MATK is differentially expressed in the tumors of breast cancer patients treated with trastuzumab.

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Trastuzumab (Herceptin) is a monoclonal antibody targeting the extracellular domain of the human epidermal growth factor receptor 2 (HER2)¹ utilized for the treatment of adjuvant and metastatic breast cancer² in the United States and worldwide. We mined published microarray and gene expression data^{3,4} to discover in an unbiased manner the most striking transcriptional features of trastuzumab treatment. We identified the megakaryocyte-associated tyrosine kinase MATK^{5,6} as among the genes most differentially expressed in the primary tumors of patients with breast cancer treated with trastuzumab. The primary tumors of breast cancer patients treated with trastuzumab expressed higher levels of MATK messenger RNA than did patients not treated with trastuzumab, and a single administration of trastuzumab was sufficient to result in differential expression of MATK in primary tumors of the breast, demonstrating that a platelet-expressed tyrosine kinase^{5,6} that interacts with the receptor for the stem cell factor⁷ is likely transcriptionally induced in primary tumors of the breast by trastuzumab.

Keywords: trastuzumab, breast cancer, MATK, megakaryocyte-associated tyrosine kinase, systems biology of breast cancer, targeted therapeutics in breast cancer.

The mechanism of action ascribed to trastuzumab function is thought to be binding of the F_{ab} domain of trastuzumab to the extracellular region of the human epidermal growth factor receptor 2 (HER2)¹, but the transcriptional consequences resulting from signaling downstream of trastuzumab binding to HER2 is less well understood. Through unbiased, systems-level comparative transcriptome analysis of published microarray and gene expression data^{3,4}, we report here that MATK is a differentially expressed gene in the tumors of trastuzumab-treated patients: patients treated with trastuzumab expressed significantly higher levels of MATK than did those of patients not treated with trastuzumab.

Methods

We used datasets GSE38057³ and GSE114082⁴ this differential gene expression analysis of the transcriptional response to trastuzumab treatment in patients with breast cancer. GSE38057 was generated using DASL Human Cancer Panel by Probe technology with $n=6$ primary breast tumors from patients treated with induction chemotherapy and/or hormone therapy without trastuzumab and $n=35$ primary breast tumors from patients treated with induction chemotherapy and/or hormone therapy in addition to trastuzumab, both of which developed brain metastases; analysis was performed using platform GPL5826. GSE114082 was generated using Illumina HumanHT-12 WG-DASL V4.0 R2 expression beadchip technology with $n=17$ primary breast tumors from patients before trastuzumab treatment and $n=17$ primary tumors from patients after trastuzumab treatment, analysis performed using platform GPL14951. 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 or multiplexed 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 MATK gene expression was significantly between primary breast tumors of patients receiving trastuzumab 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 harnessed the power of blind, comparative transcriptome analysis using published microarray and gene expression data^{3,4} to identify the most significant transcriptional features of the primary breast tumors of patients treated with trastuzumab (Herceptin).

MATK is differentially expressed in the tumors of patients treated with trastuzumab.

We identified the megakaryocyte-associated tyrosine kinase MATK as among the genes whose expression changed most significantly in the tumors of breast cancer patients treated with trastuzumab in a multiplexed gene expression dataset³ (Table 1). When sorting each of the genes expressed in the primary tumors of breast cancer patients treated with trastuzumab based on significance of change as compared to that of patients not treated with trastuzumab, MATK ranked 44 out of 1506 total transcripts (Table 1), equating to 97.1% differential expression. MATK differential expression in the tumors of patients treated with trastuzumab was statistically significant (Table 1; $p=0.04173$).

