MICALCL 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 MICAL C-terminal-like, encoded by MICALCL, 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. MICALCL mRNA was present at increased quantities in brain metastatic tissues as compared to primary tumors of the breast. Expression of MICALCL in primary tumors was significantly correlated with patient overall survival. Modulation of MICALCL 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, MICAL C-terminal-like, MICALCL, 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 MICAL C-terminal-like, MICALCL, 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 MICALCL 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 MICALCL mRNA expression levels with overall survival in $n=626$ 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.

MICALCL 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 MICAL C-terminal-like, encoded by MICALCL, 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, MICALCL ranked 179 out of 17418 total transcripts (Chart 1), equating to __% differential expression. Differential expression of MICALCL in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=7.48e-04$).

To attempt to validate differential transcriptome-wide differential expression of MICALCL in brain metastases in human metastatic breast cancer, we queried a second microarray dataset⁵; again, we identified MICALCL 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, MICALCL ranked 7131 out of 61359 total transcripts (Chart 2), equating to ___% differential expression. Differential expression of MICALCL in the brain metastases of patients with metastatic breast cancer approached statistical significance (Chart 2; $p=0.05576998$). Thus, transcriptome-wide differential expression of MICALCL 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.

MICALCL is expressed at higher levels in the brain metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for MICALCL, 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 MICALCL expression in brain metastatic tissues. We observed significantly higher expression of MICALCL in the brain metastases of patients with breast cancer as compared to primary tumors of the breast: MICALCL was expressed at 0.78 ± 0.94 arbitrary units (AU) in primary tumors of the breast, while it was expressed at 3.55 ± 1.67 AU in brain metastatic tissues. The difference in MICALCL mRNA levels between primary tumors of the breast and brain metastatic tissues was statistically significant (Figure 1; $p=0.002198$).

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

We performed Kaplan-Meier survival analysis⁸ in 626 breast cancer patients in total, to evaluate whether MICALCL tumor expression was correlated with survival outcomes in breast cancer. We observed a statistically significant correlation between primary tumor expression of MICALCL and overall survival (OS) in patients with breast cancer (Figure 2). Patients whose primary tumors expressed low levels of MICALCL possessed median OS of 67.4 months, while patients whose tumors expressed high levels of MICALCL possessed median OS of 110.4 months. This difference in OS based on MICALCL tumor expression in patients with breast cancer was statistically significant (Figure 2, Chart 3; logrank p -value: 0.016; hazard ratio: 0.68 (0.5-0.93)).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified MICAL C-terminal-like, encoded by MICALCL, 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 increased expression of MICALCL in brain metastases as compared to primary tumors of the breast. Further, we found a significant correlation between MICALCL expression and patient survival outcomes, as overall survival was significantly greater in patients whose tumors expressed higher levels of MICALCL as compared to patients whose tumors expressed lower levels of MICALCL.

Discussion

We provided evidence here that MICAL C-terminal-like, encoded by MICALCL, is among the genes whose expression is most different in the brain metastases of patients with brain metastatic breast cancer, that MICALCL mRNA is present at significantly increased quantities in brain metastatic tissues

1 as compared to primary tumors of the breast, and that primary tumor MICALCL expression is
2 significantly correlated with patient survival outcomes in human breast cancer. Evaluation of the effects of
3 genetic depletion of MICALCL in mouse models of metastatic breast cancer on metastasis to the central
4 nervous system is merited. Modulation of MICALCL expression may be relevant to the processes by
5 which breast cancer cells exit the breast, enter the vasculature and/or lymphatics, reside in the lymph
6 nodes, evade immune clearance, breach the blood-brain barrier and colonize the brain.
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Rank: 179
Probe ID: 6722
p-value: 7.48e-04
t: -4.23
B: -0.2992
Gene: MICALCL
Gene name: MICAL C-terminal-like

Chart 1: MICALCL 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: 7131
probe ID: Hs.97459.0.A1_3p_at
p-value: 0.05576998
t: 1.966245
B: -3.96941
Gene: MICALCL
Gene name: MICAL C-terminal-like

Chart 2: MICALCL 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: MICALCL is expressed at significantly higher levels in the brain metastases of patients with metastatic breast cancer when compared to primary tumors of the breast.

The mRNA expression level of MICALCL 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 MICALCL expression between primary tumors of the breast and brain metastases is $p=0.002198$.

Figure 2: Significant correlation between MICALCL primary tumor expression and overall survival in patients with breast cancer.

Depicted in this Kaplan-Meier plot is the probability of overall survival for $n=626$ total patients with breast cancer stratified into two groups, based on low or high expression of MICALCL in patient primary tumors. The log rank p -value denoting statistical significance of difference in overall 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 MICALCL 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.

Low MICALCL expression: 67.4 months
High MICALCL expression: 110.4 months

Chart 3: Median overall survival is inferior in patients with low primary tumor expression of MICALCL.

The median OS (overall survival) of patients with low primary tumor expression of MICALCL and high primary tumor expression of MICALCL is listed in this chart, for $n=626$ breast cancer patients.