast cancer of an unknown stage who had received no previous therapies. The second cell line was derived from a 64-year-old woman with stage II breast cancer who had undergone chemotherapy and surgery treatment. The third sample was derived from a 58-year-old woman with stage II/III breast cancer who had been subjected to partial mastectomy and who had also undergone immunotherapy. The next patient was a 45-year-old woman with stage IV breast cancer. She had undergone adjuvant chemotherapy followed by radiotherapy. She had also received a modified radical mastectomy 5 years earlier. The last cell line was derived from a 43-year-old woman with stage IV breast cancer.

Each patient has consented writing and has given their permission for storage of samples as for their use in Research and Development purposes. This study is not a clinical trial and does not include intervention in patients. All procedures were conducted according to the standards of Safety, Bioethics, and Validation.

Evaluation of cells

Cells were tested using both cellular and molecular assays. The cellular assays were based on the ability of CSCs to form

microspheres in semisuspension, as detected with an inverted light microscope. The cultivated cells have previously been evaluated with molecular analysis, including gene expression analysis for specific transcription factors.^{15–18} The authentication of the control cell line was tested each time using molecular-based assays, such as short tandem repeats profiling, which was compared with the manufacturer's profile. The cultivation step was continued for >30 passages to exclude the possibility of any embryonic stem cells (ESCs) being included. CSCs are immortal, unlike ESCs.

RNA extraction

RNA was extracted from cells using a Magnetic mRNA Isolation Kit (S1550S; New England Biolabs, Hertfordshire, UK). The RNA samples were evaluated both spectrophotometrically and on agarose gels by checking the 18S–28S rRNA bands.

DNA microarrays

A total of 1 µg of the extracted RNA was prepared for DNA microarray experiments using the Amino Alkyl MessageAmp II kit (AM1753; Ambion, TX, USA) according to the manufacturer's protocol. The dye was performed by using the Amersham CyDye Post-labeling Reactive Dye Pack (RPN5661; GE Healthcare, Freiburg, Germany). The noncancerous sample was labeled with Cy3, while the breast samples were labeled with Cy5. For each sample, the noncancerous and cancerous samples were mixed together and hybridized on a Human Ready Array platform (HS1100; Microarrays Inc., AL, USA). The prehybridization, hybridization, and washing procedures were automated on the HS400Pro (TECAN, Switzerland). Finally, the slides were imaged on the InnoScan 710 (Innopsys, France) with 5 µM resolution.

Data analysis

Scanned microarray image data were used to process expression data by Array-Pro Analyzer 6.3 Software. The microarray gene expression data were normalized using background subtraction. All data were represented as a log₂ ratio for the expression analysis of gene transcription. Analysis of variance and *t*-test were used to evaluate the variant significance of gene expression in different groups. Genes with log₂ ratios of means >2 in all samples were further examined.

Molecular analysis

A total of 1 µg of RNA of each sample was used as a template for cDNA synthesis using an iScript cDNA synthesis kit (1708891; Bio-Rad Laboratories Inc., CA, USA). Genomic

DNA had been previously removed using an RNase-Free DNase Set (79254; Qiagen NV, Venlo, the Netherlands). The top strand was used as template for the real-time polymerase chain reaction (PCR) reaction, which was performed using iTaq Universal SYBR Green Supermix (1725124; Bio-Rad Laboratories Inc.). Specific primers for each marker and for the endogenous control gene (18S rRNA) were designed with Genamics Expression 1.1 software. The sequence of primers was run on BLAST to exclude those that amplified undesired genes. The sequences of the primers are presented in Table 1.

The PCR reaction program was set as follows: initial denaturation at 95°C, 50 cycles of denaturation at 95°C for 10 seconds followed by annealing at 59°C for 30 seconds. A final extension step was performed at 72°C for 10 minutes followed by melting curve analysis. Data were analyzed according to the Livak method.¹⁹ In all PCR reactions, positive and negative controls were used. The positive control was cDNA from a Universal Human Reference RNA (740000-41; Agilent Technologies, Santa Clara, CA, USA), and negative controls were no-template, no-enzyme, and controls that included human genomic DNA (G304A; Promega, WI, USA). Finally, a no-reverse transcription control was used in cDNA synthesis.

