KRT14 is differentially expressed in metastatic breast cancer, both in metastases to the brain and to the lymph nodes.

Shahan Mamoor, MS¹

¹shahanmamoor@gmail.com

East Islip, NY USA

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 to discover genes associated with brain metastasis in patients with metastatic breast cancer. We found that keratin 14, encoded by KRT14, was among the genes whose expression was most different in the metastatic tumor tissues of patients with metastatic breast cancer, both in metastases to brain and to the lymph nodes when compared to primary tumors of the breast or normal breast tissue, respectively. We observed significant down-regulation of KRT14 in metastasis to the brain. Molecular functions and down-regulation of keratin 14 may be important for metastasis of primary tumor-derived cancer cells to the lymph nodes and to the brain in humans with metastatic breast cancer and these data suggest some level of common origin for metastases that reside in the lymph nodes and colonize the brain.

Keywords: breast cancer, metastasis, brain metastasis, central nervous system metastasis, lymph node metastasis, KRT14, keratin 14, systems biology of breast cancer, targeted therapeutics in breast cancer.

One report described a 34% incidence of central nervous system metastases in trastuzumab-treated patients with breast cancer². This alarmingly high frequency of CNS metastasis 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 metastatic breast cancer^{4,5}. We discovered transcriptome-wide differential expression of KRT14 in brain and lymph node metastases of patients with metastatic breast cancer.

Methods

We used datasets GSE125989⁴ and GSE124648⁵ for this global differential gene expression analysis of brain metastatic breast cancer in conjunction with GEO2R. GSE125989 was generated using Affymetrix Human Genome U133A 2.0 Array technology with $n=16$ primary tumors from patients with breast cancer and $n=16$ brain metastases from patients with brain metastatic breast cancer. GSE124648, a microarray dataset, 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; platform GPL96 was used for this analysis. 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 KRT14 gene expression was significantly between primary breast tumors and brain metastases in humans with breast cancer using a two-tailed, unpaired t-test with Welch's correction. We used PRISM for all statistical analyses of differential gene expression in human breast cancer (Version 8.4.0)(455).

Results

We performed global comparative transcriptome analysis of the primary and metastatic tumor tissues of patients with brain and lymph node metastatic breast cancer using published microarray data^{4,5} to describe the transcriptional landscape of metastasis in human breast cancer in an unbiased fashion and for the discovery of novel therapeutic targets.

KRT14 is differentially expressed in the brain metastases of patients with brain metastatic breast cancer.

We identified keratin 14, encoded by KRT14, as among the genes whose expression was most significantly different in the brain metastases of patients with brain metastatic breast cancer⁴ (Table 1). When sorting each of the genes expressed in brain metastases based on significance of difference as compared to the primary tumors of patients with brain metastatic breast cancer, KRT14 ranked 140 out of 22277 total transcripts (Table 1), equating to 99.4% differential expression. Differential expression of KRT14 in the brain metastases of patients with brain metastatic breast cancer was statistically significant (Table 1; $p=7.72E-04$).

We asked whether we could validate differential expression of KRT14 was specific to brain metastasis or if we could observe differential expression of KRT14 in lymph node metastasis. Comparison of global gene expression profiles of 10 normal breast tissues to 44 lymph node metastases⁵ revealed that KRT14 was among the genes whose expression was most significantly different transcriptome-wide between the breast and lymph node metastases in patients with metastatic breast cancer (Table 2).

When sorting each of the genes expressed in lymph node metastases based on significance of difference in expression as compared to normal breast tissues, KRT14 ranked 8 out of 22283 total transcripts (Table 2), equating to 99.96% differential expression. Differential expression of KRT14 in lymph node metastases from patients with metastatic breast cancer was statistically significant (Table 2; $p=5.64E-23$).

KRT14 is expressed at significantly lower levels in the brain metastases of patients with brain metastatic breast cancer.

We obtained exact mRNA expression levels for KRT14, in primary tumors of the breast and in brain metastasis of patients with brain metastatic breast cancer to determine magnitude and direction of change in KRT14 expression in brain metastatic tissues. KRT14 was expressed at lower levels in the brain metastases of patients with breast cancer as compared to primary tumors of the breast, and this difference was statistically significant (Figure 1; $p=0.0008$). We calculated a mean fold change of 0.62 ± 0.35 in KRT14 expression when comparing primary tumors of the breast to brain metastatic tissues in patients with breast cancer (Table 1).

We also obtained exact mRNA expression levels for KRT14, in normal breast tissue and in lymph node metastases of patients with metastatic breast cancer to determine magnitude and direction of change in KRT14 expression in lymph node metastases. KRT14 was expressed at lower levels in the lymph node metastases of patients with breast cancer as compared to normal breast tissue, and this difference was statistically significant (Figure 2; $p<0.0001$). We calculated a mean fold change of 0.36 ± 0.12 in KRT14 expression when comparing normal breast tissue to lymph node metastases in patients with breast cancer (Table 2).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified KRT14 as a differentially expressed gene in metastatic breast cancer, both in brain metastases and in lymph node metastases when compared to tissues of the breast, transformed and benign; KRT14 was expressed at significantly lower levels in brain and lymph node metastases as compared to primary tumors of the breast.

