Over-expression of CDK1 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 the cell cycle component cyclin-dependent kinase 1, encoded by CDK1, as among the most differentially expressed genes, transcriptome-wide, in cancers of the endometrium. CDK1 was expressed at significantly higher levels in endometrial tumor tissues as compared to the endometrium. Importantly, high primary tumor expression of CDK1 was correlated with worse overall survival in patients with endometrial cancer. Together, the data reveal over-expression of CDK1 in human endometrial cancer and describe specific activation of the cell cycle in cancers of the endometrium.

Keywords: endometrial cancer, gynecologic cancers, endometrium, CDK1, cyclin-dependent kinase 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 cyclin-dependent kinase 1 (CDK1) 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 CDK1 gene expression was significantly different between primary tumors of the breast and brain metastases in humans with breast cancer using a two-tailed t-test. For Kaplan-Meier survival analysis, we used the Kaplan-Meier plotter tool⁷ for correlation of CDK1 mRNA expression levels with overall 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.

CDK1 is differentially expressed in endometrial cancer.

We identified cyclin-dependent kinase 1, encoded by CDK1, 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, CDK1 ranked 96 out of 22273 transcripts, equating to 99.6% differential expression (Chart 1). Differential expression of CDK1 in human endometrial cancers was statistically significant (Chart 1; $p=8.71\text{e-}05$).

We queried a second microarray data to validate differential expression of CDK1 in endometrial cancer. Again, we observed differential expression of CDK1 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, CDK1 ranked 998 out of 54675 transcripts, equating to 98.2% differential expression (Chart 2). Differential expression of CDK1 in human endometrial cancers trended towards statistical significance (Chart 2; $p=1.14e-04$).

CDK1 is expressed at significantly higher levels in endometrial cancers as compared to benign endometrial tissue.

We obtained exact mRNA expression levels for CDK1 in endometrial tumor tissues and from benign endometrial tissue to evaluate direction and statistical significance of change in expression of CDK1 in human endometrial cancer. We observed significantly higher expression of CDK1 in the endometrial tumor tissues of patients with endometrial cancer as compared to control endometrial tissues: CDK1 was expressed at 5.96 ± 0.60 arbitrary units (AU) in endometrial tumor tissues, while it was expressed at 8.13 ± 0.76 AU in control endometrial tissues (Figure 1). The difference in CDK1 mRNA levels between endometrial tumor tissues and control endometrial tissues was statistically significant (Figure 1; $p=0.000341$).

CDK1 expression is correlated with patient survival outcomes in endometrial cancer.

We performed Kaplan-Meier survival analysis to evaluate correlation between CDK1 primary tumor expression and survival outcomes in 543 patients with endometrial cancer. We observed a correlation between primary tumor expression of CDK1 and overall survival in patients with endometrial cancer, in the lower survival quartile (Figure 2). The difference in overall survival based on CDK1 tumor expression in patients with endometrial cancer was not statistically significant (Figure 2, Chart 3; logrank p -value: 0.1; hazard ratio: 1.57 (0.91-2.69)).

Thus, by mining published microarray data^{5,6} in an unbiased and systematic fashion, we identified cyclin-dependent kinase 1, encoded by CDK1, 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 CDK1 in endometrial tumor tissue as compared to benign endometrial tissue. Further, we found a correlation between CDK1 expression and patient survival outcomes in human endometrial cancer, as overall survival was greater in patients whose tumors expressed lower levels of CDK1 as compared to patients whose tumors expressed higher levels of CDK1.

Discussion

We provided evidence here that the cell cycle component cyclin-dependent kinase 1 is among the genes most differentially expressed in human endometrial cancer, that mRNA for CDK1 is present at significantly increased quantity in endometrial tumor tissue as compared to benign endometrium, and that CDK1 primary tumor expression is correlated with overall survival in patients with endometrial cancer. These data, by demonstrating transcriptome-wide differential over-expression of cell cycle machinery, describe a specific mechanism by which the endometrial cell cycle is dysregulated, potentially to support transformation and/or tumor maintenance.

References

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Rank: 96
Probe ID: 203214_x_at
p-value: 8.71e-05
t: -5.7487845
B: 1.77226
Gene: CDK1
Gene name: cyclin-dependent kinase 1

Chart 1: CDK1 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: 998
probe ID: 203213_at
p-value: 1.14e-04
t: -4.0203796
B: 1.02196
Gene: CDK1
Gene name: cyclin-dependent kinase 1

Chart 2: CDK1 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.

CDK1: Cyclin-dependent kinase 1

Figure 1: CDK1 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 CDK1 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 CDK1 expression between benign endometrial tissue and primary tumors of the endometrial tissue is $p=0.000341$.

Figure 2: Correlation between CDK1 primary tumor expression and overall survival in patients with endometrial cancer.

Depicted in this Kaplan-Meier plot is the probability of overall survival for $n=543$ total endometrial cancer patients stratified into two groups, based on low or high expression of CDK1 in patient primary tumors, for patients in the lower survival quartile. The log rank p -value denoting statistical significance of difference in overall 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 CDK1 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.