Over-expression of desumoylating isopeptidase 1 in human endometrial cancer.

Shahan Mamoor, MS¹
¹shahanmamoor@gmail.com
East Islip, NY USA

Gynecologic cancers including cancers of the endometrium are a clinical problem¹⁻⁴. We mined published microarray data^{5,6} to discover genes associated with endometrial cancers by comparing transcriptomes of the normal endometrium and endometrial tumors from humans. We identified desumoylating isopeptidase 1, encoded by DESI1, as among the most differentially expressed genes, transcriptome-wide, in cancers of the endometrium. DESI1 was expressed at significantly higher levels in endometrial tumor tissues as compared to the endometrium. Importantly, in human endometrial cancer, primary tumor expression of DESI1 was correlated with recurrence-free survival in black patients with high mutational burden. DESI1 may be a molecule of interest in understanding the etiology or progression of human endometrial cancer.

Keywords: endometrial cancer, gynecologic cancers, endometrium, DESI1, desumoylating isopeptidase 1, systems biology of endometrial cancer, targeted therapeutics in endometrial cancer.

Endometrial cancer is the most common gynecologic cancer in the developed world¹. Over the last three decades, the incidence of endometrial cancer has increased 21%⁴ and the death rate has increased 100%³. We harnessed the power of independently published microarray datasets^{5,6} to determine in an unbiased fashion and at the systems-level genes most differentially expressed in endometrial tumors. We report here the differential and increased expression of the desumoylating isopeptidase 1 (DESI1) in human endometrial cancer.

Methods

We utilized datasets GSE63678⁵ and GSE17025⁶ for this global differential gene expression analysis of human endometrial cancer in conjunction with GEO2R. GSE63678 was generated using Affymetrix Human Genome U133A 2.0 Array technology with $n=5$ control endometrial tissues (including $n=4$ uterine myomas and $n=1$ benign cyst) and $n=7$ endometrial cancers (including $n=2$ endometrial adenocarcinomas, $n=3$ mixed endometrioid adenocarcinomas, and $n=2$ adenocarcinomas with squamous differentiation); analysis was performed using platform GPL571. GSE17025 was generated using Affymetrix Human Genome U133 Plus 2.0 Array technology with $n=5$ normal endometrial tissues (inactive endometrium) and $n=91$ endometrial cancers; 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 DESI1 gene expression was significantly different between control endometrial tissue and endometrial tumor tissue in humans using a two-tailed t-test. For Kaplan-Meier survival analysis, we used the Kaplan-Meier plotter tool⁷ for correlation of DESI1 mRNA expression levels with recurrence-free survival in $n=543$ endometrial cancer patients.

Results

We harnessed the power of blind comparative transcriptome analysis using published microarray data^{5,6} to discover in an unbiased fashion genes associated with endometrial cancer in humans.

DESI1 is differentially expressed in endometrial cancer.

We identified desumoylating isopeptidase 1, encoded by DESI1, as among the genes most differentially expressed in cancers of the endometrium when compared to benign endometrial tissues (Chart 1). When sorting each of the genes expressed in endometrial tumor tissue based on significance of change in expression as compared to benign endometrial tissue, DESI1 ranked 71 out of 22273 transcripts, equating to 99.7% differential expression (Chart 1). Differential expression of DESI1 in human endometrial cancers was statistically significant (Chart 1; $p=6.75E-05$).

We queried a second microarray data to validate differential expression of DESI1 in endometrial cancer. Again, we observed differential expression of DESI1 when comparing endometrial tumor tissue to benign endometrial tissue (Chart 2). When sorting each of the genes expressed in endometrial tumor tissue based on significance of change in expression as compared to benign endometrial tissue, DESI1 ranked 4147 out of 54675 transcripts, equating to 92.4% differential expression (Chart 2). Differential expression of DESI1 in human endometrial cancers was not deemed statistically significant (Chart 2; $p=5.96E-03$).

DESI1 is expressed at significantly higher levels in endometrial cancers as compared to benign endometrial tissue.

We obtained exact mRNA expression levels for DESI1 in endometrial tumor tissues and from benign endometrial tissue to evaluate direction and statistical significance of change in expression of DESI1 in human endometrial cancer. DESI1 was expressed at higher levels in endometrial tissue as compared to normal endometrial tissue, and this difference was statistically significant (Figure 1; $p=0.0002$). We calculated a mean fold change of 1.25 in DESI1 mRNA levels in human endometrial cancer, as DESI1 was expressed at 6.07 ± 0.44 arbitrary units (A.U.) in control endometrial tissue but at 7.61 ± 0.49 A.U. in endometrial tumor tissue.

DESI1 expression is correlated with patient survival outcomes in endometrial cancer.

We performed Kaplan-Meier survival analysis to evaluate correlation between DESI1 primary tumor expression and survival outcomes in 543 patients with endometrial cancer. We observed a correlation between primary tumor expression of DESI1 and recurrence-free survival in patients with endometrial cancer, in black patients with high mutational burden (Figure 2). DESI1 primary tumor mRNA levels were a positive prognostic indicator in black endometrial cancer patients with high mutational burden. Black patients with high mutational burden whose primary tumors expressed low levels of DESI1 possessed, on average, markedly shorter median RFS as compared to black patients with high mutational burden whose tumors expressed high levels of DESI1 (Figure 2). This difference in RFS based on DESI1 tumor expression in black patients with endometrial cancer with high mutational burden was statistically significant (Figure 2, Chart 3; logrank p -value: 0.022; hazard ratio: 0.15 (0.02-0.95)). DESI1 primary endometrial tumor expression was not correlated with recurrence-free survival in black patients with low mutational burden (Figure 2, Chart 3; logrank p -value: 0.46; hazard ratio: 0.55 (0.11-2.76)), nor in white patients with high (Figure 2, Chart 3; logrank p -value: 0.23; hazard ratio: 0.56 (0.22-1.45)) or low mutational burden (Figure 2, Chart 3; logrank p -value: 0.83; hazard ratio: 0.91 (0.39-2.15)).