Knockdown

During the exponential phase of proliferation, commercial breast CSCs cells were plated in 24-well plates (E36102-29-24Well; Celprogen) and transfected with gene-specific small interfering RNAs (siRNAs) using Lipofectamine 2000 Reagent (11668-027; Thermo Fisher Scientific), according to the manufacturer's instructions. The siRNA molecules were designed in accordance with the rules of Reynolds et al.²⁰ The siRNA sequences were as follows:

HP: 5' UAAGGCUGUUGGAGAUAAAdTdT 3',
SMPD1: 5' UGAGGCUGCUGUCCUUUCAdTdT 3',
SCRIB: 5' GGACACACCUCACUACAAAdTdT 3',
KCMF1: 5' CCAAUGCAGUGCAUAUUAAdTdT 3',
FAM155B: 5' ACCUCGUGCUGCAUAAAUAdTdT 3',
PTGER3: 5' GAAUGCAACUUCUUCUUAAdTdT 3',
GPR3: 5' CAAAGACAGUGUCUAUUUAAdTdT 3',
TMX2: 5' UGCAGCUUCUGAUUUUAAAdTdT 3', and
DDX49: 5' CACGAGGACUGGUCCAUAUAdTdT 3'.

All sequences were run on BLAST to ensure that there was no risk of off-target effects. Following 48 hours incubation, cells were harvested by trypsinization (15090-046; Thermo Fisher Scientific). Samples incubated with Lipofectamine alone (without siRNA) were also tested to study the effect

Table 1 Primer pairs used in qPCR analysis

| Gene | Primer | Sequence (5'–3') | Amplicon length |
|----------|---------|----------------------------|-----------------|
| 18S rRNA | Forward | TGCCCTATCAACTTTCGATGGTAGTC | 112 bp |
| | Reverse | TTGGATGTGGTAGCCGTTTCTCA | |
| NANOG | Forward | TGAGATGCCTCACACGGAGACTG | 138 bp |
| | Reverse | GGGTTGTTTGCCTTTGGGACTG | |
| OCT3/4 | Forward | GGTGCCCTGCCCTTCTAGGAATG | 97 bp |
| | Reverse | TGCCCCACCCCTTTGTGTTC | |
| SOX2 | Forward | CAACGGCAGCTACAGCATGATG | 91 bp |
| | Reverse | GCGAGCTGGTCATGGAGTTGTA | |
| CD34 | Forward | CCCATGCTGGAGGTGACATCTC | 130 bp |
| | Reverse | CCAGGGAGCCGAATGTGTAAG | |
| HP | Forward | CTGTCATTGCCCTCCTGCTCTG | 131 bp |
| | Reverse | GCGAACCAGTGCTCCACATAG | |
| SMPD1 | Forward | CTCTGTCTGACTCTCGGGTCTCTG | 168 bp |
| | Reverse | CGAGGTTGATGGCGGTGAATAG | |
| SCRIB | Forward | TGCTGACGACCTGCGGAAGA | 158 bp |
| | Reverse | GTGGCTGCTCATCCTCCTGTTC | |
| KCMF1 | Forward | TGGGAGGGCAGTTTTTGAATG | 191 bp |
| | Reverse | TGAAGAAACGGAGATACACGGACAG | |
| FAM155B | Forward | TGGAGATACGGAAGGGGGAGAG | 114 bp |
| | Reverse | ACCTCAACACTTATCGCCCATCTC | |
| PTGER3 | Forward | GCTGGTCTCCGCTCCTGATAATG | 91 bp |
| | Reverse | TCTTTCTGCTTCTCCGTGTGTGTC | |
| GPR3 | Forward | GATGCCACTCTCCACCTCTCTAC | 144 bp |
| | Reverse | GAAGAGGAACAGCAGCAGCAGAC | |
| TMX2 | Forward | CATCACCCCTCACCAAGCAACTC | 118 bp |
| | Reverse | TCCTCAGAGAAGGTCCATGAGACAG | |
| DDX49 | Forward | GCCAAGTTCAAGTCCAGCATCTACC | 87 bp |
| | Reverse | GACCACCTGTACCGTAGGGATGTC | |

