Differential expression of PQ loop repeat-containing 2-like 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 PQ loop repeat-containing 2-like, PQLC2L, when comparing primary tumors of the breast to the tissue of origin, the normal breast. PQLC2L was also differentially expressed in the brain metastases of patients with metastatic breast cancer. PQLC2L 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 PQLC2L in primary tumors of the breast was correlated with recurrence-free survival in patients with luminal A subtype cancer, demonstrating a relationship between primary tumor expression of a differentially expressed gene and patient survival outcomes influenced by PAM50 molecular subtype. PQLC2L may be of relevance to initiation, maintenance or progression of cancers of the female breast.

Keywords: breast cancer, PQLC2L, PQ loop repeat-containing 2-like, 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. PQ loop repeat-containing 2-like emerged as among the most differentially expressed genes in cancer of the female breast.

Methods

We utilized datasets GSE42568² and GSE43837³ 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. GSE43837 was generated using Affymetrix Human X3P Array technology with $n=19$ primary tumors of the breast and $n=19$ 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 PQLC2L 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 PQLC2L mRNA expression levels with recurrence-free survival (RFS) in $n=442$ patients with basal-like subtype cancer, $n=631$ patients with luminal A subtype cancer, $n=566$ patients with luminal B subtype cancer, $n=358$ 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}.

PQLC2L 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 PQ loop repeat-containing 2-like, PQLC2L, 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, PQLC2L ranked 67 out of 54675 total transcripts, equating to 99.9% differential expression (Chart 1). Differential expression of PQLC2L in female breast cancer was statistically significant (Chart 1; $p=3.82E-33$).

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 PQLC2L 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, PQLC2L ranked 9863 out of 61359 total transcripts, equating to 83.9% differential expression (Chart 2). Differential expression of PQLC2L in the brain metastases of patients with breast cancer trended towards statistical significance (Chart 2; $p=0.08300168$). These data suggested that differential expression of PQLC2L 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.

PQLC2L is expressed at significantly lower levels in breast tumors as compared to the breast.

We obtained exact mRNA expression levels for PQLC2L from the breast and from breast tumors to understand the magnitude and direction of PQLC2L expression change. PQLC2L was expressed at lower levels in tumors of the breast as compared to normal breast tissue (Figure 1). Decreased expression of PQLC2L in primary breast tumors was statistically significant (Figure 1: $p<0.0001$). PQLC2L was expressed at 4.69 ± 1.35 arbitrary units (AU) in normal breast tissue, while it was expressed at 2.38 ± 0.21 AU in tumors of the breast. We calculated a mean fold change of 0.51 in PQLC2L mRNA levels when comparing primary tumors of the breast to normal breast tissues.

PQLC2L expression correlates with survival outcomes in luminal A subtype human breast cancer.

We performed Kaplan-Meier survival analysis to study relationships between tumor PQLC2L mRNA expression levels and survival outcomes in patients with breast cancer. We observed a correlation between PQLC2L expression and recurrence-free survival (RFS) in patients with luminal A subtype breast cancer which was statistically significant (Figure 2; log rank p -value: 0.0019 for recurrence-free survival, hazard ratio: 0.57 (0.4-0.82) (Fig. 2)). PQLC2L mRNA levels were a positive prognostic indicator in luminal A subtype breast cancer patients. RFS was markedly shorter for luminal A patients with low tumor expression of PQLC2L as compared to luminal A patients with high tumor expression of PQLC2L (Chart 3). PQLC2L primary tumor expression was not correlated with recurrence-free survival in basal-like breast cancer (Figure 2; log rank p -value: 0.88 for RFS, hazard ratio: 0.98 (0.72-1.33) (Fig. 2)), luminal B subtype breast cancer (Figure 2; log rank p -value: 0.52 for RFS, hazard ratio: 0.92 (0.71-1.19) (Fig. 2)), in HER2+ breast cancer (Figure 2; log rank p -value: 0.44 for RFS, hazard ratio: 0.88 (0.63-1.22) (Fig. 2)) or in patients with normal-like breast cancer (Figure 2; log rank p -value: 0.86 for RFS, hazard ratio: 1.09 (0.41-2.92) (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 PQLC2L was among the most significant transcriptional features in primary tumors from patients with breast cancer. PQLC2L expression in primary tumors of the breast was correlated with recurrence-free survival in patients with luminal A subtype disease, with mRNA levels of PQLC2L a positive prognostic indicator for luminal A 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 PQ loop repeat-containing 2-like, encoded by PQLC2L, 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. PQLC2L was

expressed at significantly lower levels in primary tumors from patients with breast cancer as compared to normal breast tissue. Importantly, in patients with luminal A subtype breast cancers, expression of PQLC2L was correlated with recurrence-free survival. PQ loop repeat-containing 2-like 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: 67
Probe ID: 1558552_s_at
p-value: 3.82E-33
t: 1.67E+01
B: 64.8329106
Gene: PQLC2L
Gene name: PQ loop repeat-containing 2-like

Chart 1: PQLC2L 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: 9863
Probe ID: Hs.103823.0.S1_3p_at
p-value: 0.08300168
t: 1.7749995
B: -4.25924
Gene: PQLC2L
Gene name: PQ loop repeat-containing 2-like

Chart 2: PQLC2L 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: PQLC2L is expressed at significantly lower levels in primary breast tumors as compared to normal breast tissue.

The mRNA expression level of PQLC2L 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 PQLC2L expression between normal breast tissue and primary tumors of the breast, a *p*-value, listed above.

Figure 2: PQLC2L expression correlates with recurrence-free survival in patients with luminal A subtype breast cancer, but not in patients with basal, luminal B, HER2+, or normal-like subtype cancer.

Depicted in this Kaplan-Meier plot is the probability of recurrence-free survival (RFS) for $n=442$ patients with basal-like breast cancer (upper left), $n=358$ patients with HER2+ breast cancer (upper right), $n=631$ patients with luminal A breast cancer (middle left), $n=566$ patients with luminal B 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 PQLC2L in

patient primary tumors. The log rank p-value denoting statistical significance of difference in recurrence-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 PQLC2L 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.