Differential expression of METTL7A in cancer of the vulva.

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In these brief notes we document work using published microarray data (1, 2) to pioneer integrative transcriptome analysis comparing vulvar carcinoma to its tissue of origin, the vulva. We report the differential expression of methyltransferase-like 7A, encoded by METTL7A, in cancer of the vulva. METTL7A may be of pertinence to understanding transformation and disease progression in vulvar cancer (3).

Keywords: vulvar cancer, vulvar carcinoma, METTL7A, methyltransferase-like 7A.

Gynecologic cancers include cervical cancer, ovarian cancer, endometrial (uterine) cancer, and vulvar cancer (4, 3). Vulvar cancer is thought to be the least prevalent of these, with 6190 cases reported in the United States in 2018 (5). We integrated separate published microarray datasets to understand, at the systems level, the transcriptional landscape of vulvar carcinoma.

Methods

We utilized microarray datasets GSE63678 (1) and GSE5563 (2) for this integrated, transcriptome-level differential gene expression analysis of human vulvar cancers in conjunction with GEO2R. GSE63678 was generated using Affymetrix Human Genome U133A 2.0 Array technology with $n=7$ normal vulvar tissues and $n=6$ vulvar carcinoma tissues; analysis was performed using platform GPL571. GSE5563 was generated using Affymetrix Human Genome U133 Plus 2.0 Array technology with $n=10$ normal vulvar tissues and $n=9$ VIN (vulvar intraepithelial neoplasia) tissues; analysis was performed using platform GPL570. 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 METTL7A expression was significantly different between normal vulvar tissue and vulvar carcinoma using a two-tailed t -test.

Results

We mined published microarray data (1, 2) to understand the most significant transcriptional changes between the normal vulva and cancer of the vulva.

METTL7A is differentially expressed in vulvar cancer.

We found that methyltransferase-like 7A, encoded by METTL7A, was among the most differentially expressed genes, transcriptome-wide, in cancer of the vulva (1). When sorting each transcript whose expression was measured across the transcriptome based on significance of change between the normal vulva and vulvar cancer tissues, METTL7A ranked 25 out of 22277 total transcripts, equating to 99.9% differential expression (Chart 1) (1). Differential expression of METTL7A was statistically significant (Chart 1; $p=1.26E-06$).

We validated our findings by performing a similar analysis using a second published microarray dataset (2), but here measuring gene expression in vulvar intraepithelial neoplasia, a dysplastic cell state from which vulvar carcinomas are said to originate from (6). When sorting each transcript whose expression was measured across the transcriptome based on significance of change between the normal vulva and vulvar cancer tissues, METTL7A ranked 124 out of 54662 total transcripts (Chart 2) (2), equating to 99.8% differential expression. Differential expression of METTL7A was again statistically significant (Chart 2; $p=5.21E-07$).

METTL7A expression is higher in cancer tissue as compared to the vulva.

We obtained exact mRNA expression data from the first microarray dataset we mined to directly compare expression levels between control and cancer tissues. METTL7A was expressed at significantly

1 higher levels in cancer of the vulva as compared to normal vulva. METTL7A was expressed at $11.21 \pm$
2 0.37 arbitrary units (A.U.) in normal vulva, but at 8.45 ± 0.86 A.U. in vulvar cancer tissues (Figure 1).
3 We calculated a mean fold change of 0.75 in METTL7A expression when comparing vulvar carcinoma to
4 vulva.

5 **Discussion**

6 We documented here that METTL7A is differentially expressed at the transcriptome level in cancer
7 and dysplasia of the human vulva (1, 2). METTL7A is a candidate gene of interest in understanding the
8 transcriptional biology of vulvar cancer.
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Rank: 25
Probe ID: 207761_s_at
p-value: 1.26E-06
t: 8.250974
B: 5.73511
Gene: METTL7A
Gene name: methyltransferase-like 7A

Chart 1: Differential expression of METTL7A in vulvar cancer.

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.

Rank: 124
Probe ID: 207761_s_at
p-value: 5.21E-07
t: 7.3238192
B: 6.423399
Gene: METTL7A
Gene name: methyltransferase-like 7A

Chart 2: Differential expression of METTL7A in VIN tissues.

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: METTL7A is expressed at significantly higher levels in vulvar cancer as compared to normal vulva.

The mRNA expression level of METTL7A in the normal vulva (left) and in vulvar carcinoma (right) is graphically depicted with the result of a statistical test evaluating significance of difference in METTL7A expression between the two groups, a *p*-value, listed above.