Differential expression of laeverin 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 laeverin, LVRN, when comparing primary tumors of the breast to the tissue of origin, the normal breast. LVRN was also differentially expressed in the brain metastases of patients with metastatic breast cancer. LVRN 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 LVRN in primary tumors of the breast was correlated with overall survival in patients with normal-like subtype cancer, demonstrating a relationship between primary tumor expression of a differentially expressed gene and patient survival outcomes influenced by PAM50 molecular subtype. LVRN may be of relevance to initiation, maintenance or progression of cancers of the female breast.

Keywords: breast cancer, LVRN, laeverin, 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. Laeverin emerged as among the most differentially expressed genes in cancer of the female breast.

Methods

We utilized datasets GSE42568² and GSE52604³ for this global differential gene expression analysis of female breast cancer. GSE42568 was generated using Affymetrix Human Genome U133 Plus 2.0 array technology with $n=17$ normal breast tissue biopsies and $n=104$ primary breast tumor biopsies from patients with breast cancer; analysis was performed using platform GPL570; the majority of patients whose tumors were analyzed were age 50 or older. GSE52604 was generated using Agilent-014850 Whole Human Genome Microarray 4x44K G4112F with $n=10$ normal breast tissues and $n=35$ brain metastases from patients with breast cancer; 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 LVRN expression was significantly different between primary breast tumors and normal breast tissue using a two-tailed t-test. For Kaplan-Meier survival analysis, we used the Kaplan-Meier plotter online tool⁷ for correlation of LVRN mRNA expression levels with overall survival (OS) in $n=417$ patients with basal-like subtype cancer, $n=952$ patients with luminal A subtype cancer, $n=465$ patients with normal-like subtype cancer, $n=198$ patients with HER2+ cancer, and $n=999$ patients with normal-like subtype cancer.

Results

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

LVRN is differentially expressed in primary tumors of the breast.

Studying the global gene expression profiles of 104 breast cancers from patients aged 31 to 89 revealed that the gene encoding laeverin, LVRN, 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, LVRN ranked 13 out of 54675 total transcripts, equating to 99.98% differential expression (Chart 1). Differential expression of LVRN in female breast cancer was statistically significant (Chart 1; $p=1.89\text{E-}38$).

Analysis of a second microarray dataset³, here studying global gene expression patterns in the brain metastases of patients with metastatic breast cancer, again revealed significant differential expression of LVRN in tumor tissue of patients with human breast cancer (Chart 2). When sorting each of the genes expressed in the brain metastases of patients with breast cancer based on significance of difference as compared to normal breast tissue, LVRN ranked 2065 out of 41093 total transcripts, equating to 95.0%

differential expression (Chart 2). Differential expression of LVRN in the brain metastases of patients with breast cancer was statistically significant (Chart 2; $p=4.50E-06$). These data suggested that differential expression of LVRN was not an artifact of a single microarray dataset, nor was it strictly associated with primary tumors of the breast, rather a reflection of the spectrum of transformation in human cancer.

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

We obtained exact mRNA expression levels for LVRN from the breast and from breast tumors to understand the magnitude and direction of LVRN expression change. LVRN was expressed at lower levels in tumors of the breast as compared to normal breast tissue (Figure 1). Decreased expression of LVRN in primary breast tumors was statistically significant (Figure 1; $p<0.0001$). LVRN was expressed at 6.57 ± 1.98 arbitrary units (AU) in normal breast tissue, while it was expressed at 2.42 ± 0.42 AU in tumors of the breast. We calculated a mean fold change of 0.37 in LVRN mRNA levels when comparing primary tumors of the breast to normal breast tissues.

LVRN expression correlates with survival outcomes in normal-like subtype human breast cancer.

We performed Kaplan-Meier survival analysis to study relationships between tumor LVRN mRNA expression levels and survival outcomes in patients with breast cancer. We observed a correlation between LVRN expression and overall survival (OS) in patients with normal-like subtype breast cancer which trended towards statistical significance (Figure 2; log rank p -value: 0.07 for overall survival, hazard ratio: 3.86 (0.8-18.57) (Fig. 2)). LVRN mRNA levels were a negative prognostic indicator in normal-like subtype breast cancer patients. Median OS was, on average, markedly greater for normal-like patients with low tumor expression of LVRN as compared to normal-like patients with high tumor expression of LVRN (Chart 3). LVRN primary tumor expression was not correlated with overall survival in basal-like breast cancer (Figure 2; log rank p -value: 0.1 for OS, hazard ratio: 0.67 (0.42-1.08) (Fig. 2)), luminal A subtype breast cancer (Figure 2; log rank p -value: 0.71 for OS, hazard ratio: 1.14 (0.56-2.31) (Fig. 2)), in patients with luminal B disease (Figure 2; log rank p -value: 0.82 for OS, hazard ratio: 1.07 (0.61-1.86) (Fig. 2)), or in HER2+ breast cancer (Figure 2; log rank p -value: 0.67 for OS, hazard ratio: 0.89 (0.52-1.52) (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 LVRN was among the most significant transcriptional features in primary tumors from patients with breast cancer. LVRN expression in primary tumors of the breast was correlated with overall survival in patients with normal-like subtype disease, with mRNA levels of LVRN a negative prognostic indicator for normal-like breast cancer 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 laeverin, encoded by LVRN, is a defining transcriptional feature of human breast cancer: in patients diagnosed after age 50, and in brain metastatic tissues from patients with human breast cancer. LVRN was expressed at significantly lower levels in primary tumors from patients with breast cancer as compared to normal breast tissue.

1 Importantly, in patients with normal-like subtype breast cancers, expression of LVRN was correlated with
2 overall survival. Laeverin and the molecular processes to which it pertains to may be relevant to the
3 initiation or progression of human breast cancer.
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Rank: 13
Probe ID: 235382_at
p-value: 1.89E-38
t: 1.92E+01
B: 76.8694587
Gene: LVRN
Gene name: laeverin

Chart 1: LVRN 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.

Rank: 2065
Probe ID: A_23_P58557
p-value: 4.50E-06
t: 5.1849003
B: 3.93504
Gene: LVRN
Gene name: laeverin

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

The mRNA expression level of LVRN 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 LVRN expression between normal breast tissue and primary tumors of the breast, a *p*-value, listed above.

Figure 2: LVRN expression correlates with overall survival in patients with normal-like subtype breast cancer, but not in patients with basal, luminal A, HER2+, or normal-like subtype cancer.

Depicted in this Kaplan-Meier plot is the probability of overall survival (OS) for $n=417$ patients with basal-like breast cancer (upper left), $n=198$ patients with HER2+ breast cancer (upper right), $n=952$ patients with luminal A breast cancer (middle left), $n=465$ patients with normal-like breast cancer (middle right), and $n=999$ patients with normal-like breast cancer (below) stratified into two groups, based on low or high expression of LVRN 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 LVRN 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.