Differential expression of dCTP pyrophosphatase 1 in cancers of the breast.

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Breast cancer affects women at relatively high frequency¹. We mined published microarray datasets^{2,3} to determine in an unbiased fashion and at the systems level genes most differentially expressed in the primary tumors of patients with breast cancer. We report here significant differential expression of the gene encoding dCTP pyrophosphatase 1, DCTPP1, when comparing primary tumors of the breast to the tissue of origin, the normal breast. DCTPP1 was also differentially expressed in the tumor cells of patients with triple negative breast cancer. DCTPP1 mRNA was present at significantly higher quantities in tumors of the breast as compared to normal breast tissue. Analysis of human survival data revealed that expression of DCTPP1 in primary tumors of the breast was correlated with overall survival in patients with basal subtype cancer. DCTPP1 may be of relevance to initiation, maintenance or progression of cancers of the female breast.

Keywords: breast cancer, DCTPP1, dCTP pyrophosphatase 1, systems biology of breast cancer, targeted therapeutics in breast cancer.

Invasive breast cancer is diagnosed in over a quarter of a million women in the United States each year¹ and in 2018, breast cancer was the leading cause of cancer death in women worldwide⁴. While patients with localized breast cancer are provided a 99% 5-year survival rate, patients with regional breast cancer, cancer that has spread to lymph nodes or nearby structures, are provided an 86% 5-year survival rate^{5,6}. Patients with metastasis to distant sites, like the brain, are provided a 27% 5-year survival rate^{5,6}. Understanding how primary tumors are most transcriptionally different from the tissue from which they originate, the breast, can facilitate development of novel diagnostic and therapeutics to promote early detection and enhanced treatment, and contribute to efforts to prevent progression to metastatic stages. We mined published microarray data^{2,3} to understand at the transcriptome level and in an unbiased fashion genes most differentially expressed in primary tumors of the breast as compared to normal breast tissue. The dCTP pyrophosphatase 1 emerged as among the most differentially expressed genes in cancer of the female breast.

Methods

We utilized datasets GSE109169² and GSE38959³ for this differential gene expression analysis of female breast cancer. GSE109169 was generated using Affymetrix Human Exon 1.0 ST Array technology with $n=25$ normal breast tissue and $n=25$ tumors of the breast; analysis was performed using platform GPL5175. The tissues from this first dataset are paired tissues (25 tumors matching 25 breast tissues from 25 patients). GSE38959 was generated using Agilent-014850 Whole Human Genome Microarray 4x44K G4112F technology with $n=13$ samples of normal mammary gland ductal cells and $n=30$ samples of tumor cells from patients with triple negative breast cancer; analysis was performed using platform GPL4133. The Benjamini and Hochberg method of p -value adjustment was used for ranking of differential expression but raw p -values were used to assess statistical significance of global differential expression. Log-transformation of data was auto-detected, and the NCBI generated category of platform annotation was used. A statistical test was performed to evaluate whether DCTPP1 expression was significantly different between primary breast tumors and breast tissue using a two-tailed t -test. For Kaplan-Meier survival analysis, we used the Kaplan-Meier plotter online tool⁷ for correlation of DCTPP1 mRNA expression levels with overall survival (OS) in $n=404$ patients with basal subtype cancer, $n=794$ patients with luminal A subtype cancer, $n=515$ patients with luminal B subtype cancer, and $n=166$ patients with HER2+ cancer.

Results

We performed discovery of genes associated with breast cancer in females by mining two independently published microarray datasets^{2,3}.

DCTPP1 is differentially expressed in primary tumors of the breast.

Comparison of 25 normal breast tissues to 25 tumors of the breast² from patients with early-onset breast cancer revealed that the gene encoding dCTP pyrophosphatase 1, encoded by the DCTPP1 gene, was among the genes most differentially expressed in tumors of the breast in human breast cancer (Chart 1). When sorting each of the genes expressed in tumors of the breast based on significance of difference as compared to normal breast tissue, DCTPP1 ranked 195 out of 19076 total transcripts, equating to 99.0% differential expression (Chart 1). Differential expression of DCTPP1 in female breast cancer was statistically significant (Chart 1; $p=3.62E-13$).

Analysis of a second microarray dataset³, here in tumor cells of patients with triple negative breast cancer as compared to normal mammary gland ductal cells, again revealed significant differential expression of DCTPP1 in human breast cancer (Chart 2). When sorting each of the genes expressed in the

tumor cells of patients with triple negative breast cancer based on significance of difference as compared to normal mammary gland ductal cells, DCTPP1 ranked 2215 out of 45015 total transcripts, equating to 95.1% differential expression (Chart 2). Differential expression of DCTPP1 in the tumor cells of patients with triple negative breast cancer was statistically significant (Chart 2; $p=7.32E-06$). These data suggested that differential expression of DCTPP1 was not an artifact of a single microarray dataset, nor was it associated with one type of breast cancer, rather a general feature of cancers of the breast.

DCTPP1 is expressed at significantly higher levels in breast tumors as compared to the breast.

We obtained exact mRNA expression levels for DCTPP1 from the breast and from breast tumors² to understand the magnitude and direction of DCTPP1 expression change. DCTPP1 was expressed at higher levels in tumors of the breast as compared to normal breast tissue (Figure 1). Increased expression of DCTPP1 in primary breast tumors was statistically significant (Figure 1: $p<0.0001$). DCTPP1 was expressed at 8.18 ± 0.23 arbitrary units (AU) in normal breast tissue, while it was expressed at 9.10 ± 0.42 AU in tumors of the breast. We calculated a mean fold change of 1.11 in DCTPP1 mRNA levels when comparing primary tumors of the breast to normal breast tissues.