Abbreviations: qPCR, quantitative polymerase chain reaction; *HP*, haptoglobin; *SMPD1*, sphingomyelin phosphodiesterase 1, acid lysosomal; *SCRIB*, scribbled homolog (*Drosophila*); *KCMF1*, potassium channel modulatory factor 1; *FAM155B*, family with sequence similarity 155, member B; *PTGER3*, prostaglandin E receptor 3 (subtype EP3); *GPR3*, G protein-coupled receptor 3; *TMX2*, thioredoxin-related transmembrane protein 2; *DDX49*, DEAD (Asp-Glu-Ala-Asp) box polypeptide 49; *18SrRNA*, 18S ribosomal RNA; *NANOG*, Homeobox protein *NANOG*; *OCT3/4*, Octamer-binding transcription factor 3/4; *SOX2*, sex determining region Y-box 2; *CD34*, Hematopoietic progenitor cell antigen CD34.

of compound alone on gene expression. Finally, samples incubated with nonspecific siRNA were tested to study the specificity of the particular siRNA. The mRNA knockdown was calculated relative to a nontargeting control siRNA in each experiment. The experiments were repeated three times in triplicate. The expression level of the gene of interest and its percentage knockdown was calculated using the comparative threshold cycle (Ct) method:

$$\Delta Ct = Ct_{\text{target}} - Ct_{18\text{SrRNA}}$$

$$\Delta\Delta Ct = \Delta Ct_{(\text{siRNA treated})} - \Delta Ct_{(\text{siRNA nontreated})}$$

$$\text{Relative expression level} = 2^{-\Delta\Delta Ct}$$

$$\%KD = 100 \times (1 - 2^{-\Delta\Delta Ct})$$

Statistical analysis

The quantitative PCR (qPCR) results were assessed according to the Kolmogorov–Smirnov test; all samples had normal distribution. Median values were used for the analysis.

Mann–Whitney tests were also performed on the qPCR data. All the reactions (molecular assays, knockdown) were performed in triplicate three times. A *P*-value of <0.05 was considered significant. To ensure the differential expression of genes in knockdown experiments, *t*-test was run and the statistical significance was set to 0.05.

Results

DNA microarray

DNA microarray analysis of breast CSCs and patient cell lines demonstrated nine different genes with log ratios of >2. These genes included haptoglobin (*HP*), sphingomyelin phosphodiesterase 1, acid lysosomal (*SMPD1*), scribbled homolog (*Drosophila*) (*SCRIB*), potassium channel modulatory factor 1 (*KCMF1*), family with sequence similarity 155, member B (*FAM155B*), prostaglandin E receptor 3 (subtype EP3) (*PTGER3*), G protein-coupled receptor 3 (*GPR3*), thioredoxin-related transmembrane protein 2 (*TMX2*), and DEAD (Asp-Glu-Ala-Asp) box polypeptide 49 (*DDX49*). The positive controls,

