BICD1 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 bicaudal D homolog 1, encoded by BICD1, 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. BICD1 mRNA was present at decreased quantities in brain metastatic tissues as compared to primary tumors of the breast. Importantly, expression of BICD1 in primary tumors was correlated with patient distant metastasis-free survival. Modulation of BICD1 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, bicaudal D homolog 1, BICD1, 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 bicaudal D homolog 1, BICD1, 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 BICD1 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. For Kaplan-Meier survival analysis, we used the Kaplan-Meier plotter online tool⁷ for correlation of BICD1 mRNA expression levels with distant metastasis-free survival in $n=1803$ 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 brain metastasis in human breast cancer in an unbiased fashion and for the discovery of novel therapeutic targets.

BICD1 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 bicaudal D homolog 1, encoded by BICD1, 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, BICD1 ranked 84 out of 17418 total transcripts (Chart 1), equating to 99.5% differential expression. Differential expression of BICD1 in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=1.72\text{e-}04$).

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 BICD1 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 BICD1 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, BICD1 ranked 15492 out of 41093 total transcripts (Chart 2), equating to 62.3% differential expression. Differential expression of BICD1 in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 2; $p=3.23e-02$). Thus, differential expression of BICD1, 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 BICD1 differential expression in human brain metastatic breast cancer is a *bona fide* biological process.

BICD1 is expressed at lower levels in the brain metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for BICD1, 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 BICD1 expression in brain metastatic tissues. We observed significantly lower expression of BICD1 in the brain metastases of patients with breast cancer as compared to primary tumors of the breast: BICD1 was expressed at 0.03 ± 0.24 arbitrary units (AU) in primary tumors of the breast, while it was expressed at -0.92 ± 0.47 AU in brain metastatic tissues. The difference in BICD1 mRNA levels between primary tumors of the breast and brain metastatic tissues was statistically significant (Figure 1; $p=0.000166$).

BICD1 expression is correlated with survival outcomes in human breast cancer.

We performed Kaplan-Meier survival analysis⁷ in $n=1803$ breast cancer patients in total, to evaluate whether BICD1 tumor expression was correlated with survival outcomes in breast cancer. We observed a statistically significant correlation between primary tumor expression of BICD1 and distant metastasis-free survival (PPS) in patients with breast cancer (Figure 2). Patients whose primary tumors expressed low levels of BICD1 possessed median PPS of 118.51 months, while patients whose primary tumors expressed high levels of BICD1 possessed median PPS of 79.46 months. This difference in PPS based on BICD1 tumor expression in patients with breast cancer trended towards statistical significance (Figure 2, Chart 3; logrank p -value: 0.098; hazard ratio: 1.18 (0.97-1.42)).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified bicaudal D homolog 1, encoded by BICD1, 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 BICD1 in brain metastases as compared to primary tumors of the breast. Further, we found a correlation between BICD1 expression and patient survival outcomes, as distant metastasis-free survival was greater in patients whose primary tumors expressed lower levels of BICD1 as compared to patients whose primary tumors expressed higher levels of BICD1.

Discussion

We provided evidence here that bicaudal D homolog 1, encoded by BICD1, is among the genes whose expression is most different in the brain metastases of patients with brain metastatic breast cancer, that BICD1 mRNA is present at significantly decreased quantities in brain metastatic tissues as compared to primary tumors of the breast, and that primary tumor BICD1 expression is significantly correlated with patient survival outcomes in human breast cancer. Evaluation of the effects of genetic depletion of BICD1 in mouse models of metastatic breast cancer on metastasis to the central nervous system is merited. Bicaudal-D1 is a coiled-coil protein that functions in the attachment of specific cargoes to dynein-dynactin motor complexes, such as in the context of COPI-independent Golgi-ER vesicular trafficking involving Rab6a⁸. Modulation of BICD1 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: 84
Probe ID: 11560
p-value: 1.72e-04
t: 4.89
B: 1.030729
Gene: BICD1
Gene name: bicaudal D homolog 1

Chart 1: BICD1 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: 15492
probe ID: A_24_P916586
p-value: 3.23e-02
t: -2.205808
B: -4.396576
Gene: BICD1
Gene name: bicaudal D homolog 1

Chart 2: BICD1 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: BICD1 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 BICD1 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 BICD1 expression between primary tumors of the breast and brain metastases, a p -value, is $p=0.000166$.

Figure 2: Correlation between BICD1 primary tumor expression and distant metastasis-free survival in patients with breast cancer.

Depicted in this Kaplan-Meier plot is the probability of distant metastasis-free survival for $n=1803$ total patients stratified into two groups, based on low or high expression of BICD1 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 BICD1 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.

1 Low BICD1 expression: 118.51 months

2 High BICD1 expression: 79.46 months

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4 **Chart 3: Median distant metastasis-free survival is inferior in patients with high primary tumor expression of BICD1.**

5 The median DMFS (distant metastasis-free survival) of patients with low primary tumor expression of
6 BICD1 and high primary tumor expression of BICD1 is listed in this chart, for $n=1803$ breast cancer
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