DCTPP1 expression correlates with survival outcomes in basal subtype human breast cancer.

We performed Kaplan-Meier survival analysis in an attempt to correlate DCTPP1 mRNA expression levels with survival outcomes in patients with breast cancer, evaluating correlations between molecular subtype and overall survival. We observed a correlation between DCTPP1 expression and overall survival (OS) in patients with basal subtype breast cancer which trended towards statistical significance (Figure 2; log rank p -value: 0.072 for overall survival, hazard ratio: 1.42 (0.97-2.08) (Fig. 2)). DCTPP1 mRNA levels were a negative prognostic indicator in basal subtype breast cancer patients. Median OS was 77.4 months for basal patients with low tumor expression of DCTPP1 as compared to basal patients with high tumor expression of DCTPP1, who possessed median OS of 44.4 months (Chart 3). DCTPP1 primary tumor expression was not correlated with overall survival in luminal A subtype (Figure 2; log rank p -value: 0.79 for OS, hazard ratio: 1.04 (0.76-1.43) (Fig. 2), luminal B subtype (Figure 2; log rank p -value: 0.16 for OS, hazard ratio: 1.28 (0.91-1.82) (Fig. 2) or in HER2+ breast cancer (Figure 2; log rank p -value: 0.56 for OS, hazard ratio: 1.18 (0.67-2.08) (Fig. 2)).

Thus, through comparative transcriptome analysis of primary tumors of the breast and normal breast tissue, we found that differential expression and up-regulation of DCTPP1 was among the most significant transcriptional features in primary tumors from patients with breast cancer. DCTPP1 expression in primary tumors of the breast was correlated with overall survival in patients with basal subtype cancers, with DCTPP1 primary tumor mRNA levels a negative prognostic indicator for basal patients.

Discussion

Invasive breast cancer is a medical problem with a 27% 5-year survival rate for women whose disease has spread to distant sites^{5,6}. To facilitate understanding of the basic transcriptional differences between primary tumors of the breast and the tissues from which these tumors originate, normal breast tissues, we performed comparative transcriptome analysis using two independently published microarray datasets^{2,3}, providing evidence here that dCTP pyrophosphatase 1, encoded by DCTPP1, is a defining transcriptional feature of human breast cancer: in early onset-breast cancer, and in triple negative breast cancer. DCTPP1 was expressed at significantly higher levels in primary tumors from patients with breast cancer, as compared to normal breast. In patients with basal subtype breast cancer, primary tumor expression of DCTPP1 was correlated with overall survival. The dCTP pyrophosphatase 1, and the molecular processes to which it pertains to, may be relevant to the initiation or progression of human breast cancer.

References

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Rank: 195
Probe ID: 3687789
p-value: 3.62E-13
t: -9.7
B: 19.793101
Gene: DCTPP1
Gene name: dCTP pyrophosphatase 1

Chart 1: DCTPP1 is differentially expressed in the primary tumors of patients with early-onset human breast cancer.

Rank of differential expression, probe ID, p-value of global differential expression, t, a moderated t-statistic, B, the log-odds of differential expression between the groups compared, gene and gene name are listed in this chart.

Rank: 2215
Probe ID: 38860
p-value: 7.32E-06
t: -5.0661085
B: 3.453747
Gene: DCTPP1
Gene name: dCTP pyrophosphatase 1

Chart 2: DCTPP1 is differentially expressed in the tumor cells of patients with triple-negative breast cancer.

Rank of differential expression, probe ID, p-value of global differential expression, t, a moderated t-statistic, B, the log-odds of differential expression between the groups compared, gene and gene name are listed in this chart.

Figure 1: DCTPP1 is expressed at significantly higher levels in primary breast tumors as compared to normal breast tissue.

The mRNA expression level of DCTPP1 in normal breast tissue (left) and in primary tumors of the breast (right) is graphically depicted with the result of a statistical test evaluating significance of difference in DCTPP1 expression between normal breast tissue and primary tumors of the breast, a p -value, is $p < 0.00001$.

Figure 2: DCTPP1 expression correlates with overall survival in patients with basal subtype breast cancer, but not in patients with luminal A, luminal B or HER2+ cancer.

Depicted in this Kaplan-Meier plot is the probability of overall survival (OS) for $n=404$ patients with basal subtype breast cancer (upper left), $n=166$ patients with HER2+ breast cancer (upper right), $n=794$ patients with luminal A breast cancer (lower left), and $n=515$ patients with luminal B breast cancer (lower right), stratified into two groups, based on low or high expression of DCTPP1 (also known as CDA03) in patient primary tumors. The log rank p-value denoting statistical significance of difference in overall survival when comparing the two groups, as well as hazard ratio for this comparison is listed above. Listed below is the number of patients at risk (number of patients alive) per interval, after stratification based on DCTPP1 expression; in the first interval, number at risk is number of patients alive; in each subsequent interval, number at risk is the number at risk less those who have expired or are censored.

1 Low DCTPP1 expression: 77.4 months

2 High DCTPP1 expression: 44.4 months

3 **Chart 3: Median overall survival is superior in basal subtype breast cancer patients with low**
4 **primary tumor expression of DCTPP1.**

5 The overall survival of $n=404$ basal subtype breast cancer patients based on stratification into low or high
6 tumor expression of DCTPP1 is listed in this chart.