Over-expression of pituitary tumor-transforming 1 in human endometrial cancer.

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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 pituitary tumor-transforming 1, encoded by PTTG1, as among the most differentially expressed genes, transcriptome-wide, in cancers of the endometrium. PTTG1 was expressed at significantly higher levels in endometrial tumor tissues as compared to the endometrium. Importantly, primary tumor expression of PTTG1 was correlated with recurrence-free survival in patients with endometrial cancer. PTTG1 may be a molecule of interest in understanding the etiology or progression of human endometrial cancer.

Keywords: endometrial cancer, gynecologic cancers, endometrium, PTTG1, pituitary tumor-transforming 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 pituitary tumor-transforming 1 (PTTG1) 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 PTTG1 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 PTTG1 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.

PTTG1 is differentially expressed in endometrial cancer.

We identified pituitary tumor-transforming 1, encoded by PTTG1, 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, PTTG1 ranked 204 out of 22273 transcripts, equating to 99.1% differential expression (Chart 1). Differential expression of PTTG1 in human endometrial cancers was statistically significant

(Chart 1; $p=7.64E-07$).

We queried a second microarray data to validate differential expression of PTTG1 in endometrial cancer. Again, we observed differential expression of PTTG1 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, PTTG1 ranked 22 out of 54675 transcripts, equating to 99.96% differential expression (Chart 2). Differential expression of PTTG1 in human endometrial cancers trended towards statistical significance (Chart 2; $p=1.57E-05$).

PTTG1 is expressed at significantly higher levels in endometrial cancers as compared to benign endometrial tissue.

We obtained exact mRNA expression levels for PTTG1 in endometrial tumor tissues and from benign endometrial tissue to evaluate direction and statistical significance of change in expression of PTTG1 in human endometrial cancer. PTTG1 was expressed at higher levels in endometrial tissue as compared to normal endometrial tissue, and this difference was statistically significant (Figure 1; $p<0.0001$). We calculated a mean fold change of 1.42 in PTTG1 mRNA levels in human endometrial cancer, as PTTG1 was expressed at 6.84 ± 0.52 arbitrary units (A.U.) in control endometrial tissue but at 9.72 ± 0.91 A.U. in endometrial tumor tissue.

PTTG1 expression is correlated with patient survival outcomes in endometrial cancer.

We performed Kaplan-Meier survival analysis to evaluate correlation between PTTG1 primary tumor expression and survival outcomes in 543 patients with endometrial cancer. We observed a correlation between primary tumor expression of PTTG1 and recurrence-free survival (RFS) in patients with endometrial cancer (Figure 2). Patients whose primary tumors expressed low levels of PTTG1 possessed, on average, markedly greater median RFS as compared to patients whose tumors expressed high levels of PTTG1 (Figure 2). This difference in RFS based on PTTG1 tumor expression in patients with endometrial cancer was statistically significant (Figure 2, Chart 3; logrank p -value: 0.017; hazard ratio: 1.93 (1.11-3.35)).

Thus, by mining published microarray data^{5,6} in an unbiased and systematic fashion, we identified pituitary tumor-transforming 1, encoded by PTTG1, as among the genes whose expression was most different, transcriptome-wide, in the endometrial tumor tissue of patients with endometrial cancer when compared to benign endometrial tissue; we observed significantly increased expression of PTTG1 in endometrial tumor tissue as compared to benign endometrial tissue. Further, we found a correlation between PTTG1 expression and patient survival outcomes in human endometrial cancer, as recurrence-free survival was inferior in patients whose tumors expressed higher levels of PTTG1 as compared to patients whose tumors expressed lower levels of PTTG1.

Discussion

We provided evidence here that pituitary tumor-transforming 1 is among the genes most differentially expressed in human endometrial cancer, that mRNA for PTTG1 is present at significantly increased quantity in endometrial tumor tissue as compared to benign endometrium, and that PTTG1 primary tumor expression is correlated with recurrence-free survival in patients with endometrial cancer. These data suggest PTTG1 may be of importance to fundamental biological processes that underlie the initiation, progression or maintenance of human endometrial cancer.

References

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Rank: 22
Probe ID: 203554_x_at
p-value: 1.57E-05
t: -6.886501
B: 3.34502
Gene: PTTG1
Gene name: pituitary tumor-transforming 1

Chart 1: PTTG1 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: 204
probe ID: 203554_x_at
p-value: 7.64E-07
t: -5.2827637
B: 5.64612
Gene: PTTG1
Gene name: pituitary tumor-transforming 1

Chart 2: PTTG1 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: PTTG1 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 PTTG1 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 PTTG1 expression between benign endometrial tissue and primary tumors of the endometrial tissue is $p < 0.0001$.

Figure 2: Correlation between PTTG1 primary tumor expression and recurrence-free survival in patients with endometrial cancer.

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 PTTG1 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 PTTG1 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.