Discussion

We provided evidence here that keratin 14, encoded by KRT14 is among the genes whose expression is most different in the brain and lymph node metastases of patients with metastatic breast cancer. A study has reported that in a mouse model of breast cancer induced by mouse mammary tumor virus promoter driving expression of the polyoma virus middle T antigen, in circulating tumor cells and in micrometastases of the lung, keratin 14+ cells were enriched for: while 0.9% of primary tumor cells were K14+, greater than 50% of lung micrometastases were KRT14+⁶. A possible explanation for apparent discrepancies observed in the lung micrometastases of the MMTV-PyMT mouse model and the patterns of KRT14 expression we have observed here in lymph node metastases include species-specificity to relative gene expression changes between mouse and human; it could also be that these lung micrometastases are still expressing relatively lower levels of keratin 14 as compared to the primary tumor of origin; the data previously presented describe frequency of cells in a given population expressing some level of KRT14, rather than transcriptome-wide differential expression and down-regulation of KRT14 between a metastatic tissue and benign breast tissue as we have observed here in human breast cancer through analysis of published microarray data. Moreover, the analysis we performed here compared benign breast tissue to lymph node metastasis as opposed to primary tumor. Nevertheless, KRT14 may be of relevance to any number of steps required for metastasis to the lymph nodes and to the brain, and differential expression of KRT14 in both metastasis to the lymph nodes and the brain suggests some level of common origin for metastases that reside in the lymph nodes and colonize the brain.

References

1. Lin, N.U., Amiri-Kordestani, L., Palmieri, D., Liewehr, D.J. and Steeg, P.S., 2013. CNS metastases in breast cancer: old challenge, new frontiers.
2. Bendell, J.C., Domchek, S.M., Burstein, H.J., Harris, L., Younger, J., Kuter, I., Bunnell, C., Rue, M., Gelman, R. and Winer, E., 2003. Central nervous system metastases in women who receive trastuzumab-based therapy for metastatic breast carcinoma. *Cancer*, 97(12), pp.2972-2977.
3. Tsukada, Y., Fouad, A., Pickren, J.W. and Lane, W.W., 1983. Central nervous system metastasis from breast carcinoma autopsy study. *Cancer*, 52(12), pp.2349-2354.
4. Iwamoto, T., Niikura, N., Ogiya, R., Yasojima, H., Watanabe, K.I., Kanbayashi, C., Tsuneizumi, M., Matsui, A., Fujisawa, T., Iwasa, T. and Shien, T., 2019. Distinct gene expression profiles between primary breast cancers and brain metastases from pair-matched samples. *Scientific reports*, 9(1), pp. 1-8.
5. Sinn, B.V., Fu, C., Lau, R., Litton, J., Tsai, T.H., Murthy, R., Tam, A., Andreopoulou, E., Gong, Y., Murthy, R. and Gould, R., 2019. SET ER/PR: a robust 18-gene predictor for sensitivity to endocrine therapy for metastatic breast cancer. *NPJ breast cancer*, 5(1), pp.1-8.
6. Cheung, K.J., Padmanaban, V., Silvestri, V., Schipper, K., Cohen, J.D., Fairchild, A.N., Gorin, M.A., Verdone, J.E., Pienta, K.J., Bader, J.S. and Ewald, A.J., 2016. Polyclonal breast cancer metastases arise from collective dissemination of keratin 14-expressing tumor cell clusters. *Proceedings of the National Academy of Sciences*, 113(7), pp.E854-E863.

Rank	ID	p-value	t	B	FC	Gene	Gene name
140	209351_at	7.72E-04	-3.6879173	-0.5088	0.62 ± 0.35	KRT14	keratin 14

Table 1: KRT14 is differentially expressed in brain metastases in metastatic breast cancer when compared to primary tumors of the breast.

Rank of differential expression, probe ID, *p*-value with respect to differential expression, t, a moderated t-statistic, B, the log-odds of differential expression between the two groups compared, fold change (FC) of KRT14 expression between the brain metastases of patients with breast cancer and primary tumors of the breast, gene and gene name are listed in this chart.

Rank	ID	p-value	t	B	FC	Gene	Gene name
8	209351_at	5.64E-23	16.430534	41.829557	0.36 ± 0.12	KRT14	keratin 14

Table 2: KRT14 is differentially expressed in lymph node metastases in metastatic breast cancer when compared to normal breast tissues.

Rank of differential expression, probe ID, *p*-value with respect to differential expression, t, a moderated t-statistic, B, the log-odds of differential expression between the two groups compared, fold change (FC) of KRT14 expression between the lymph node metastases of patients with breast cancer and normal breast tissues, gene and gene name are listed in this chart.

Figure 1: KRT14 is expressed at significantly lower levels in the brain metastases of patients with brain metastatic breast cancer.

The mRNA expression level of KRT14 in primary tumors of the breast (left) and in the brain metastases of brain metastatic breast cancer patients (right) is graphically represented here with mean KRT14 levels marked and the result of a statistical test evaluating difference in mRNA expression level between brain metastases and primary tumors of the breast, a *p*-value, listed above.

Figure 2: KRT14 is expressed at significantly lower levels in the lymph node metastases of patients with metastatic breast cancer as compared to normal breast tissues.

The mRNA expression level of KRT14 in normal breast tissue (left) and in the lymph node metastases of metastatic breast cancer patients (right) is graphically represented here with mean KRT14 levels marked and the result of a statistical test evaluating difference in mRNA expression level between lymph node metastases and normal breast tissue, a *p*-value, listed above.