Differential expression of TUFT1 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 the tuftelin 1, TUFT1, when comparing primary tumors of the breast to the tissue of origin, the normal breast. TUFT1 was also differentially expressed in the tumor cells of patients with triple negative breast cancer. TUFT1 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 TUFT1 in primary tumors of the breast was correlated with distant metastasis-free survival in patients with basal and luminal A subtype cancer. TUFT1 may be of relevance to initiation, maintenance or progression of cancers of the female breast.

Keywords: breast cancer, TUFT1, tuftelin 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 tuftelin 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 TUFT1 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 TUFT1 mRNA expression levels with distant metastasis-free 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}.

TUFT1 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 the tuftelin 1, encoded by the TUFT1 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, TUFT1 ranked 173 out of 19076 total transcripts, equating to 99.1% differential expression (Chart 1). Differential expression of TUFT1 in female breast cancer was statistically significant (Chart 1; $p=1.86E-13$).

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 TUFT1 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, TUFT1 ranked 6475 out of 45015 total transcripts, equating to 85.6% differential expression (Chart 2). Differential expression of TUFT1 in the tumor cells of patients with triple negative breast cancer was statistically significant (Chart 2; $p=1.44E-03$). These data suggested that differential expression of TUFT1 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.

TUFT1 is expressed at significantly higher levels in breast tumors as compared to the breast.

We obtained exact mRNA expression levels for TUFT1 from the breast and from breast tumors² to understand the magnitude and direction of TUFT1 expression change. TUFT1 was expressed at higher levels in tumors of the breast as compared to normal breast tissue (Figure 1). Increased expression of TUFT1 in primary breast tumors was statistically significant (Figure 1: $p<0.0001$). TUFT1 was expressed at 7.44 ± 0.29 arbitrary units (AU) in normal breast tissue, while it was expressed at 8.87 ± 0.67 AU in tumors of the breast. We calculated a mean fold change of 1.19 in TUFT1 mRNA levels when comparing primary tumors of the breast to normal breast tissues.

TUFT1 expression correlates with survival outcomes in basal and luminal A human breast cancer.

We performed Kaplan-Meier survival analysis in an attempt to correlate TUFT1 mRNA expression levels with survival outcomes in patients with breast cancer, evaluating correlations between molecular subtype and distant metastasis-free survival. We observed a statistically significant correlation between TUFT1 expression and distant metastasis-free survival (DMFS) in patients with basal subtype breast cancer (Figure 2; log rank p -value: 0.05 for distant metastasis-free survival, hazard ratio: 1.37 (1-1.87) (Fig. 2)). TUFT1 mRNA levels were a negative prognostic indicator in basal subtype breast cancer patients. Median DMFS was 78 months for basal patients with low tumor expression of TUFT1 while median DMFS was 28.75 months for basal patients with high tumor expression of TUFT1 (Chart 3). We also observed a statistically significant correlation between TUFT1 expression and distant metastasis-free survival (DMFS) in patients with luminal A breast cancer (Figure 2; log rank p -value: 0.0059 for distant metastasis-free survival, hazard ratio: 1.29 (0.99-1.67) (Fig. 2)). TUFT1 mRNA levels were also a negative prognostic indicator in luminal A subtype breast cancer patients. Median DMFS was 191.21 months for luminal A subtype patients with low tumor expression of TUFT1 while median DMFS was 137 months for luminal A subtype patients with high tumor expression of TUFT1 (Chart 3). TUFT1 primary tumor expression was not correlated with distant metastasis-free survival in luminal B subtype (Figure 2; log rank p -value: 0.5 for DMFS, hazard ratio: 0.91 (0.69-1.2) (Fig. 2)), or in HER2+ breast cancer (Figure 2; log rank p -value: 0.17 for DMFS, hazard ratio: 1.42 (0.86-2.34) (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 TUFT1 was among the most significant transcriptional features in primary tumors from patients with breast cancer. TUFT1 expression in primary tumors of the breast was correlated with distant metastasis-free survival in patients with basal and luminal A subtype cancers, with low expression of TUFT1 associating with superior survival in both breast cancer subtypes.

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

1 datasets^{2,3}, providing evidence here that tuftelin 1, encoded by the TUFT1, is a defining transcriptional
2 feature of human breast cancer: in early onset-breast cancer, and in triple negative breast cancer. TUFT1
3 was expressed at significantly higher levels in primary tumors from patients with breast cancer as
4 compared to normal tissues of the breast. In patients with luminal A or basal subtype breast cancers, low
5 expression of TUFT1 was associated with superior distant metastasis-free survival. TUFT1 and the
6 molecular processes to which it pertains to may be relevant to the initiation or progression of human breast
7 cancer.
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Rank: 173
Probe ID: 2358993
p-value: 1.86E-13
t: -9.89
B: 20.451715
Gene: TUFT1
Gene name: tuftelin 1

Chart 1: TUFT1 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: 6475
Probe ID: 5593
p-value: 1.44E-03
t: -3.3943952
B: -1.593013
Gene: TUFT1
Gene name: tuftelin 1

Chart 2: TUFT1 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: TUFT1 is expressed at significantly higher levels in primary breast tumors as compared to normal breast tissue.

The mRNA expression level of TUFT1 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 TUFT1 expression between normal breast tissue and primary tumors of the breast, a p -value, is $p < 0.0001$.

Figure 2: TUFT1 expression correlates with distant metastasis-free survival in patients with basal subtype or luminal A subtype breast cancer, but not in patients with luminal B or HER2+ cancer.

Depicted in this Kaplan-Meier plot is the probability of distant metastasis-free survival (DMFS) 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 TUFT1 in patient primary tumors. The log rank p-value denoting statistical significance of difference in distant metastasis-free 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 TUFT1 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

Low TUFT1 expression: 78 months

High TUFT1 expression: 28.75 months

Luminal A

Low TUFT1 expression: 191.21 months

High TUFT1 expression: 137 months

Chart 3: In basal subtype and in luminal A subtype breast cancer, median distant metastasis-free survival is superior in patients with low primary tumor expression of TUFT1.

The distant metastasis-free survival of $n=571$ basal subtype breast cancer patients and $n=1260$ luminal A subtype breast cancer patients based on stratification into low or high tumor expression of TUFT1 is listed in this chart.