Differential expression of GSTM5 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 glutathione S-transferase mu 5, GSTM5, when comparing primary tumors of the breast to the tissue of origin, the normal breast. GSTM5 mRNA was present at significantly lower quantities in tumors of the breast as compared to normal breast tissue. Analysis of human survival data revealed that expression of GSTM5 in primary tumors of the breast was correlated with overall survival in patients with basal subtype cancer, demonstrating a relationship between primary tumor expression of a differentially expressed gene and patient survival outcomes influenced by molecular subtype. GSTM5 may be of relevance to initiation, maintenance or progression of cancers of the female breast.

Keywords: breast cancer, GSTM5, glutathione S-transferase mu 5, 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. glutathione S-transferase mu 5 emerged as among the most differentially expressed genes in cancer of the female breast.

Methods

We utilized datasets GSE109169² and GSE72653³ 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). GSE72653 was generated using Agilent-014850 Whole Human Genome Microarray 4x44K G4112F with $n=8$ normal epithelium and $n=8$ tumors of the breast from patients with breast cancer; the tissues from this second dataset are paired tissues (8 tumors matching 8 normal breast epithelial tissues from 8 patients); analysis was performed using platform GPL6480. 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 GSTM5 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 GSTM5 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}.

GSTM5 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 glutathione S-transferase mu 5, encoded by the GSTM5 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, GSTM5 ranked 237 out of 19076 total transcripts, equating to 98.8% differential expression (Chart 1). Differential expression of GSTM5 in female breast cancer was statistically significant (Chart 1; $p=1.01E-12$).

To attempt to validate differential transcriptome-wide differential expression of GSTM5 in human breast cancer, we queried a second microarray dataset³, here comparing normal breast tissues and primary tumors of the breast. Again, we identified GSTM5 as a differentially expressed gene in the

tumor tissues of patients with breast cancer (Chart 2). When sorting each of the genes expressed in primary tumors of the breast based on significance of difference as compared to normal breast tissues, GSTM5 ranked 2579 out of 41093 total transcripts (Chart 2), equating to 93.7% differential expression. Differential expression of GSTM5 in the primary tumors of patients with breast cancer was statistically significant (Chart 2; $p=2.42E-09$). These data indicated that differential expression of GSTM5 was not an artifact of a single microarray dataset, and perhaps a general feature of cancers of the breast.

GSTM5 is expressed at significantly lower levels in breast tumors as compared to the breast.

We obtained exact mRNA expression levels for GSTM5 from the breast and from breast tumors² to understand the magnitude and direction of GSTM5 expression change. GSTM5 was expressed at lower levels in tumors of the breast as compared to normal breast tissue (Figure 1). Decreased expression of GSTM5 in primary breast tumors was statistically significant (Figure 1; $p<0.0001$). GSTM5 was expressed at 8.25 ± 1.38 arbitrary units (AU) in normal breast tissue, while it was expressed at 5.11 ± 1.03 AU in tumors of the breast. We calculated a mean fold change of 0.62 in GSTM5 mRNA levels when comparing primary tumors of the breast to normal breast tissues.

GSTM5 expression correlates with survival outcomes in basal subtype human breast cancer.

We performed Kaplan-Meier survival analysis in an attempt to correlate GSTM5 mRNA expression levels with survival outcomes in patients with breast cancer, evaluating correlations between molecular subtype and overall survival. We observed a statistically significant correlation between GSTM5 expression and overall survival (OS) in patients with basal subtype breast cancer (Figure 2; log rank p -value: 0.075 for overall survival, hazard ratio: 1.41 (0.96-2.07) (Fig. 2)). GSTM5 mRNA levels were a negative prognostic indicator in basal subtype breast cancer patients. Median OS was 85.2 months for basal subtype patients with low tumor expression of GSTM5 while median OS was 52.92 months for basal subtype patients with high tumor expression of GSTM5 (Chart 3). GSTM5 primary tumor expression was not correlated with overall survival in luminal A subtype breast cancer (Figure 2; log rank p -value: 0.64 for OS, hazard ratio: 0.93 (0.68-1.27) (Fig. 2)), luminal B subtype breast cancer (Figure 2; log rank p -value: 0.84 for OS, hazard ratio: 0.96 (0.68-1.37) (Fig. 2)), or in HER2+ breast cancer (Figure 2; log rank p -value: 0.23 for OS, hazard ratio: 0.71 (0.4-1.25) (Fig. 2)).

Thus, through comparative transcriptome analysis of primary tumors of the breast and normal breast tissue, we found that differential expression and down-regulation of GSTM5 was among the most significant transcriptional features in primary tumors from patients with breast cancer. GSTM5 expression in primary tumors of the breast was correlated with overall survival in patients with basal subtype cancers, with GSTM5 primary tumor mRNA levels a negative prognostic indicator for basal subtype 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 differential expression of glutathione S-transferase mu 5, encoded by GSTM5, is a defining transcriptional feature of human breast cancer. GSTM5 was expressed at significantly lower levels in primary tumors from patients with breast cancer, as compared to normal breast. In patients with basal subtype breast cancers, primary tumor expression of GSTM5 was correlated with overall survival. glutathione S-transferase mu 5, 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: 237
Probe ID: 2351004
p-value: 1.01E-12
t: 9.4
B: 18.786719
Gene: GSTM5
Gene name: glutathione S-transferase mu 5

Chart 1: GSTM5 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: 2579
Probe ID: 205752_s_at
p-value: 2.42E-09
t: 7.06
B: 13.7038131
Gene: GSTM5
Gene name: glutathione S-transferase mu 5

Chart 2: GSTM5 is differentially expressed in the primary tumors of patients with 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: GSTM5 is expressed at significantly lower levels in primary breast tumors as compared to normal breast tissue.

The mRNA expression level of GSTM5 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 GSTM5 expression between normal breast tissue and primary tumors of the breast, a *p*-value, is $p<0.0001$.

Figure 2: GSTM5 expression correlates with overall survival in patients with basal subtype breast cancer, but not in patients with luminal A, luminal B, or HER2+ subtype breast 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 GSTM5 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 GSTM5 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.

Basal subtype patients

Low GSTM5 expression: 85.2 months

High GSTM5 expression: 52.92 months

Chart 3: In basal subtype breast cancer, median overall survival is superior in patients with low primary tumor expression of GSTM5.

The overall survival of $n=404$ basal subtype breast cancer patients based on stratification into low or high tumor expression of GSTM5 is listed in this chart.