Thus, by mining published microarray data^{5,6} in an unbiased and systematic fashion, we identified desumoylating isopeptidase 1, encoded by DESI1, as among the genes whose expression was most different, transcriptome-wide, in the endometrial tumor tissue of patients

1 with endometrial cancer when compared to benign endometrial tissue; we observed
2 significantly increased expression of DESI1 in endometrial tumor tissue as compared to benign
3 endometrial tissue. Further, we found a correlation between DESI1 expression and patient
4 survival outcomes in human endometrial cancer, as recurrence-free survival was superior in
5 patients whose tumors expressed higher levels of DESI1 as compared to patients whose tumors
6 expressed lower levels of DESI1, in black patients with high mutational burden, but not in black
7 patients with low mutational burden, nor in white patients with high or low mutational burden.

8 **Discussion**

9 We provided evidence here that desumoylating isopeptidase 1 is among the genes most
10 differentially expressed in human endometrial cancer, that mRNA for DESI1 is present at
11 significantly increased quantity in endometrial tumor tissue as compared to benign endometrium,
12 and that DESI1 primary tumor expression is correlated with recurrence-free survival in black
13 endometrial cancer patients with high mutational burden. These data suggest DESI1 may be of
14 importance to fundamental biological processes that underlie the initiation, progression or
15 maintenance of human endometrial cancer.
16
17
18
19
20
21
22
23
24
25
26
27
28

References

1. Amant, F., Moerman, P., Neven, P., Timmerman, D., Van Limbergen, E. and Vergote, I., 2005. Endometrial cancer. *The Lancet*, 366(9484), pp.491-505.
2. Sorosky, J.I., 2008. Endometrial cancer. *Obstetrics & Gynecology*, 111(2), pp.436-447.
3. Morice, P., Leary, A., Creutzberg, C., Abu-Rustum, N. and Darai, E., 2016. Endometrial cancer. *The Lancet*, 387(10023), pp.1094-1108.
4. Sorosky, J.I., 2012. Endometrial cancer. *Obstetrics & Gynecology*, 120(2 Part 1), pp.383-397.
5. Pappa, K.I., Polyzos, A., Jacob-Hirsch, J., Amariglio, N., Vlachos, G.D., Loutradis, D. and Anagnou, N.P., 2015. Profiling of discrete gynecological cancers reveals novel transcriptional modules and common features shared by other cancer types and embryonic stem cells. *PLoS One*, 10(11), p.e0142229.
6. Day, R.S., McDade, K.K., Chandran, U.R., Lisovich, A., Conrads, T.P., Hood, B.L., Kolli, V.K., Kirchner, D., Litzi, T. and Maxwell, G.L., 2011. Identifier mapping performance for integrating transcriptomics and proteomics experimental results. *BMC bioinformatics*, 12(1), p.213.
7. Nagy, A., Munkacsy, G. and Gyorffy, B., 2020. Pancancer survival analysis of cancer hallmark genes. *bioRxiv*.

Rank: 71
Probe ID: 212527_at
p-value: 6.75E-05
t: -5.910474
B: 2.00857
Gene: DESI1
Gene name: desumoylating isopeptidase 1

Chart 1: DESI1 is differentially expressed in endometrial cancer when comparing primary endometrial tumors to benign endometrial tissue.

The rank of global differential expression, probe/transcript ID, the *p*-value with respect to differential expression transcriptome-wide, *t*, a moderated *t*-statistic, *B*, the log-odds of differential expression between the groups compared, the gene and gene name are listed in this chart.

Rank: 4147
probe ID: 212527_at
p-value: 5.96E-03
t: -2.8110488
B: -2.53805
Gene: DESI1
Gene name: desumoylating isopeptidase 1

Chart 2: DESI1 is differentially expressed in endometrial cancer when comparing primary endometrial tumors to benign endometrial tissue.

The rank of global differential expression, probe/transcript ID, the *p*-value with respect to differential expression transcriptome-wide, *t*, a moderated *t*-statistic, *B*, the log-odds of differential expression between the groups compared, the gene and gene name are listed in this chart.

Figure 1: DESI1 is expressed at significantly higher levels in the endometrial tumors of patients with endometrial cancer when compared to benign endometrium.

The mRNA expression level of DESI1 in benign endometrial tissue (left) and in primary tumors of the endometrium (right) is graphically depicted; the result of a statistical test evaluating significance of difference in DESI1 expression between benign endometrial tissue and primary tumors of the endometrial tissue is $p=0.0002$.

Figure 2: Correlation between DESI1 primary tumor expression and recurrence-free survival in endometrial cancer, in black patients with high mutational burden.

Depicted in this Kaplan-Meier plot is the probability of recurrence-free survival for $n=543$ total endometrial cancer patients stratified into two groups, based on low or high expression of DESI1 in patient primary tumors, in black patients with high mutational burden (top left), black patients with low mutational burden (top right), white patients with high mutational burden (bottom left), and white patients with low mutational burden (bottom right). 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 DESI1 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.