FUT4 is a differentially expressed gene in both lymph node and brain metastases in 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 fucosyltransferase 4, encoded by FUT4, was among the genes whose expression was most quantitatively different in the brain metastases of patients with metastatic breast cancer. FUT4 mRNA was present at decreased quantities in brain metastatic tissues as compared to primary tumors of the breast. Importantly, expression of FUT4 in primary tumors was significantly correlated with patient recurrence-free survival in patients with breast cancer. Modulation of FUT4 expression may be relevant to the biology by which tumor cells metastasize from the breast to the brain. These data are one piece of evidence suggesting a common ancestor or tumor clone for brain and lymph node metastases that originate from the primary tumor, alluding to patterns in developmental origin and migratory pathways through the lymph node in human brain metastatic breast cancer.

Keywords: breast cancer, metastasis, brain metastases, central nervous system metastases, fucosyltransferase 4, FUT4, 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 fucosyltransferase 4, FUT4, in brain metastatic tissues of patients with metastatic breast cancer.

Methods

We used datasets GSE10893⁴ and GSE124648⁵ 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 $n=4$ brain metastases from patients with breast cancer; analysis was performed using platform GPL885. GSE124648 was generated using Affymetrix Human Genome U133A array technology with $n=10$ normal breast tissues and $n=44$ lymph node metastases from patients with breast cancer; analysis was performed using platform GPL96. 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 FUT4 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 FUT4 mRNA expression levels in primary tumors of the breast with recurrence-free survival in $n=3951$ breast cancer patients.

Results

We performed global comparative transcriptome analysis of metastatic and primary tumor tissues of patients with metastatic breast, as well as normal tissues of the breast 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.

FUT4 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 fucosyltransferase 4, encoded by FUT4, as a differentially expressed gene in the brain 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, FUT4 ranked 66 out of 17418 total transcripts (Chart 1), equating to 99.6% differential expression. Differential expression of FUT4 in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=1.25e-04$).

FUT4 is differentially expressed in the lymph node metastases of patients with breast cancer.

To determine whether differential expression of FUT4 in human breast cancer could be validated in a second microarray dataset, and whether this was specific to brain metastases or could be observed in other anatomical locations, we queried a second microarray dataset⁵, here comparing normal breast tissues to lymph node metastases. Again, we identified FUT4 as a differentially expressed gene in the lymph node metastatic tissues of patients with breast cancer (Chart 2). When sorting each of the genes expressed in lymph node metastases based on significance of difference as compared to normal breast tissues, FUT4 ranked 3198 out of 22283 total transcripts (Chart 2), equating to 85.6% differential expression. Differential expression of FUT4 in the lymph node metastases of patients with metastatic breast cancer was statistically significant (Chart 2; $p=8.12\text{e-}04$). Thus, differential expression of FUT4, transcriptome-wide, in metastatic tissues of women with metastatic breast cancer was conserved across two independent microarray datasets, in the brain and in the lymph nodes.

FUT4 is expressed at lower levels in the brain metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for FUT4, 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 FUT4 expression in brain metastatic tissues. We observed significantly decreased expression of FUT4 in the brain metastases of patients with breast cancer as compared to primary tumors of the breast: FUT4 was expressed at 0.21 ± 0.27 arbitrary units (AU) in primary tumors of the breast, while it was expressed at -0.62 ± 0.16 AU in brain metastatic tissues (Figure 1). The difference in FUT4 mRNA levels between primary tumors of the breast and brain metastatic tissues was statistically significant (Figure 1; $p=0.000061$).

FUT4 expression is correlated with survival outcomes in human breast cancer.

We performed Kaplan-Meier survival analysis⁷ in 3951 breast cancer patients in total, to evaluate whether FUT4 tumor expression was correlated with survival outcomes in breast cancer. We observed a correlation between primary tumor expression of FUT4 and recurrence-free survival (RFS) in patients with breast cancer, in the lower survival quartile (Figure 2). Patients whose primary tumors expressed low levels of FUT4 possessed median RFS of 61 months, while patients whose tumors expressed high levels of FUT4 possessed median RFS of 46 months. This difference in RFS based on FUT4 tumor expression in patients with breast cancer was statistically significant (Figure 2, Chart 3; logrank p -value 0.022; hazard ratio: 1.16 (1.02-1.32)).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified fucosyltransferase 4, encoded by FUT4, as among the genes whose expression was most different, transcriptome-wide, in the brain and lymph node metastases of patients with breast cancer, when compared to primary tumors of the breast and to normal breast tissues, respectively; we observed significantly decreased expression of FUT4 in brain metastases as compared to primary tumors of the breast. Further, we found a correlation between FUT4 expression and patient survival outcomes, as recurrence-free survival was greater in patients whose primary tumors expressed higher levels of FUT4 as compared to patients whose primary tumors expressed lower levels of FUT4.

Discussion

We provided evidence here that FUT4 is among the genes whose expression is most different in the brain and lymph node metastases of patients with metastatic breast cancer, that FUT4 mRNA is present at significantly decreased quantity in brain metastatic tissues as compared to primary tumors of the breast, and that primary tumor FUT4 expression is significantly correlated with patient survival outcomes in human breast cancer. Evaluation of the effects of genetic depletion of FUT4 in mouse models of metastatic breast cancer on metastasis to the central nervous system is merited. Modulation of FUT4 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: 66
Probe ID: 21669
p-value: 1.25e-04
t: 5.04
B: 1.321746
Gene: FUT4
Gene name: fucosyltransferase 4

Chart 1: FUT4 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: 3198
probe ID: 209892_at
p-value: 8.12e-04
t: 3.542579
B: -1.26517
Gene: FUT4
Gene name: fucosyltransferase 4

Chart 2: FUT4 is differentially expressed in the lymph node metastases of patients with breast cancer when comparing lymph node 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: FUT4 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 FUT4 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 FUT4 expression between primary tumors and brain metastases is $p=0.000061$.

Figure 2: Significant correlation between FUT4 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 breast cancer patients stratified into two groups, based on low or high expression of FUT4 (also known as FCT3A) in patient primary tumor. 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, in the lower survival quartile. Listed below is the number of patients at risk (number of patients alive) per interval, after stratification based on FUT4 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 FUT4 expression: 61 months

2 High FUT4 expression: 46 months

3
4 **Chart 3: Median recurrence-free survival is inferior in patients with high primary tumor expression of FUT4.**

5 The median RFS (recurrence-free survival) of patients with low primary tumor expression of FUT4 and
6 high primary tumor expression of FUT4 is listed in this chart, for $n=3951$ breast cancer patients, in the
7 lower survival quartile.