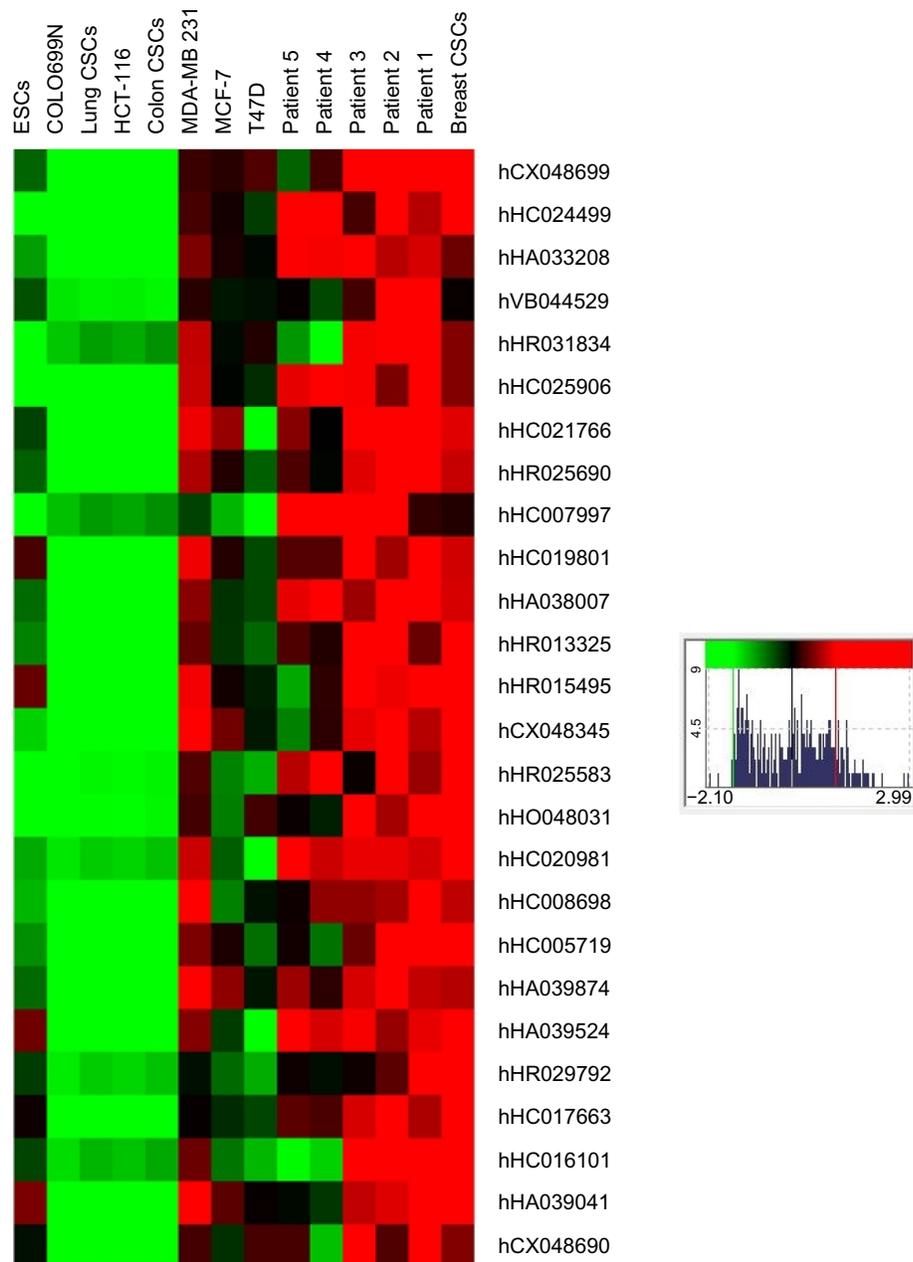


Figure 1 Microarray clustering analysis.

Notes: The color represents the expression level of the gene. Red represents high expression, while green represents low expression. The expression levels are continuously mapped on the color scale provided at the right of the figure. On the left the experiments are presented as heat maps with the name of samples on the top, and the names of probes on the right.

Abbreviations: ESCs, embryonic stem cells; CSCs, cancer stem cells.

as well the housekeeping genes, were expressed in all samples, while the negative controls were not. The heat map of genes with log ratio >2 are presented in Figure 1.

qPCR validation of DNA microarrays

The above genes were validated with qPCR assays for all samples. qPCR assays were also performed on other samples including normal samples, ESCs, colorectal and lung cancer cells, and CSCs of other cell lines representing lung and colorectal

cancer. The relative analysis revealed that some of the genes were expressed only in breast cancer while others were also expressed in lung and colon cancer. Among them, *HP*, *SMPDI*, and *FAM155B* were overexpressed in MCF-7 and MDA-MB 231 cell lines and in all patients. A lower level of overexpression was also observed in ESCs. *SCRIB* was overexpressed in four of the patients and in MCF-7 and MDA-MB 231 cell lines, as well as in ESCs. Low levels were evident in differentiated lung and colorectal cell lines. *KCMF1* was overexpressed in

