TAF11 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 transcription initiation factor TFIID subunit 11, encoded by TAF11, 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. TAF11 mRNA was present at decreased quantities in brain metastatic tissues as compared to primary tumors of the breast. Expression of TAF11 in primary tumors was significantly correlated with patient recurrence-free survival. Modulation of TAF11 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 metastases, central nervous system metastases, transcription initiation factor TFIID subunit 11, TAF11, 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 increased expression of the gene encoding transcription initiation factor TFIID subunit 11, TAF11, in brain metastatic tissues of patients with metastatic breast cancer.

Methods

We used datasets GSE10893⁴ and GSE43837⁵ 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. GSE43837 was generated using Affymetrix Human X3P Array technology with $n=19$ primary tumors of the breast and $n=19$ 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 TAF11 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 TAF11 mRNA expression levels with recurrence-free survival in $n=3951$ patients; auto cut-off was selected.

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.

TAF11 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 transcription initiation factor TFIID subunit 11, encoded by TAF11, 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, TAF11 ranked 46 out of 17418 total transcripts (Chart 1), equating to 99.7% differential expression. Differential expression of TAF11 in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=6.97e-05$).

To attempt to validate differential transcriptome-wide differential expression of TAF11 in brain metastases in human metastatic breast cancer, we queried a second microarray dataset⁵; again, we identified TAF11 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 primary tumors of the breast, TAF11 ranked 1264 out of 61359 total transcripts (Chart 2), equating to 97.9% differential expression. Differential expression of TAF11 in the brain metastases of patients with metastatic breast cancer approached statistical significance (Chart 2; $p=0.0073605$). Thus, transcriptome-wide differential expression of TAF11 in the brain metastases of women with metastatic breast cancer was conserved across two independent microarray datasets, indicating that this may likely be a *bona fide* biological phenomena associated with metastatic breast cancer in humans.

TAF11 is expressed at lower levels in the brain metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for TAF11, 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 TAF11 expression in brain metastatic tissues. We observed significantly lower expression of TAF11 in the brain metastases of patients with breast cancer as compared to primary tumors of the breast: TAF11 was expressed at -0.23 ± 0.57 arbitrary units (AU) in primary tumors of the breast, while it was expressed at -2.40 ± 1.14 AU in brain metastatic tissues. The difference in TAF11 mRNA levels between primary tumors of the breast and brain metastatic tissues was statistically significant (Figure 1; $p=0.00024$).

TAF11 expression is significantly correlated with survival outcomes in human breast cancer.

We performed Kaplan-Meier survival analysis⁸ in 3951 breast cancer patients in total, to evaluate whether TAF11 tumor expression was correlated with survival outcomes in breast cancer. We observed a statistically significant correlation between primary tumor expression of TAF11 and recurrence-free survival (OS) in patients with breast cancer (Figure 2). Patients whose primary tumors expressed low levels of TAF11 possessed median OS of 69.2 months, while patients whose tumors expressed high levels of TAF11 possessed median OS of 36 months. This difference in OS based on TAF11 tumor expression in patients with breast cancer was statistically significant (Figure 2, Chart 3; logrank p -value: $4.1e-10$; hazard ratio: 1.42 (1.27-1.58)).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified transcription initiation factor TFIID subunit 11, encoded by TAF11, as among the genes whose expression was most different, transcriptome-wide, in the brain metastases of patients with breast cancer when compared to primary tumors of the breast; we observed significantly decreased expression of TAF11 in brain metastases as compared to primary tumors of the breast. Further, we found a significant correlation between TAF11 expression and patient survival outcomes, as recurrence-free survival was significantly greater in patients whose tumors expressed lower levels of TAF11 as compared to patients whose tumors expressed higher levels of TAF11.

Discussion

We provided evidence here that transcription initiation factor TFIID subunit 11, encoded by TAF11, is among the genes whose expression is most different in the brain metastases of patients with

1 brain metastatic breast cancer, that TAF11 mRNA is present at significantly decreased quantities in brain
2 metastatic tissues as compared to primary tumors of the breast, and that primary tumor TAF11 expression
3 is significantly correlated with patient survival outcomes in human breast cancer. Evaluation of the effects
4 of genetic depletion of TAF11 in mouse models of metastatic breast cancer on metastasis to the central
5 nervous system is merited. Modulation of TAF11 expression may be relevant to the processes by which
6 breast cancer cells exit the breast, enter the vasculature and/or lymphatics, reside in the lymph nodes,
7 evade immune clearance, breach the blood-brain barrier and colonize the brain.
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Rank: 46
Probe ID: 5915
p-value: 6.97e-05
t: 5.34
B: 1.854346
Gene: TAF11
Gene name: transcription initiation factor TFIID subunit 11

Chart 1: TAF11 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: 1264
probe ID: Hs2.379936.1.A1_3p_at
p-value: 0.0073605
t: 2.8139417
B: -2.41866
Gene: TAF11
Gene name: transcription initiation factor TFIID subunit 11

Chart 2: TAF11 is differentially expressed in brain metastatic breast cancer when comparing brain metastases to primary tumors of the breast.

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: TAF11 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 TAF11 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 TAF11 expression between primary tumors of the breast and brain metastases is $p=0.00024$.

Figure 2: Significant correlation between TAF11 primary tumor expression and recurrence-free survival in patients with breast cancer.

Depicted in this Kaplan-Meier plot is the probability of recurrence-free survival for $n=3951$ total patients with breast cancer stratified into two groups, based on low or high expression of TAF11 in patient primary tumors. The log rank p -value denoting statistical significance of difference in recurrence-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 TAF11 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 TAF11 expression: 69.2 months

2 High TAF11 expression: 36 months

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4 **Chart 3: Median recurrence-free survival is inferior in patients with high primary tumor expression of TAF11.**

5 The median RFS (recurrence-free survival) of patients with low primary tumor expression of TAF11 and
6 high primary tumor expression of TAF11 is listed in this chart, for $n=3951$ breast cancer patients.