Differential expression of H2BFS 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 H2B histone family member S, encoded by H2BFS, in cancer of the vulva. H2BFS may be of pertinence to understanding transformation and disease progression in vulvar cancer (3).

Keywords: vulvar cancer, vulvar carcinoma, H2BFS, H2B histone family member S.

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 H2BFS 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.

H2BFS is differentially expressed in vulvar cancer.

We found that H2B histone family member S, encoded by H2BFS, 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, H2BFS ranked 227 out of 22277 total transcripts, equating to 99.0% differential expression (Chart 1) (1). Differential expression of H2BFS was statistically significant (Chart 1; $p=6.99E-05$).

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, H2BFS ranked 2122 out of 54662 total transcripts (Chart 2) (2), equating to 96.1% differential expression. Differential expression of H2BFS was again statistically significant (Chart 2; $p=9.44E-04$).

H2BFS 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. H2BFS was expressed at significantly

higher levels in cancer of the vulva as compared to normal vulva. H2BFS was expressed at 8.32 ± 0.65 arbitrary units (A.U.) in normal vulva, but at 10.36 ± 0.74 A.U. in vulvar cancer tissues (Figure 1). We calculated a mean fold change of 1.25 in H2BFS expression when comparing vulvar carcinoma to vulva.

Discussion

We documented here that H2BFS is differentially expressed at the transcriptome level in cancer and dysplasia of the human vulva (1, 2). H2BFS is a candidate gene of interest in understanding the transcriptional biology of vulvar cancer.

References

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Rank: 227
Probe ID: 208579_x_at
p-value: 6.99E-05
t: -5.647549
B: 1.92154
Gene: H2BFS
Gene name: H2B histone family member S

Chart 1: Differential expression of H2BFS 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: 2122
Probe ID: 208579_x_at
p-value: 9.44E-04
t: -3.8913326
B: -0.747166
Gene: H2BFS
Gene name: H2B histone family member S

Chart 2: Differential expression of H2BFS 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: H2BFS is expressed at significantly higher levels in vulvar cancer as compared to normal vulva.

The mRNA expression level of H2BFS 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 H2BFS expression between the two groups, a *p*-value, listed above.