FAM22F expression associates with survival in triple negative breast cancer.

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We mined published microarray data (1) to understand the most significant gene expression differences in the tumors of triple negative breast cancer patients based on survival following treatment: dead or alive. We observed significant transcriptome-wide differential expression of family with sequence similarity 22, member F, encoded by FAM22F when comparing the primary tumors of triple negative breast cancer patients dead or alive. FAM22F may be of relevance as a biomarker or as a molecule of interest in understanding the etiology or progression of triple negative breast cancer.

Keywords: triple negative breast cancer, TNBC, systems biology of breast cancer, targeted therapeutics in breast cancer, FAM22F, family with sequence similarity 22, member F.

Triple negative breast cancer is defined by lack of expression of the receptors for the hormones progesterone and estrogen (PR negative and ER negative), as well as for the human epidermal growth factor receptor 2 (HER2 negative) (2, 3). Though not completely identical, triple negative breast cancer shares significant overlap with the basal or basal-like molecular subtype of human breast cancer (3). TNBC is more frequently diagnosed in women of African descent (black women) for reasons not understood, and their disease course is similarly more aggressive than in white women with triple negative breast cancer (2, 3). To understand the transcriptional biology of triple negative breast cancer in an unbiased fashion and at the systems level, we mined published microarray data paired with patient survival data (1), performing comparative transcriptome analysis based on survival at time of data collection: dead or alive. We present here a finding from the results of this analysis.

Methods

We used dataset GSE142102 (1) for this differential gene expression analysis in conjunction with GEO2R. GSE142102 was generated using Affymetrix Human Gene 2.1 ST Array technology; in this analysis, we used data from $n=87$ tumors from TNBC patients that were dead at time of analysis and $n=123$ tumors from TNBC patients that were alive at time of 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 FAM22F expression was significantly different between the primary tumors of TNBC patients that were dead or alive using a two-tailed t-test.

Results

We performed comparative transcriptome analysis using published microarray data (1) to understand in an unbiased fashion the most significant gene expression differences in the primary tumors of patients with triple negative breast cancer based on survival outcomes.

FAM22F is differentially expressed in triple negative breast cancer and negatively correlates with survival.

When comparing primary tumors of 87 live patients with triple negative breast cancer with that of 123 dead TNBC patients we identified family with sequence similarity 22, member F, *FAM22F*, as among the most significant transcriptional differences based on survival in human triple negative breast cancer. When ranking each of the transcripts whose expression was measured by microarray based on significance of difference in expression between the tumors of patients dead and alive, FAM22F ranked 79 out of 53617 total transcripts, equivalent to 99.9% differential expression (Chart 1). FAM22F differential expression in the tumors of patients based on survival outcomes was statistically significant (Figure 1; $p=0.00191337$).

FAM22F is expressed at significantly lower levels in the breast tumors of TNBC patients when comparing based on survival.

We obtained exact mRNA expression levels for FAM22F from breast tumors of TNBC patients dead and alive to understand the magnitude and direction of FAM22F expression change based on survival outcomes. FAM22F was expressed at lower levels in tumors of TNBC patients alive as compared to that of TNBC patients dead (Figure 1). Decreased expression of FAM22F in primary breast tumors was

1 statistically significant (Figure 1: $p=0.0019$). FAM22F was expressed at 0.22 ± 0.98 arbitrary units (AU)
2 in the primary tumors of TNBC patients dead, while it was expressed at -0.21 ± 0.98 AU in the primary
3 tumors of TNBC patients alive.

4 Thus, we found through unbiased comparative transcriptome analysis that FAM22F was among the
5 genes whose expression was most significantly different in the primary tumors of triple negative breast
6 cancer patients alive when compared to that of TNBC patients dead, and that FAM22F was expressed at
7 significantly lower levels in the primary tumors of TNBC patients alive as compared to TNBC patients
8 dead.

9 **Discussion**

10 It is not understood why women of African descent (black women) are diagnosed with triple
11 negative breast cancer more frequently than white women, and why this disease is more aggressive in
12 black women. FAM22F may be of relevance as a biomarker in identifying patients who are more likely to
13 survive, perhaps as part of a panel of genes used for prognostic stratification, and the molecule itself may
14 be important to the biology of triple negative breast cancer etiology or more likely its progression. Blind
15 systems-level analyses, like this, can help shed light on the fundamental molecular characteristics of a
16 disease whose racial propensities demand further explanation.
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References

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Rank: 79
Probe ID: 17096004
p-value: 0.00191337
t: 3.1033597
B: -3.17
Gene: FAM22F
Gene name: family with sequence similarity 22, member F

Chart 1: FAM22F is differentially expressed at the transcriptome-level when comparing the primary tumors of TNBC patients dead and alive.

Rank of differential expression, probe ID, *p*-value of global differential expression, *t*, a moderated *t*-statistic, *B*, the log-odds of differential expression between the groups compared, gene and gene name are listed in this chart.

Figure 1: FAM22F is expressed at significantly lower levels in the primary tumors of TNBC patients alive as compared to the primary tumors of TNBC patients dead.

The mRNA expression level of FAM22F in the primary tumors of TNBC patients dead (left) and in primary tumors of TNBC patients alive (right) is graphically depicted with the result of a statistical test evaluating significance of difference in FAM22F expression between the primary tumors of TNBC patients dead and alive, a p -value, listed here: $p=0.0019$.