four patients, in MCF-7 and MDA-MB 231 cell lines, and at lower levels in ESCs. *PTGER3* was overexpressed in two of the patients and in T47D cells. Upregulation was observed in three of the patients for *GPR3*. The expression rates were similar in MDA-MB 231 cells and lower in MCF-7 and ESCs. *TMX2* was overexpressed in all breast samples, both in patient-derived and commercial cell lines, but was not expressed in ESCs and in lung and colon cancer. Almost the same results were obtained for *DDX49*. Among all the patients, the expression levels did not show great difference (Figure 2).

Knockdown assays

The knockdown experiments were satisfactory only for *FAM155B*, *PTGER3*, *GPR3*, *TMX2*, and *DDX49*. The reduction in expression ranged from 20% to 40% for *FAM155B*, 35%–40% for *PTGER3*, 35%–50% in *GPR3*, 10%–25% in *TMX2*, and around 40% for *DDX49*. The phenotype of the cells was not particularly affected, except in those in which *TMX2* was knocked down (Figure 3). After *TMX2* knockdown, the cells seem to obtain more rounded formation, compared with the control. However, the change is not too great, so be considered significant. The cell population also was not affected in all cells.

Relative gene expression in stemness transcription factors

In the knocked-down samples, further qPCR experiments were performed to study the gene expression of *NANOG*, *OCT3/4*, *SOX2*, and *CD34*, both pre- and postknockdown. The knockdown of *FAM155B* led to a decrease in *CD34* and a small increase in the other transcription factors. The reduction in *GPR3* gene expression led to upregulation of *NANOG* transcription factor, and *OCT3/4* and *CD34* to lesser extent; no change was observed for *SOX2*. An increase in gene expression of *NANOG* and *OCT3/4* was observed post-*PTGER3* knockdown, while a decrease was observed in *CD34*. The reduction in *NANOG* was observed only after the knockdown of *TMX2*. Following suppression of *TMX2*, a decrease in *OCT3/4* and *SOX2* was also observed. Finally, the suppression of *DDX49* led to the lowest levels of *SOX2* and *OCT3/4* in parallel with an increase in *NANOG* and *CD34* (Figure 4).

Discussion

Breast cancer affects the highest proportion of women compared with other types of cancers. Although progress has been made in its diagnosis and treatment, much research continues

