CD22 is differentially expressed in the lymph nodes of patients with metastatic breast cancer.

Shahan Mamoor, MS¹

¹shahanmamoor@gmail.com

East Islip, NY USA

Metastasis to the brain is a clinical problem in patients with breast cancer¹⁻³. Between the breast and the brain reside the secondary lymphoid organ, the lymph nodes. We mined published microarray data^{4,5} to compare primary and metastatic tumor transcriptomes for the discovery of genes associated with metastasis to the lymph nodes in humans with metastatic breast cancer. We found that cluster of differentiation 22, CD22, was among the genes whose expression was most different in the lymph node metastases of patients with metastatic breast cancer as compared to primary tumors of the breast. CD22 mRNA was present at increased quantities in lymph node metastases as compared to primary tumors of the breast. Importantly, expression of CD22 in primary tumors of the breast was correlated with patient recurrence-free survival, more significantly in lymph node positive patients than in lymph node negative patients. Modulation of CD22 expression may be relevant to the biology by which tumor cells metastasize from the breast to the lymph nodes and the brain in humans with metastatic breast cancer.

Keywords: breast cancer, metastasis, brain metastasis, central nervous system metastasis, lymph node metastasis, cluster of differentiation 22, CD22, 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 and lymph node metastatic tissues to support identification of therapeutic targets, whether they are treatment related or not. The lymph nodes reside between the breast and the brain. We performed a global comparative analysis of lymph node metastatic tumor tissues in patients with metastatic breast cancer, compared to primary tumors and normal breast tissues^{4,5}. We discovered transcriptome-wide differential expression of the gene encoding cluster of differentiation 22, CD22, in lymph node 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 $n=71$ primary breast tumors and $n=7$ lymph node metastases from patients with breast cancer; analysis was performed using platform GPL887. 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 CD22 gene expression was significantly different between primary tumors of the breast and lymph node 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 CD22 mRNA expression levels with recurrence-free survival in $n=3951$ breast cancer patients.

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 metastasis in human breast cancer in an unbiased fashion and for the discovery of novel therapeutic targets.

CD22 is differentially expressed in the lymph node metastases of patients with metastatic breast cancer.

Through blind, systems-level analysis of published microarray data⁴, we identified cluster of differentiation 22, encoded by CD22, as a differentially expressed gene in the lymph node metastatic tissues of humans with breast cancer (Table 1). When sorting each of the genes expressed in lymph node metastases based on significance of difference as compared to primary tumors of the breast in patients with breast cancer, CD22 ranked 16 out of 18034 total transcripts (Chart 1), equating to 99.9% differential expression. Differential expression of CD22 in the lymph node metastases of patients with metastatic breast cancer was statistically significant (Chart 1; $p=2.17e-05$).

We queried a second microarray dataset⁵ to attempt to validate transcriptome-wide differential expression of CD22 in the lymph node metastases of patients with metastatic breast cancer. We again observed CD22 to be among the genes expressed most quantitatively differently in the lymph node metastases of patients with metastatic breast cancer as compared to primary tumors of the breast. When sorting each of the genes expressed in lymph node metastases based on significance of difference as compared to normal breast tissues, CD22 ranked 4940 out of 22283 total transcripts (Chart 2), equating to 77.8% differential expression. Differential expression of CD22 in the lymph node metastases of patients with metastatic breast cancer approached the level of statistical significance (Chart 2; $p=6.38e-03$).

CD22 is expressed at higher levels in the lymph node metastases of patients with metastatic breast cancer.

We obtained exact mRNA expression levels for CD22, in primary tumors of the breast and in lymph node metastases of patients with metastatic breast cancer to determine direction and statistical significance of change in CD22 expression in lymph node metastatic tissues. We observed significantly increased expression of CD22 in the lymph node metastases of patients with breast cancer as compared to primary tumors of the breast: CD22 was expressed at 0.28 ± 0.29 arbitrary units (AU) in primary tumors of the breast, while it was expressed at 0.83 ± 0.46 AU in lymph node metastatic tissues (Figure 1). The difference in CD22 mRNA levels between primary tumors of the breast and lymph node metastases was statistically significant (Figure 1; $p=0.000017$).

CD22 expression is significantly correlated with survival outcomes in human breast cancer.

We performed Kaplan-Meier survival analysis⁷ in $n=3951$ breast cancer patients in total, to evaluate whether CD22 tumor expression was correlated with survival outcomes in breast cancer. We observed a statistically significant correlation between primary tumor expression of CD22 and recurrence-free survival (RFS) in patients with breast cancer (Figure 2). Patients whose primary tumors expressed low levels of CD22 possessed median RFS of 216.66 months, while patients whose tumors expressed high levels of CD22 possessed median RFS of 228.85 months. This difference in RFS based on CD22 tumor expression in patients with breast cancer was statistically significant (Figure 2, Chart 3; logrank p -value: $3.9e-07$; hazard ratio: 0.75 (0.68-0.84)).

