PGM2L1 expression associates with survival in triple negative breast cancer.

Shahan Mamoor, MS¹

¹shahanmamoor@gmail.com

East Islip, NY USA

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 phosphoglucomutase 2-like 1, encoded by PGM2L1 when comparing the primary tumors of triple negative breast cancer patients dead or alive. Importantly, PGM2L1 expression was correlated with overall survival in basal subtype breast cancer, a molecular subtype sharing significant overlap with triple negative breast cancer. PGM2L1 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, PGM2L1, phosphoglucomutase 2-like 1.

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 PGM2L1 expression was significantly different between the primary tumors of TNBC patients that were dead or alive using a two-tailed t-test. For Kaplan-Meier survival analysis, we used the Kaplan-Meier plotter tool (4) for correlation of PGM2L1 mRNA expression levels with overall survival (OS) in $n=296$ patients with basal subtype breast cancer.

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.

PGM2L1 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 phosphoglucomutase 2-like 1, *PGM2L1*, 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, PGM2L1 ranked 155 out of 53617 total transcripts, equivalent to 99.7% differential expression (Chart 1). PGM2L1 differential expression in the tumors of patients based on survival outcomes was statistically significant (Figure 1; $p=0.00381138$).

PGM2L1 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 PGM2L1 from breast tumors of TNBC patients

1 dead and alive to understand the magnitude and direction of PGM2L1 expression change based on
2 survival outcomes. PGM2L1 was expressed at lower levels in tumors of TNBC patients alive as compared
3 to that of TNBC patients dead (Figure 1). Decreased expression of PGM2L1 in primary breast tumors was
4 statistically significant (Figure 1: $p=0.0085$). PGM2L1 was expressed at 0.25 ± 1.25 arbitrary units (AU)
in the primary tumors of TNBC patients dead, while it was expressed at -0.15 ± 0.77 AU in the primary
tumors of TNBC patients alive.

5 PGM2L1 expression correlates with overall survival in basal subtype human breast cancer.

6 We referenced a bioinformatics tool containing Kaplan-Meier survival data of human breast cancer
7 patients to understand more thoroughly whether a relationship existed between PGM2L1 primary tumor
8 expression and patient survival in human breast cancer. We found that PGM2L1 expression was
9 correlated with overall survival in patients with basal or basal-like human breast cancer, a breast cancer
10 molecular subtype which shares significant overlap with triple negative breast cancer (Figure 2; log rank
11 p -value: 0.0029 for overall survival, hazard ratio: 2.06 (1.27-3.36) (Fig. 2)). PGM2L1 mRNA levels were
a negative prognostic indicator in basal subtype breast cancer patients. Median OS was, on average,
markedly greater for basal subtype patients with low tumor expression of PGM2L1 as compared to basal
subtype patients with high tumor expression of PGM2L1.

12 Thus, we found through unbiased comparative transcriptome analysis that PGM2L1 was among the
13 genes whose expression was most significantly different in the primary tumors of triple negative breast
14 cancer patients alive when compared to that of TNBC patients dead, that PGM2L1 was expressed at
15 significantly lower levels in the primary tumors of TNBC patients alive as compared to TNBC patients
dead, and that PGM2L1 expression was negatively correlated with overall survival in the basal or
basal-like molecular subtype.

16 **Discussion**

17 It is not understood why women of African descent (black women) are diagnosed with triple
18 negative breast cancer more frequently than white women, and why this disease is more aggressive in
19 black women. PGM2L1 catalyzes the conversion of glucose-6-phosphate and 1,3-bisphosphoglycerate to
20 glucose 1,6-bisphosphate (5). PGM2L1 may be of relevance as a biomarker in identifying patients who
21 are more likely to survive, perhaps as part of a panel of genes used for prognostic stratification, and the
22 molecule itself may be important to the biology of triple negative breast cancer etiology or more likely its
23 progression. Blind systems-level analyses, like this, can help shed light on the fundamental molecular
24 characteristics of a disease whose racial propensities demand further explanation.
25
26
27
28

References

1. Purrington, K.S., Knight III, J., Dyson, G., Ali-Fehmi, R., Schwartz, A.G., Boerner, J.L. and Bandyopadhyay, S., 2020. CLCA2 expression is associated with survival among African American women with triple negative breast cancer. *PloS one*, 15(4), p.e0231712.
2. Foulkes, W.D., Smith, I.E. and Reis-Filho, J.S., 2010. Triple-negative breast cancer. *New England journal of medicine*, 363(20), pp.1938-1948.
3. Dietze, E.C., Sistrunk, C., Miranda-Carboni, G., O'regan, R. and Seewaldt, V.L., 2015. Triple-negative breast cancer in African-American women: disparities versus biology. *Nature Reviews Cancer*, 15(4), pp.248-254.
4. 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.
5. Veiga-da-Cunha, M., Vleugels, W., Maliekal, P., Matthijs, G. and Van Schaftingen, E., 2008. Mammalian phosphomannomutase PMM1 is the brain IMP-sensitive glucose-1, 6-bisphosphatase. *Journal of Biological Chemistry*, 283(49), pp.33988-33993.

Rank: 155
Probe ID: 16742086
p-value: 0.00381138
t: 2.8933653
B: -3.38
Gene: PGM2L1
Gene name: phosphoglucomutase 2-like 1

Chart 1: PGM2L1 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: PGM2L1 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 PGM2L1 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 PGM2L1 expression between the primary tumors of TNBC patients dead and alive, a p -value, listed here: $p=0.0085$.

Figure 2: PGM2L1 expression correlates with overall survival in basal subtype human breast cancer.

Depicted in this Kaplan-Meier plot is the probability of overall survival (OS) for $n=296$ breast cancer patients of basal subtype, based on low or high expression of PGM2L1 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 PGM2L1 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.