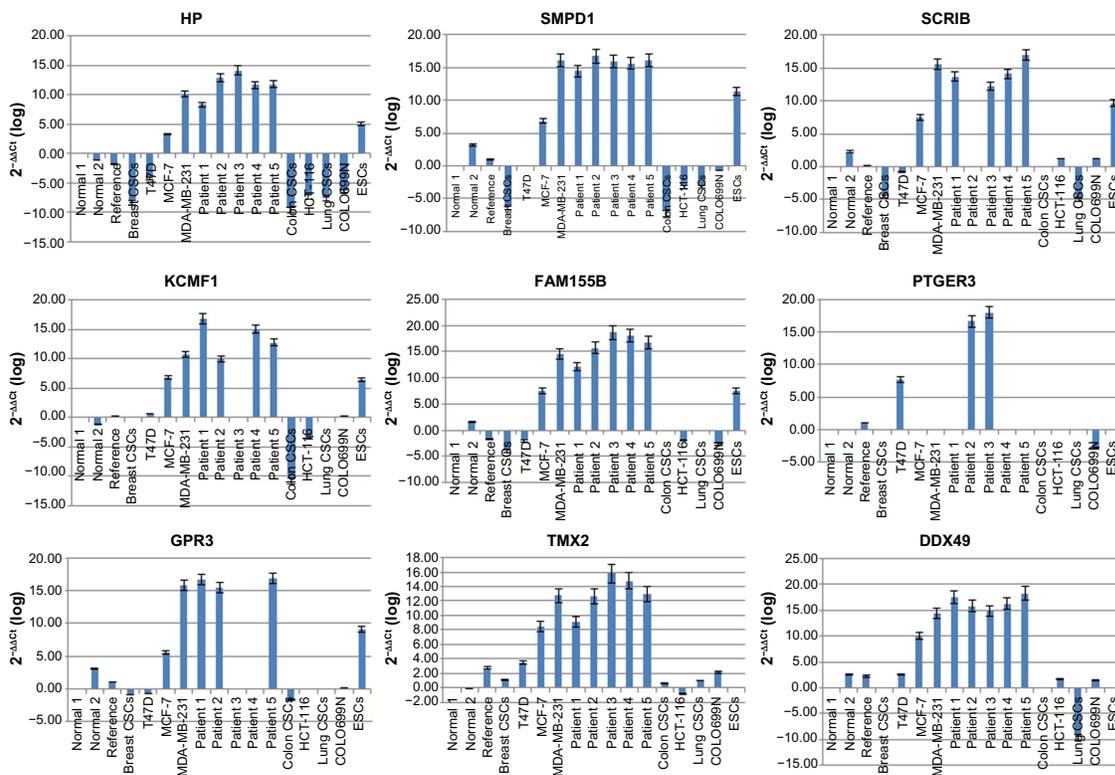


Figure 2 Gene expression among different cancer types.

Notes: Relative gene expression analysis of nine genes that were overexpressed in breast cancer and breast CSCs. The gene expression also was studied in colon and lung cancer, colon CSCs, lung CSCs, embryonic stem cells, and in a reference sample. The experiments were performed in triplicate and a *P*-value of <0.05 was considered significant.

Abbreviations: CSCs, cancer stem cells; ESCs, embryonic stem cells; *HP*, haptoglobin; *SMPD1*, sphingomyelin phosphodiesterase I, acid lysosomal; *SCRIB*, scribbled homolog (*Drosophila*); *KCMF1*, potassium channel modulatory factor 1; *FAM155B*, family with sequence similarity 155, member B; *PTGER3*, prostaglandin E receptor 3 (subtype EP3); *GPR3*, G protein-coupled receptor 3; *TMX2*, thioredoxin-related transmembrane protein 2; *DDX49*, DEAD (Asp-Glu-Ala-Asp) box polypeptide 49.

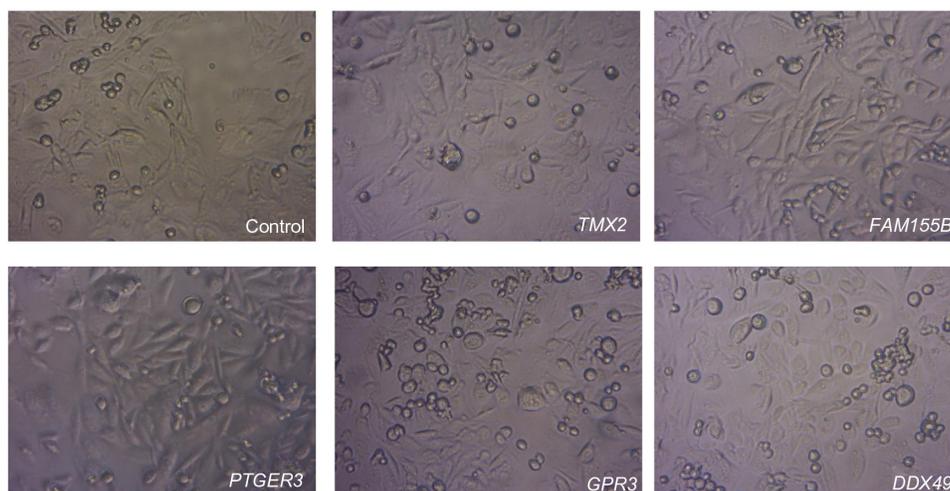


Figure 3 Breast CSCs pre- and post-siRNA knockdown.

Note: Representative images showing breast CSCs pre- and post-siRNA knockdown.

