Paraneoplastic antigen-like 5 (PNMA5) 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 significant transcriptional changes associated with trastuzumab treatment. We identified the paraneoplastic antigen-like 5, encoded by PNMA5 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 PNMA5 messenger RNA than did patients not treated with trastuzumab, and a single administration of trastuzumab was sufficient to result in differential expression of PNMA5 in primary tumors of the breast, demonstrating increased expression of a paraneoplastic antigen described to possess specific expression in association areas of the neocortex of the primate brain⁵ as a direct transcriptional consequence of treatment with trastuzumab.

Keywords: trastuzumab, breast cancer, PNMA5, paraneoplastic-like 5, 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 PNMA5 is a differentially expressed gene in the tumors of trastuzumab-treated patients: patients treated with trastuzumab expressed significantly higher levels of PNMA5 than did those of patients not treated with trastuzumab.

Methods

We used datasets GSE130788³, and GSE114082⁴ for this differential gene expression analysis of the transcriptional response to trastuzumab treatment in patients with breast cancer. GSE130788 was generated using Agilent-014850 Whole Human Genome Microarray 4x44K G4112F technology with *n*=11 primary breast tumors from patients treated with trastuzumab and *n*=36 primary tumors from patients treated with trastuzumab, analysis performed using platform GPL6480. 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 PNMA5 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 performed unbiased 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).

PNMA5 is differentially expressed in the tumors of patients treated with trastuzumab.

We identified paraneoplastic antigen-like 5, encoded by PNMA5 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, PNMA5 ranked 241 out of 41000 total transcripts (Table 1), equating to 99.4% differential expression. PNMA5 differential expression in the tumors of patients treated with trastuzumab trended towards statistical significance (Table 1; *p*=3.61E-44).

We turned to a second microarray dataset to validate our findings of PNMA5 differential expression in the patients treated with trastuzumab. 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

1 in this dataset, occurring after only a single treatment of trastuzumab, are more likely to be a direct
2 transcriptional result of trastuzumab binding events. We found again that PNMA5 was among the genes
3 most differentially expressed in the tumors of patients administered a single treatment of trastuzumab
4 (Table 2). When sorting each of the genes expressed in the tumors of patients administered a single
5 treatment of trastuzumab, PNMA5 ranked 8099 out of 29377 total transcripts (Table 2), equating to
6 72.4% differential expression. Differential expression of PNMA5 in the primary tumors of breast cancer
7 patients following treatment with trastuzumab was statistically significant (Table 2; $p=2.75E-02$).

8 **PNMA5 is expressed at significantly higher levels in the tumors of breast cancer patients treated**
9 **with trastuzumab than in the tumors of those not treated with trastuzumab.**

10 We obtained exact mRNA expression levels for PNMA5 from tumors of patients treated with
11 trastuzumab and from the tumors of patients not treated with trastuzumab to directly evaluate direction
12 and statistical significance of change in expression of PNMA5 based on history of trastuzumab treatment.
13 PNMA5 was expressed at higher levels in the tumors of patients treated with trastuzumab as compared to
14 those of patients not treated with trastuzumab, and this difference was statistically significant (Figure 1;
15 $p<0.0001$).

16 Thus, we found using published multiplexed gene expression and microarray data^{3,4} that PNMA5
17 was among the genes most differentially expressed in the tumors of patients treated with trastuzumab, that
18 PNMA5 was expressed at higher levels in the tumors of patients treated with trastuzumab as compared to
19 those not treated with trastuzumab, and that this transcriptional change was likely a direct result of
20 trastuzumab treatment as opposed to a gene expression change associated with clonal selection and
21 evolution of the tumor across the course of treatment.

22 **Discussion**

23 We provided evidence here that PNMA5 is a differentially expressed gene in the tumors of
24 patients treated with trastuzumab, and expressed at significantly higher levels in the primary tumors of
25 breast cancer patients treated with trastuzumab as compared to patients not treated with trastuzumab.
26 Thus, trastuzumab, a treatment associated with a 34% rate of central nervous system metastases⁶,
27 administration in patients with breast cancer results in increased primary tumor expression of a
28 paraneoplastic antigen reported to possess specific expression in a sub-region of the primate neocortex⁵.

References

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Rank	ID	p-value	t	B	Gene	Gene name
241	A_23_P352950	3.61E-44	18.304814	89.881809	PNMA5	paraneoplastic Ma antigen family member 5

Table 1: PNMA5 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, gene and gene name are listed in this chart.

Rank	ID	p-value	t	B	Gene
8099	ILMN_1750337	2.75E-02	2.2981342	-3.85738	PNMA5

Table 2: A single exposure to trastuzumab is sufficient to drive differential expression of PNMA5 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: PNMA5 is expressed at significantly higher levels in the primary tumors of patients treated with trastuzumab.

The mRNA expression level of PNMA5 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 PNMA5 expression in the primary tumors of patients treated with trastuzumab or not, a *p*-value, listed above.