TRBV5-4 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 T cell receptor beta variable 5-4, TRBV5-4, 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 TRBV5-4 was also differentially expressed in brain metastatic tissues. TRBV5-4 mRNA was present at increased quantities in lymph node metastases as compared to primary tumors of the breast. Thus, up-regulation of a variable segment of the beta chain of the T-cell receptor in tumor cells of the breast may be relevant to the biology by which cells from tumors of the breast metastasize 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, T cell receptor beta variable 5-4, TRBV5-4, 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 T cell receptor beta variable 5-4, TRBV5-4, 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 TRBV5-4 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.

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.

TRBV5-4 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 T cell receptor beta variable 5-4, encoded by TRBV5-4, 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, TRBV5-4 ranked 218 out of 18034 total transcripts (Chart 1), equating to 98.8% differential expression. Differential expression of TRBV5-4 in the lymph node metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=2.70e-03$).

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 TRBV5-4 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 TRBV5-4 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, TRBV5-4 ranked 7364 out of 41093 total transcripts (Chart 2), equating to 82.1% differential expression. Differential expression of TRBV5-4 in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 2; $p=1.23e-03$). Thus, differential expression of TRBV5-4, 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 TRBV5-4 differential expression in human metastatic breast cancer is a *bona fide* biological process and that differential expression of TRBV5-4 in metastatic breast cancer is shared between the brain and the lymph nodes.

TRBV5-4 is expressed at higher levels in the lymph node metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for TRBV5-4, 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 TRBV5-4 expression in lymph node metastatic tissues. We observed significantly increased expression of TRBV5-4 in the lymph node metastases of patients with breast cancer as compared to primary tumors of the breast: TRBV5-4 was expressed at -2.20 ± 0.97 arbitrary units (AU) in primary tumors of the breast, while it was expressed at -1.00 ± 1.20 AU in lymph node metastatic tissues (Figure 1). The difference in TRBV5-4 mRNA levels between primary tumors of the breast and lymph node metastases was statistically significant (Figure 1; $p=0.003158$).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified TRBV5-4 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 TRBV5-4 in lymph node metastases as compared to primary tumors of the breast.

Discussion

We provided evidence here that T cell receptor beta variable 5-4, TRBV5-4, 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 TRBV5-4 is also differentially expressed in brain metastatic tissues in human breast cancer, and that TRBV5-4 mRNA is present at significantly increased quantities in lymph node metastatic tissues as compared to primary tumors of the breast. Evaluation of the effects of genetic depletion of TRBV5-4 in mouse models of metastatic breast cancer on metastasis to the lymph nodes and to the central nervous system is merited. Modulation of TRBV5-4 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: 218
Probe ID: 20899
p-value: 2.70e-03
t: -3.0976589
B: -1.6482
Gene: TRBV5-4
Gene name: T cell receptor beta variable 5-4

Chart 1: TRBV5-4 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: 7364
Probe ID: A_23_P352861
p-value: 1.23e-03
t: 3.4408268
B: -1.4195
Gene: TRBV5-4
Gene name: T cell receptor beta variable 5-4

Chart 2: TRBV5-4 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: TRBV5-4 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 TRBV5-4 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 TRBV5-4 expression between primary tumors of the breast and lymph node metastases, a p -value, is $p=0.003158$.