Abbreviations: CSCs, cancer stem cells; siRNA, small interfering RNA; *TMX2*, thioredoxin-related transmembrane protein 2; *FAM155B*, family with sequence similarity 155, member B; *PTGER3*, prostaglandin E receptor 3 (subtype EP3); *GPR3*, G protein-coupled receptor 3; *DDX49*, DEAD (Asp-Glu-Ala-Asp) box polypeptide 49.

on its recurrence and drug resistance mechanisms. According to previous experiments, CSCs may provide clues. By exhibiting specific features, such as self-renewal, initiation of cancer, and propagation of metastasis, they may be the ideal target for new therapeutic approaches.²¹

However, CSCs are affected by many factors, and many signal transduction pathways are implicated in their function. Notch1 is implicated in breast tumorigenesis, thus new molecules against Notch1 are a research focus.²² According to another study based on colon CSCs, the suppression of Notch receptors led to an increase in stemness transcription factors.²³ Wnt1 and STAT1/3 are involved in drug and radio resistance.^{24,25} Amplification or overexpression of human

epidermal growth factor receptor 2 (HER2) has been shown to play an important role in the progression of breast cancer, and it is also implicated in resistance to chemotherapeutics.²⁶

Microarray technology enables the study of thousands of genes and the outcome of gene expression signatures in many types of cancer. There are many studies relating to specific gene expression signatures among different phenotype characteristics, histology subtypes, and invasiveness.²⁷ However, there are few existing data with reference to gene expression patterns in breast CSCs. The present study aimed to examine which genes are overexpressed in breast CSCs derived from patients and compare them with differentiated breast cancer cells as well as with colorectal and lung cancer.

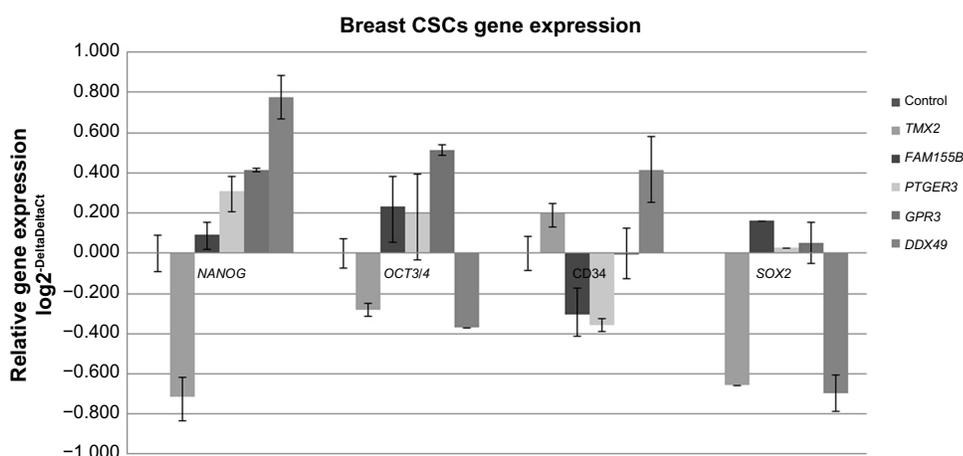


Figure 4 Gene expression of stemness transcription factors in breast CSCs.

Notes: Relative gene expression of transcription factors in breast CSCs following knockdown. The $\Delta\Delta C_t$ method was used to perform the analysis. Each bar represents the average of the Ct values. The assays were performed in triplicate and a P -value of <0.05 was considered to be significant. The assays are presented in a \log_2 scale. Thus, positive values indicate overexpression while negative values indicate underexpression.

Abbreviations: CSCs, cancer stem cells; *TMX2*, thioredoxin-related transmembrane protein 2; *FAM155B*, family with sequence similarity 155, member B; *PTGER3*, prostaglandin E receptor 3 (subtype EP3); *GPR3*, G protein-coupled receptor 3; *DDX49*, DEAD (Asp-Glu-Ala-Asp) box polypeptide 49; *NANOG*, Homeobox protein NANOG; *OCT3/4*, Octamer-binding transcription factor 3/4; *SOX2*, sex determining region Y-box 2; *CD34*, Hematopoietic progenitor cell antigen CD34.