The first dataset, although measuring the expression of over 1500 genes, was still limited. We turned to a second microarray dataset⁴, this measuring the expression of genes across the transcriptome - 29377 genes in total. The tumors compared in this dataset were sampled from the same patient before and after a single, brief exposure to trastuzumab, not comparing tumors from different patients treated with a

course of trastuzumab or not. Thus, while differentially expressed genes when comparing tumors based on trastuzumab treatment can result from a variety of sources, including gene expression changes resulting from tumor evolution over the course of treatment, changes identified in this dataset, occurring after only a single treatment of trastuzumab, are more likely to be a direct transcriptional result of trastuzumab binding events. We found again that MATK was among the genes most differentially expressed in the tumors of patients administered a single treatment of trastuzumab (Table 2). When sorting each of the genes expressed in the tumors of patients administered a single treatment of trastuzumab, MATK ranked 6792 out of 29377 total transcripts (Table 2), equating to 76.9% differential expression. Differential expression of MATK in the primary tumors of breast cancer patients following treatment with trastuzumab was statistically significant (Table 2; $p=1.61E-02$).

MATK is expressed at significantly higher levels in the tumors of breast cancer patients treated with trastuzumab than in the tumors of those not treated with trastuzumab.

We obtained exact mRNA expression levels for MATK from tumors of patients treated with trastuzumab and from the tumors of patients not treated with trastuzumab to directly evaluate magnitude and change of expression in MATK based on history of trastuzumab treatment. MATK was expressed at higher levels in the tumors of patients treated with trastuzumab as compared to those of patients not treated with trastuzumab, and this difference was statistically significant (Figure 1; $p=0.0036$). We calculated a mean fold change of 1.63 ± 0.98 in MATK expression in the primary tumors of patients treated with trastuzumab relative to that of patients not treated with trastuzumab.

Thus, we found using published multiplexed gene expression and microarray data^{3,4} that MATK was among the genes most differentially expressed in the tumors of patients treated with trastuzumab, that MATK was expressed at significantly higher levels in the tumors of patients treated with trastuzumab as compared to those not treated with trastuzumab, and that this transcriptional change was likely a direct result of trastuzumab treatment as opposed to a gene expression change associated with clonal selection and evolution of the tumor across the course of treatment.

Discussion

MATK can interact with c-Kit⁷ and can phosphorylate the Src tyrosine kinase⁸. The data presented here demonstrate that a cellular component that can contribute to Src signaling⁸ is differentially expressed and transcriptionally induced by treatment with trastuzumab; we have recently illustrated transcriptional induction of the Src tyrosine kinase itself in the primary tumors of patients treated with trastuzumab⁹.

We provided evidence here that MATK, a tyrosine kinase otherwise thought to possess specific expression in cells of the megakaryocytic lineage^{5,6}, is a differentially expressed gene in the tumors of patients treated with trastuzumab, and that the primary tumors of breast cancer patients treated with trastuzumab expressed higher levels of MATK in their primary tumors than did patients not treated with trastuzumab.

References

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Rank	ID	p-value	t	B	FC	Gene
44	GI_21450843-A-4	0.04173	2.099071	-4.33	1.63 ± 0.98	MATK

Table 1: MATK is differentially expressed in the primary tumors of breast cancer patients treated with trastuzumab.

The rank of differential expression, probe ID, p-value with respect to global differential expression, t, a moderated t-statistic, B, the log-odds of differential expression between the two groups compared, fold change of expression in MATK between the tumors of patients treated with trastuzumab and the tumors of patients not treated with trastuzumab, and gene are listed in this chart.

Rank	ID	p-value	t	B	Gene
6792	ILMN_1803615	1.61E-02	-2.5258936	-3.39022	MATK

Table 2: A single exposure to trastuzumab is sufficient to drive differential expression of MATK in the primary tumors of patients with breast cancer.

The rank of differential expression, probe ID, p-value with respect to global 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: MATK is expressed at higher levels in the primary tumors of patients treated with trastuzumab.

The mRNA expression level of MATK is graphically depicted in this chart in the primary tumors of breast cancer patients not treated with trastuzumab (left) and in the primary tumors of breast cancer patients treated with trastuzumab (right), with mean mRNA expression level marked and the result of a statistical test evaluating significance of difference between MATK expression in the primary tumors of patients treated with trastuzumab or not, a *p*-value, listed above.