Lumican 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 lumican, encoded by LUM, 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. Molecular functions and down-regulation of LUM 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 suggests 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, LUM, lumican, 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 LUM 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 LUM 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.

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

We identified lumican, encoded by LUM, 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, LUM ranked 12 out of 22297 total transcripts (Table 1), equating to 99.95% differential expression. Differential expression of LUM in the brain metastases of patients with brain metastatic breast cancer was statistically significant (Table 1; $p=1.1E-06$).

We asked whether we could validate differential expression of LUM was specific to brain metastasis or if we could observe differential expression of LUM in lymph node metastasis. Comparison of global gene expression profiles of 10 normal breast tissues to 44 lymph node metastases⁵ revealed that LUM 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 tissues of the breast, LUM ranked 529 out of 22283 total transcripts (Table 2), equating to 97.6% differential expression. Differential expression of LUM in lymph node metastases from patients with metastatic breast cancer was statistically significant (Table 2; $p=1.17E-08$).

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

We obtained exact mRNA expression levels for LUM, 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 LUM expression in brain metastatic tissues. LUM 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; $p=0.0001$). We calculated a mean fold change of 0.76 ± 0.16 in LUM expression when comparing primary tumors of the breast to brain metastatic tissues in patients with breast cancer (Table 1).

Thus, by mining published microarray data^{4,5} in an unbiased and systematic fashion, we identified LUM 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; LUM was expressed at significantly lower levels in brain metastases as compared to primary tumors of the breast.

Discussion

We provided evidence here that the lumican, encoded by LUM is among the genes whose expression is most different in the brain and lymph node metastases of patients with metastatic breast cancer. LUM may be of relevance to any number of steps required for metastasis to the lymph nodes and to the brain, and suggests some level of common origin for metastases that originate in the breast, reside in the lymph nodes and colonize the brain.

References

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Rank	ID	p-value	t	B	FC	Gene	Gene name
12	201744_s_at	1.1E-06	-5.8986103	5.2573	0.76 ± 0.16	LUM	lumican

Table 1: LUM 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 LUM 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	Gene	Gene name
529	201744_s_at	1.17E-08	6.689318	9.536641	LUM	lumican

Table 2: LUM is differentially expressed in lymph node 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, gene and gene name are listed in this chart.

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

The mRNA expression level of LUM 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 LUM 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.