CNTNAP3 is a differentially expressed gene in brain metastatic human breast cancer.

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Metastasis to the brain is a clinical problem in patients with breast cancer¹⁻³. We mined published microarray data^{4,5} to compare primary and metastatic tumor transcriptomes for the discovery of genes associated with brain metastasis in humans with metastatic breast cancer. We found that contactin associated protein-like 3, encoded by CNTNAP3, was among the genes whose expression was most different in the brain metastases of patients with metastatic breast cancer as compared to primary tumors of the breast. CNTNAP3 mRNA was present at decreased quantities in brain metastatic tissues as compared to primary tumors of the breast. Modulation of CNTNAP3 expression may be relevant to the biology by which tumor cells metastasize from the breast to the brain in humans with metastatic breast cancer.

Keywords: breast cancer, metastasis, brain metastasis, central nervous system metastasis, contactin associated protein-like 3, CNTNAP3, 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 metastatic tissues to support identification of therapeutic targets, whether they are treatment related or not. We performed a global comparative analysis of primary and metastatic tumors in patients with brain metastatic breast cancer^{4,5}. We discovered differential and decreased expression of the gene encoding contactin associated protein-like 3, CNTNAP3, in brain 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 $n=11$ primary breast tumors and $n=3$ brain metastases from patients with breast cancer; analysis was performed using platform GPL885. 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 CNTNAP3 gene expression was significantly different between primary tumors of the breast and brain 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 brain metastasis in human breast cancer in an unbiased fashion and for the discovery of novel therapeutic targets.

CNTNAP3 is differentially expressed in the brain metastases of patients with brain metastatic breast cancer.

Through blind, systems-level analysis of published microarray data⁴, we identified the contactin associated protein-like 3, encoded by CNTNAP3, as a differentially expressed gene in the breast metastatic tissues of humans with breast cancer (Table 1). When sorting each of the genes expressed in brain metastases based on significance of difference as compared to primary tumors of the breast in patients with breast cancer, CNTNAP3 ranked 92 out of 17418 total transcripts (Chart 1), equating to 99.5% differential expression. Differential expression of CNTNAP3 in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=1.82e-04$).

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 CNTNAP3 in brain metastases in human metastatic 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 CNTNAP3 as a differentially expressed gene 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, CNTNAP3 ranked 2270 out of 41093 total transcripts (Chart 2), equating to 94.5% differential expression. Differential expression of CNTNAP3 in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 2; $p=7.13\text{e-}06$). Thus, differential expression of CNTNAP3, transcriptome-wide, in the brain metastases of women with metastatic breast cancer was conserved across two independent microarray datasets, both when compared to benign and transformed breast tissues. This suggests that CNTNAP3 differential expression in human brain metastatic breast cancer is a *bona fide* biological process.

CNTNAP3 is expressed at lower levels in the brain metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for CNTNAP3, in primary tumors of the breast and in brain metastasis of patients with brain metastatic breast cancer to determine direction and statistical significance of change in CNTNAP3 expression in brain metastatic tissues. We observed significantly lower expression of CNTNAP3 in the brain metastases of patients with breast cancer as compared to primary tumors of the breast: CNTNAP3 was expressed at -0.08 ± 0.31 arbitrary units (AU) in primary tumors of the breast, while it was expressed at -1.09 ± 0.43 AU in brain metastatic tissues. The difference in CNTNAP3 mRNA levels between primary tumors of the breast and brain metastatic tissues was statistically significant (Figure 1; $p=0.000217$).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified contactin associated protein-like 3, encoded by CNTNAP3, as among the genes whose expression was most different, transcriptome-wide, in the brain metastases of patients with breast cancer, both when compared to primary tumors of the breast and to normal breast tissues; we observed significantly decreased expression of CNTNAP3 in brain metastases as compared to primary tumors of the breast.

Discussion

We provided evidence here that contactin associated protein-like 3, encoded by CNTNAP3, is among the genes whose expression is most different in the brain metastases of patients with brain metastatic breast cancer, and that CNTNAP3 mRNA is present at significantly decreased quantities in brain metastatic tissues as compared to primary tumors of the breast. Evaluation of the effects of genetic depletion of CNTNAP3 in mouse models of metastatic breast cancer on metastasis to the central nervous system is merited. CNTNAP3 is expressed in the mouse basal ganglia during early post-natal development and is a cell-adhesion/recognition molecule of the Caspr family with expression in the nervous system where it has been described to interact with PDZ domain-containing proteins in a manner similar to neuroligin proteins^{7,8}. Modulation of CNTNAP3 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: 92
Probe ID: 19666
p-value: 1.82e-04
t: 4.86
B: 0.978361
Gene: CNTNAP3
Gene name: contactin associated protein-like 3

Chart 1: CNTNAP3 is differentially expressed in brain metastatic breast cancer when comparing brain 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: 2270
probe ID: A_24_P418203
p-value: 7.13e-06
t: 5.049828
B: 3.491806
Gene: CNTNAP3
Gene name: contactin associated protein-like 3

Chart 2: CNTNAP3 is differentially expressed in brain metastatic breast cancer when comparing brain metastases to normal breast tissues.

The rank of global differential expression, 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: CNTNAP3 is expressed at significantly lower levels in the brain metastases of patients with metastatic breast cancer when compared to primary tumors of the breast.

The mRNA expression level of CNTNAP3 in primary tumors of the breast (left) and in brain metastases of women with metastatic breast cancer (right) is graphically depicted; the result of a statistical test evaluating significance of difference in CNTNAP3 expression between primary tumors of the breast and brain metastases, a *p*-value, is *p*=0.000217.