We also performed Kaplan-Meier survival analysis⁷ in $n=1133$ lymph node positive breast cancer patients and $n=2020$ lymph node negative breast cancer patients, to evaluate whether lymph node status influenced correlation of CD22 tumor expression with survival outcomes in human breast cancer. We observed a statistically significant correlation between primary tumor expression of CD22 and recurrence-free survival (RFS) in lymph node positive breast cancer (Figure 2). Patients whose primary tumors expressed low levels of CD22 possessed median RFS of 113.1 months, while patients whose tumors expressed high levels of CD22 possessed median RFS of 171.43 months. This difference in RFS based on CD22 tumor expression in patients with breast cancer was statistically significant (Figure 2, Chart 3; logrank p -value: 0.0014; hazard ratio: 0.73 (0.6-0.88)). Thus, recurrence-free survival based on CD22 primary tumor expression was markedly shorter in lymph node positive patients than in the general breast cancer patient population. While we also observed a correlation between primary tumor expression of CD22 and recurrence-free survival in lymph node negative breast cancer patients (Figure 2), this correlation approached statistical significance but was not statistically significant (Figure 2, Chart 3; logrank p -value: 0.059; hazard ratio: 0.85 (0.72-1.01)).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified CD22 as among the genes whose expression was most different, transcriptome-wide, in the 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 increased expression of CD22 in lymph node

metastases as compared to primary tumors of the breast. Further, we found a significant correlation between CD22 expression and patient survival outcomes, as recurrence-free survival was significantly greater in patients whose primary tumors expressed higher levels of CD22 as compared to patients whose primary tumors expressed lower levels of CD22, and this correlation was more significant in lymph node positive patients than in lymph node negative patients.

Discussion

We provided evidence here that cluster of differentiation 22, CD22, is among the genes whose expression is most different in the lymph node metastases of patients with metastatic breast cancer as compared to primary tumors of the breast and to normal breast tissues, that CD22 mRNA is present at significantly increased quantities in lymph node metastatic tissues as compared to primary tumors of the breast, and that primary tumor CD22 expression is significantly correlated with patient survival outcomes in human breast cancer, more significantly so in lymph node positive patients than in lymph node negative patients. Evaluation of the effects of genetic depletion of CD22 in mouse models of metastatic breast cancer on metastasis to the central nervous system is merited. Modulation of CD22 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

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. Weigman, V.J., Chao, H.H., Shabalin, A.A., He, X., Parker, J.S., Nordgard, S.H., Grushko, T., Huo, D., Nwachukwu, C., Nobel, A. and Kristensen, V.N., 2012. Basal-like Breast cancer DNA copy number losses identify genes involved in genomic instability, response to therapy, and patient survival. *Breast cancer research and treatment*, 133(3), pp.865-880.
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. Awada, A., Colomer, R., Inoue, K., Bondarenko, I., Badwe, R.A., Demetriou, G., Lee, S.C., Mehta, A.O., Kim, S.B., Bachelot, T. and Goswami, C., 2016. Neratinib plus paclitaxel vs trastuzumab plus paclitaxel in previously untreated metastatic ERBB2-positive breast cancer: the NEfERT-T randomized clinical trial. *JAMA oncology*, 2(12), pp.1557-1564.
7. Györfy, B., Lanczky, A., Eklund, A.C., Denkert, C., Budczies, J., Li, Q. and Szallasi, Z., 2010. An online survival analysis tool to rapidly assess the effect of 22,277 genes on breast cancer prognosis using microarray data of 1,809 patients. *Breast cancer research and treatment*, 123(3), pp.725-731.

Rank: 16
Probe ID: 11791
p-value: 2.17e-05
t: -4.5159451
B: 2.4653
Gene: CD22
Gene name: cluster of differentiation 22

Chart 1: CD22 is differentially expressed in lymph node metastatic breast cancer when comparing lymph node 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: 4940
Probe ID: 204581_at
p-value: 6.38e-03
t: -2.835333
B: -3.182763
Gene: CD22
Gene name: cluster of differentiation 22

Chart 2: CD22 is differentially expressed in lymph node metastatic breast cancer when comparing lymph node metastases to normal breast tissues.

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.

Figure 1: CD22 is expressed at significantly higher levels in the lymph node metastases of patients with metastatic breast cancer when compared to primary tumors of the breast.

The mRNA expression level of CD22 in primary tumors of the breast (left) and in lymph node metastases of women with metastatic breast cancer (right) is graphically depicted; the result of a statistical test evaluating significance of difference in CD22 expression between primary tumors of the breast and lymph node metastases, a *p*-value, is *p*=0.000017.

Figure 2: A significant correlation between CD22 primary tumor expression and recurrence-free survival in patients with breast cancer which is more significant in lymph node positive patients than in lymph node negative patients.

Depicted in this Kaplan-Meier plot (**above**) is the probability of recurrence-free survival for $n=3951$ total patients stratified into two groups, based on low or high expression of CD22 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 CD22 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. Below, Kaplan-Meier plots for probability of recurrence-free survival in $n=1133$ lymph node positive patients (**left**) and $n=2020$ lymph node negative patients (**right**).

All patients

Low CD22 expression: 216.66 months

High CD22 expression: 228.85 months

Lymph node positive patients

Low CD22 expression: 113.1 months

High CD22 expression: 171.43 months

Lymph node negative patients

Low CD22 expression: 216.66 months

High CD22 expression: 228.85 months

Chart 3: Median recurrence-free survival is inferior in patients with low primary tumor expression of CD22.

The median RFS (recurrence-free survival) of patients with low primary tumor expression of CD22 and high primary tumor expression of CD22 is listed in this chart, for $n=3951$ breast cancer patients, for $n=1133$ lymph node positive patients, and $n=2020$ lymph node negative patients.