It is noteworthy that the genes that were overexpressed in all samples (CSCs) were not directly correlated with breast cancer. Moreover, some were found to not be involved in signal transduction pathways, and others were not included in hormone metabolism.

Abundant levels of HP are associated with advanced breast cancer; furthermore, it is also used as a marker in squamous cell carcinoma of the lung.²⁸ However, according to Gast et al, the HP phenotype cannot be used as a predictor of recurrence-free survival in high-risk breast cancer.²⁹ Our study confirms the increased expression of HP in breast and breast CSCs and its absence in NSCLC. The *SMPD1* gene has been linked with Parkinson's disease,³⁰ but other studies have linked ceramides with cell signaling pathways.³¹ In a previous epidemiology study, it was demonstrated that among patients with a primary diagnosis of Parkinson's disease, increased risks were observed for breast cancer.³² Asymmetric cell division plays an important role in the CSC hypothesis,³³ and *SCRIB* seems to be involved in this process, as it was found that it regulates cortical polarity and mitotic asymmetry in *Drosophila* neuroblasts.³⁴ The *KCMF1* is a critical factor for cancer development in pancreatic cancer,³⁵ and it affects the proliferation and colony formation of human colon CSCs.³⁶ In the present study, its overexpression was also observed in breast CSCs and in ESCs, confirming its role in development. The transmembrane protein, *FAM155B*, has been demonstrated to be affected by a microduplication at X chromosome in breast cancer patients.³⁷ The *PTGER3* gene is upregulated in triple-negative breast cancer subtypes,³⁸ but it was also upregulated in nontriple-negative breast cancer subtypes in the present study. Another transmembrane protein, *GPR3*, which is involved in signal transduction, was overexpressed in breast CSCs and ESCs. This is a critical factor for the maintenance of meiotic prophase arrest in oocytes; however, it also seems to interact with stemness transcription factors by affecting *NANOG* and *OCT3/4*.³⁹

DDX49 is a helicase that is upregulated in lymphocytes irradiated with γ rays.⁴⁰ There are no reports in the literature correlating breast cancer with *DDX49*; however, knockdown experiments revealed that *SOX2* and *OCT3/4* transcription factors were downregulated, and *NANOG* was upregulated upon its suppression. *DDX49* gene expression was not observed in ESCs, in contrast to the above genes, indicating that it may only be involved in breast CSCs and not in stem cells.

Finally, the *TMX2* gene seems to be implicated in a stemness pathway to a greater extent than any of the other factors, by affecting *NANOG*, *OCT3/4*, and *SOX2* in the same way.

TMX2 is a thioredoxin-related transmembrane protein that possesses not only a thioredoxin consensus pattern, but also an endoplasmic reticulum membrane retention signal, an N-terminal signal peptide, and a Myb DNA-binding domain repeat signature.⁴¹ The participation of thioredoxin in redox reactions explains its role in cell signaling and homeostasis. Any abnormal regulation could contribute to carcinogenesis. Direct or indirect interaction with stemness transcription factors could explain the role of *TMX2* in carcinogenesis.

According to the above data, it seems that many little-studied genes that were not correlated directly with breast cancer and basic transduction pathways are overexpressed only in breast cancer and breast CSCs. Some of these might affect the stemness pathway and are thus involved in disease progression. Although qPCR data are informative and quantitative, further experiments at the protein level need to be performed. More experiments on a larger number of patients will also provide more precise data to draw reliable conclusions.

Conclusion

The identification of novel biomarkers for breast cancer has been a focus for research for many years. The implication of CSCs in drug resistance and recurrence is also well known. Because the gene expression of *NANOG*, *OCT3/4*, *SOX2*, and *CD34* stemness transcription factors is implicated in the progression of breast cancer, the identification of genes that affect the above factors is essential. The present study aimed to determine genes that were overexpressed in breast cancer and particularly in breast CSCs and to determine their relationship with stemness pathways. We detected two main groups of genes: those that were expressed only in breast CSCs and that could be used as potential biomarkers and those that affect specific transcription factors, that are essential for stemness maintenance, and that might be used as new therapeutic targets.

Disclosure

The authors report no conflicts of interest in this work.

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