CRK is differentially expressed 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 the v-crK sarcoma virus CT10 oncogene homolog, encoded by CRK, was among the genes whose expression was most quantitatively different in the brain metastases of patients with metastatic breast cancer. CRK mRNA was present at decreased quantities in brain metastatic tissues as compared to primary tumors of the breast. Importantly, expression of CRK in primary tumors was significantly correlated with patient recurrence-free survival in patients with breast cancer. Modulation of CRK expression may be relevant to the biology by which tumor cells metastasize from the breast to the brain.

Keywords: breast cancer, metastasis, brain metastases, central nervous system metastases, proto-oncogene c-Crk, CRK, 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 proto-oncogene c-Crk, CRK, 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 CRK 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 CRK 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.

CRK 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 v-crk sarcoma virus CT10 oncogene homolog, encoded by CRK, 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, CRK ranked 173 out of 17418 total transcripts (Chart 1), equating to 99.0% differential expression. Differential expression of CRK in the brain metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=4.42e-04$).

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

To determine whether differential expression of CRK 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 CRK 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, CRK ranked 4109 out of 22283 total transcripts (Chart 2), equating to 81.6% differential expression. Differential expression of CRK in the lymph node metastases of patients with metastatic breast cancer was statistically significant (Chart 2; $p=2.71\text{e-}03$). Thus, differential expression of CRK, 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.

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

We obtained exact mRNA expression levels for CRK, 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 CRK expression in brain metastatic tissues. We observed significantly decreased expression of CRK in the brain metastases of patients with breast cancer as compared to primary tumors of the breast: CRK was expressed at -0.20 ± 0.31 arbitrary units (AU) in primary tumors of the breast, while it was expressed at -1.13 ± 0.45 AU in brain metastatic tissues (Figure 1). The difference in CRK mRNA levels between primary tumors of the breast and brain metastatic tissues was statistically significant (Figure 1; $p=0.000516$).

CRK 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 CRK tumor expression was correlated with survival outcomes in breast cancer. We observed a correlation between primary tumor expression of CRK and recurrence-free survival (RFS) in patients with breast cancer (Figure 2). Patients whose primary tumors expressed low levels of CRK possessed median RFS of 43.56 months, while patients whose tumors expressed high levels of CRK possessed median RFS of 57 months. This difference in RFS based on CRK tumor expression in patients with breast cancer was statistically significant (Figure 2, Chart 3; logrank p -value 0.0041; hazard ratio: 0.85 (0.76-0.95)).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified proto-oncogene c-Crk, encoded by CRK, 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 and to normal breast tissues, respectively; we observed significantly decreased expression of CRK in brain metastases as compared to primary tumors of the breast. Further, we found a correlation between CRK expression and patient survival outcomes, as recurrence-free survival was greater in patients whose primary tumors expressed higher levels of CRK as compared to patients whose primary tumors expressed lower levels of CRK.

Discussion

We provided evidence here that CRK is among the genes whose expression is most different in the brain metastases of patients with metastatic breast cancer, that CRK mRNA is present at significantly decreased quantity in brain metastatic tissues as compared to primary tumors of the breast, that CRK was also differentially expressed in the lymph nodes, and that primary tumor CRK expression is correlated with patient survival outcomes in human breast cancer. Evaluation of the effects of genetic depletion of CRK in mouse models of metastatic breast cancer on metastasis to the central nervous system is merited. Modulation of CRK 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: 173
Probe ID: 4615
p-value: 4.42e-04
t: 4.42
B: 0.160709
Gene: CRK
Gene name: v-crk sarcoma virus CT10 oncogene homolog

Chart 1: CRK 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: 4109
probe ID: 202224_at
p-value: 2.71e-03
t: 3.139626
B: -2.393789
Gene: CRK
Gene name: CRK proto-oncogene, adaptor protein

Chart 2: CRK 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: CRK 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 CRK 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 CRK expression between primary tumors and brain metastases is $p=0.000516$.

Figure 2: CRK primary tumor expression is correlated with 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 CRK 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. Listed below is the number of patients at risk (number of patients alive) per interval, after stratification based on CRK 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 CRK expression: 43.56 months

2 High CRK expression: 57 months

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

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