CD8A is differentially expressed in the lymph nodes of patients with metastatic 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 the alpha chain of the T-cell co-stimulatory receptor CD8, CD8A, 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 CD8A was also differentially expressed in brain metastatic tissues. CD8A mRNA was present at increased quantities in lymph node metastases as compared to primary tumors of the breast. Importantly, expression of CD8A in primary tumors of the breast was significantly correlated with patient overall survival in lymph node positive patients. Modulation of CD8A 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, CD8 receptor alpha chain, CD8A, 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 the CD8 receptor alpha chain, CD8A, 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 CD8A 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 CD8A mRNA expression levels with overall survival in $n=1402$ 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.

CD8A 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 the CD8 receptor alpha chain, encoded by CD8A, 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, CD8A ranked 84 out of 18034 total transcripts (Chart 1), equating to 99.5% differential expression. Differential expression of CD8A in the lymph node metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=5.47e-04$).

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 CD8A 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 CD8A 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, CD8A ranked 3978 out of 41093 total transcripts (Chart 2), equating to 90.3% differential expression. Differential expression of CD8A in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 2; $p=7.66e-05$). Thus, differential expression of CD8A, 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 CD8A differential expression in human metastatic breast cancer is a *bona fide* biological process and that differential expression of CD8A in metastatic breast cancer is shared between the brain and the lymph nodes.

CD8A is expressed at higher levels in the lymph node metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for CD8A, 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 CD8A expression in lymph node metastatic tissues. We observed significantly increased expression of CD8A in the lymph node metastases of patients with breast cancer as compared to primary tumors of the breast: CD8A was expressed at 1.23 ± 0.72 arbitrary units (AU) in primary tumors of the breast, while it was expressed at 2.33 ± 1.25 AU in lymph node metastatic tissues (Figure 1). The difference in CD8A mRNA levels between primary tumors of the breast and lymph node metastases was statistically significant (Figure 1; $p=0.000655$).

CD8A expression is significantly correlated with survival outcomes in human breast cancer.

We performed Kaplan-Meier survival analysis⁷ in $n=1402$ breast cancer patients in total, to evaluate whether CD8A tumor expression was correlated with survival outcomes in breast cancer. We observed a statistically significant correlation between primary tumor expression of CD8A and overall survival (OS) in patients with breast cancer (Figure 2). Patients whose primary tumors expressed low levels of CD8A possessed median OS of 78 months, while patients whose tumors expressed high levels of CD8A possessed median OS of 130 months. This difference in OS based on CD8A tumor expression in patients with breast cancer was statistically significant (Figure 2, Chart 3; logrank p -value: 0.003; hazard ratio: 0.72 (0.58-0.9)).

We also performed Kaplan-Meier survival analysis⁷ in $n=313$ lymph node positive breast cancer patients and $n=594$ lymph node negative breast cancer patients, to evaluate whether lymph node status influenced correlation of CD8A tumor expression with survival outcomes in human breast cancer. We observed a correlation between primary tumor expression of CD8A and overall survival (OS) in lymph node positive breast cancer (Figure 2). Lymph node positive patients whose primary tumors expressed low levels of CD8A possessed median OS of 35.64 months, while lymph node positive patients whose tumors expressed high levels of CD8A possessed median OS of 62.07 months. This difference in OS based on CD8A tumor expression in lymph node positive patients with breast cancer trended was statistically significant (Figure 2, Chart 3; logrank p -value: 0.0039; hazard ratio: 0.56 (0.38-0.83)).

1 Thus, overall survival based on CD8A primary tumor expression was markedly longer in lymph
2 node positive patients than in the general breast cancer patient population. CD8A primary tumor
3 expression was not significantly correlated with overall survival outcomes in lymph node negative
4 patients, though it trended towards significance (Figure 2, Chart 3; logrank p -value: 0.085; hazard ratio:
0.72 (0.49-1.05)).

5 Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified
6 CD8A as among the genes whose expression was most different, transcriptome-wide, in the lymph node
7 metastases of patients with breast cancer, when compared to primary tumors; we observed significantly
8 increased expression of CD8A in lymph node metastases as compared to primary tumors of the breast.
9 Further, we found a significant correlation between CD8A expression and patient survival outcomes, as
overall survival was significantly greater in patients whose primary tumors expressed higher levels of
CD8A as compared to patients whose primary tumors expressed lower levels of CD8A, and this
correlation was markedly more significant in lymph node positive patients than in lymph node negative
patients.

10 **Discussion**

11 We provided evidence here that the CD8 receptor alpha chain, CD8A, is among the genes whose
12 expression is most different in the lymph node metastases of patients with metastatic breast cancer as
13 compared to primary tumors of the breast, that CD8A is also differentially expressed in brain metastatic
14 tissues in human breast cancer, that CD8A mRNA is present at significantly increased quantities in lymph
15 node metastatic tissues as compared to primary tumors of the breast, and that primary tumor CD8A
16 expression is significantly correlated with patient survival outcomes in human breast cancer, markedly
17 more so in lymph node positive patients than in lymph node negative patients. Evaluation of the effects of
18 genetic depletion of CD8A in mouse models of metastatic breast cancer on metastasis to the central
19 nervous system is merited. Modulation of CD8A expression may be relevant to the processes by which
20 breast cancer cells exit the breast, enter the vasculature and/or lymphatics, reside in the lymph nodes,
21 evade immune clearance, breach the blood-brain barrier and colonize the brain.
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Rank: 84
Probe ID: 18976
p-value: 5.47e-04
t: -3.6033801
B: -0.3001
Gene: CD8A
Gene name: CD8 receptor alpha chain

Chart 1: CD8A 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: 3978
Probe ID: A_32_P163247
p-value: 7.66e-05
t: 4.3346591
B: 1.209393
Gene: CD8A
Gene name: CD8 receptor alpha chain

Chart 2: CD8A 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: CD8A 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 CD8A 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 CD8A expression between primary tumors of the breast and lymph node metastases, a p -value, is $p=0.000655$.

Figure 2: Significant correlation between CD8A primary tumor expression and overall survival in patients with breast cancer, which is markedly more significant in lymph node positive patients than in lymph node negative patients.

Depicted in this Kaplan-Meier plot (**above**) is the probability of overall survival for $n=1402$ total patients stratified into two groups, based on low or high expression of CD8A 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 CD8A 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. Below, Kaplan-Meier plots for probability of overall survival in $n=313$ lymph node positive patients (**left**) and $n=594$ lymph node negative patients (**right**).

All patients

Low CD8A expression: 78 months

High CD8A expression: 130 months

Lymph node positive patients

Low CD8A expression: 35.64 months

High CD8A expression: 62.07 months

Lymph node negative patients

Low CD8A expression: 125.92 months

High CD8A expression: 175.46 months

Chart 3: Median overall survival is inferior in patients with low primary tumor expression of CD8A.

The median OS (overall survival) of patients with low primary tumor expression of CD8A and high primary tumor expression of CD8A is listed in this chart, for $n=1402$ breast cancer patients, for $n=313$ lymph node positive patients and for $n=594$ lymph node negative patients.