PLA1A is differentially expressed in lymph node metastasis in human breast cancer.

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Metastasis to the brain is a clinical problem in patients with breast cancer¹⁻³. Between the breast and the brain reside the secondary lymphoid organ, the lymph nodes. We mined published microarray data^{4,5} to compare primary and metastatic tumor transcriptomes for the discovery of genes associated with metastasis to the lymph nodes in humans with metastatic breast cancer. We found that phospholipase A1 member A, PLA1A, was among the genes whose expression was most different in the lymph node metastases of patients with metastatic breast cancer as compared to primary tumors of the breast. Analysis of a separate microarray dataset revealed that PLA1A was also differentially expressed in brain metastatic tissues. PLA1A mRNA was present at increased quantities in lymph node metastases as compared to primary tumors of the breast. Importantly, expression of PLA1A in primary tumors of the breast was correlated with patient distant metastasis-free survival, in lymph node positive patients but not in lymph node negative patients. Modulation of PLA1A expression may be relevant to the biology by which tumor cells metastasize from the breast to the lymph nodes and the brain in humans with metastatic breast cancer.

Keywords: breast cancer, metastasis, brain metastasis, central nervous system metastasis, lymph node metastasis, phospholipase A1 member A, PLA1A, systems biology of breast cancer, targeted therapeutics in breast cancer.

One report described a 34% incidence of central nervous system metastases in patients treated with trastuzumab for breast cancer². More recently, the NEfERT-T clinical trial⁶ which compared administration of either neratinib or trastuzumab in conjunction with paclitaxel demonstrated that in a randomized, controlled setting, in breast cancer patients treated with neratinib, not only was the incidence of central nervous system recurrence significantly lower, the time to central nervous system metastasis was significantly delayed as compared to patients administered trastuzumab⁶. The alarmingly high rate of central nervous system metastasis described, as well as data, both anecdotal² and from a randomized, controlled setting⁶ illustrating that treatment with trastuzumab may be associated with these events demands an enhanced understanding of the transcriptional makeup of brain and lymph node metastatic tissues to support identification of therapeutic targets, whether they are treatment related or not. The lymph nodes reside between the breast and the brain. We performed a global comparative analysis of lymph node metastatic tumor tissues in patients with metastatic breast cancer, compared to primary tumors and normal breast tissues^{4,5}. We discovered transcriptome-wide differential expression of the gene encoding phospholipase A1 member A, PLA1A, in lymph node metastatic tissues of patients with metastatic breast cancer.

Methods

We used datasets GSE10893⁴ and GSE52604⁵ for this global differential gene expression analysis of brain metastatic breast cancer in conjunction with GEO2R. GSE10893 was generated using Agilent-011521 Human 1A Microarray G4110A technology with $n=71$ primary breast tumors and $n=7$ lymph node metastases from patients with breast cancer; analysis was performed using platform GPL887. 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 PLA1A gene expression was significantly different between primary tumors of the breast and lymph node metastases in humans with breast cancer using a two-tailed t-test. For Kaplan-Meier survival analysis, we used the Kaplan-Meier plotter online tool⁷ for correlation of PLA1A mRNA expression levels with distant metastasis-free survival in $n=889$ lymph node positive patients and $n=1309$ lymph node negative breast cancer patients.

Results

We performed global comparative transcriptome analysis of metastatic tumor tissues of patients with metastatic breast cancer using published microarray data^{4,5} to describe the transcriptional landscape of metastasis in human breast cancer in an unbiased fashion and for the discovery of novel therapeutic targets.

PLA1A is differentially expressed in the lymph node metastases of patients with metastatic breast cancer.

Through blind, systems-level analysis of published microarray data⁴, we identified phospholipase A1 member A, encoded by PLA1A, as a differentially expressed gene in the lymph node metastatic tissues of humans with breast cancer (Table 1). When sorting each of the genes expressed in lymph node metastases based on significance of difference as compared to primary tumors of the breast in patients with breast cancer, PLA1A ranked 82 out of 18034 total transcripts (Chart 1), equating to 99.5% differential expression. Differential expression of PLA1A in the lymph node metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=5.44e-04$).

Differential gene expression analyses that utilize primary and metastatic tumor tissues to discover genes associated with metastasis can be challenging due to the relatively heterogeneous cellular composition and constitution of the tumor as compared to normal, untransformed (benign) tissues. Thus, to attempt to validate differential transcriptome-wide differential expression of PLA1A in metastatic tissues in human breast cancer, we queried a second microarray dataset⁵, here comparing normal breast tissues rather than primary tumors of the breast, to brain metastases. Again, we identified PLA1A as a differentially expressed gene in the metastatic tissues of humans with breast cancer, here, in the brain metastatic tissues of patients with breast cancer (Chart 2). When sorting each of the genes expressed in brain metastases based on significance of difference as compared to normal breast tissues, PLA1A ranked 7924 out of 41093 total transcripts (Chart 2), equating to 80.7% differential expression. Differential expression of PLA1A in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 2; $p=1.75e-03$). Thus, differential expression of PLA1A, transcriptome-wide, in the metastatic tissues of women with metastatic breast cancer was conserved across two independent microarray datasets, both in lymph node and brain metastases. This suggests that PLA1A differential expression in human metastatic breast cancer is a *bona fide* biological process and that differential expression of PLA1A in metastatic breast cancer is shared between the brain and the lymph nodes.

PLA1A is expressed at higher levels in the lymph node metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for PLA1A, in primary tumors of the breast and in lymph node metastases of patients with metastatic breast cancer to determine direction and statistical significance of change in PLA1A expression in lymph node metastatic tissues. We observed significantly increased expression of PLA1A in the lymph node metastases of patients with breast cancer as compared to primary tumors of the breast: PLA1A was expressed at 0.36 ± 0.63 arbitrary units (AU) in primary tumors of the breast, while it was expressed at 1.34 ± 1.22 AU in lymph node metastatic tissues (Figure 1). The difference in PLA1A mRNA levels between primary tumors of the breast and lymph node metastases was statistically significant (Figure 1; $p=0.00064$).

PLA1A expression is significantly correlated with survival outcomes in human breast cancer.

We performed Kaplan-Meier survival analysis⁷ in $n=889$ lymph node positive breast cancer patients and $n=1309$ lymph node negative breast cancer patients, to evaluate whether PLA1A tumor expression was correlated with survival outcomes in breast cancer and to evaluate whether lymph node status influenced correlation of PLA1A tumor expression with survival outcomes in human breast cancer. We observed a correlation between primary tumor expression of PLA1A and distant metastasis-free survival (DMFS) in lymph node positive breast cancer (Figure 2). Lymph node positive patients whose primary tumors expressed low levels of PLA1A possessed median DMFS of 50.07 months, while lymph node positive patients whose tumors expressed high levels of PLA1A possessed median DMFS of 32.03 months. This difference in DMFS based on PLA1A tumor expression in lymph node positive patients with breast cancer trended towards statistical significance (Figure 2, Chart 3; logrank p -value: 0.099; hazard ratio: 1.23 (0.96-1.59)). PLA1A primary tumor expression was not correlated with distant metastasis-free survival outcomes in lymph node negative patients (Figure 2, Chart 3; logrank p -value: 0.16; hazard ratio: 1.19 (0.93-1.52)).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified PLA1A as among the genes whose expression was most different, transcriptome-wide, in the lymph node metastases of patients with breast cancer, when compared to primary tumors; we observed significantly increased expression of PLA1A in lymph node metastases as compared to primary tumors of the breast.

Further, we found correlation between PLA1A expression and distant metastasis-free survival in lymph node positive patients but not in lymph node negative patients.

Discussion

We provided evidence here that phospholipase A1 member A, PLA1A, is among the genes whose expression is most different in the lymph node metastases of patients with metastatic breast cancer as compared to primary tumors of the breast, that PLA1A is also differentially expressed in brain metastatic tissues in human breast cancer, that PLA1A mRNA is present at significantly increased quantities in lymph node metastatic tissues as compared to primary tumors of the breast, and that primary tumor PLA1A expression is correlated with patient survival outcomes in human breast cancer in lymph node positive patients but not in lymph node negative patients. Evaluation of the effects of genetic depletion of PLA1A in mouse models of metastatic breast cancer on metastasis to the lymph nodes and to the central nervous system is merited. Modulation of PLA1A expression may be relevant to the processes by which breast cancer cells exit the breast, enter the vasculature and/or lymphatics, reside in the lymph nodes, evade immune clearance, breach the blood-brain barrier and colonize the brain.

References

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Rank: 82
Probe ID: 9087
p-value: 5.44e-04
t: -3.605452
B: -0.2943
Gene: PLA1A
Gene name: phospholipase A1 member A

Chart 1: PLA1A is differentially expressed in lymph node metastatic breast cancer when comparing lymph node metastases to primary tumors of the breast.

The rank of global differential expression, the probe/transcript ID, the *p*-value with respect to differential expression transcriptome-wide, *t*, a moderated *t*-statistic, *B*, the log-odds of differential expression between the groups compared, the gene and gene name are listed in this chart.

Rank: 7924
Probe ID: A_24_P294408
p-value: 1.75e-03
t: -3.3185367
B: -1.753041
Gene: PLA1A
Gene name: phospholipase A1 member A

Chart 2: PLA1A is differentially expressed in brain metastatic breast cancer when comparing brain metastases to normal breast tissues.

The rank of global differential expression, the probe/transcript ID, the *p*-value with respect to differential expression transcriptome-wide, *t*, a moderated *t*-statistic, *B*, the log-odds of differential expression between the groups compared, the gene and gene name are listed in this chart.

Figure 1: PLA1A is expressed at significantly higher levels in the lymph node metastases of patients with metastatic breast cancer when compared to primary tumors of the breast.

The mRNA expression level of PLA1A in primary tumors of the breast (left) and in lymph node metastases of women with metastatic breast cancer (right) is graphically depicted; the result of a statistical test evaluating significance of difference in PLA1A expression between primary tumors of the breast and lymph node metastases, a p -value, is $p=0.00064$.

Figure 2: PLA1A primary tumor expression is correlated with distant metastasis-free survival in patients with breast cancer, in lymph node positive patients but not in lymph node negative patients.

Depicted in these Kaplan-Meier plots is the probability of distant metastasis-free survival in $n=889$ lymph node positive patients (**left**) and $n=1309$ lymph node negative patients (**right**), based on low or high expression of PLA1A 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 PLA1A 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.

Lymph node positive patients

Low PLA1A expression: 50.07 months

High PLA1A expression: 32.03 months

Chart 3: Median distant metastasis-free survival is inferior in lymph node positive patients with high primary tumor expression of PLA1A.

The median DMFS (distant metastasis-free survival) of patients with low primary tumor expression of PLA1A and high primary tumor expression of PLA1A is listed in this chart, for $n=889$ lymph node positive breast cancer patients.