Differential expression of vascular endothelial growth factor A in human epithelial ovarian cancer.

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Epithelial ovarian cancer (EOC) is the most lethal gynecologic cancer (1). We performed discovery of genes associated with epithelial ovarian cancer and of the high-grade serous ovarian cancer (HGSC) subtype, using published microarray data (2, 3) to compare global gene expression profiles of normal ovary or fallopian tube with that of primary tumors from women diagnosed with epithelial ovarian cancer or HGSC. We identified the gene encoding vascular endothelial growth factor A, VEGFA, as among the genes whose expression was most different in epithelial ovarian cancer as compared to the normal fallopian tube. VEGFA expression was significantly higher in high-grade serous ovarian tumors relative to normal fallopian tube. VEGFA expression correlated with overall survival in patients with ovarian cancer. These data indicate that expression of VEGFA is perturbed in epithelial ovarian cancers broadly and in ovarian cancers of the HGSC subtype. VEGFA may be relevant to pathways underlying ovarian cancer initiation (transformation) or progression.

Keywords: ovarian cancer, epithelial ovarian cancer, HGSC, high-grade serous ovarian cancer, systems biology of ovarian cancer, targeted therapeutics in ovarian cancer.

The five-year survival rate for women diagnosed with high-grade serous ovarian cancer is between 30-40% and has not changed significantly in decades (4, 5). The development of novel, targeted therapeutics to treat HGSC can be facilitated by an enhanced understanding of the transcriptional behavior of ovarian tumors relative to that of the normal ovary. We mined published microarray data (2, 3) to compare global gene expression profiles between human ovarian tumors, including that of the HGSC subtype, and that of normal ovarian and fallopian tissue. We identified the gene encoding vascular endothelial growth factor A, VEGFA, as among the most differentially expressed in HGSC tumors of the ovary and in epithelial ovarian cancer broadly. VEGFA may be a gene of interest when prioritizing the study of target genes and pathways for the development of novel therapeutic interventions in epithelial ovarian cancer and specifically in high-grade serous ovarian cancers.

Methods

We used microarray data from datasets GSE124766 (2) and GSE146556 (3) for this differential gene expression analysis of epithelial ovarian cancer in conjunction with GEO2R. The Benjamini and Hochberg method of p-value adjustment was used for ranking of differential expression but raw p-values were used for assessment of statistical significance of global differential expression. Log transformation of data was auto-detected, and the NCBI generated category of platform annotation was used. GSE124766 (2) was generated using Agilent-014850 Whole Human Genome Microarray 4x44K G4112F with $n=3$ normal fallopian tube tissue (control) and $n=7$ for tumors from patients with high-grade serous ovarian cancer. GSE146556 (3) was generated using Affymetrix Human Gene 1.0 ST Array with $n=3$ for normal ovarian tissue and $n=40$ for tumors from patients with epithelial ovarian cancer: $n=26$ high-grade serous ovarian cancer; $n=3$ carcinosarcoma, $n=2$ clear cell, $n=1$ endometrioid, $n=1$ granulosa cell, $n=1$ immature teratoma, $n=4$ mixed, and $n=2$ mucinous; analysis was performed using platform GPL6244. GEO2R provides mRNA expression levels only for the top 250 most differentially expressed genes transcriptome-wide.

A statistical test was performed to evaluate whether VEGFA expression was significantly different when comparing normal ovarian tissue from control subjects and primary tumors from women diagnosed with HGSC using a two-tailed, unpaired t-test with Welch's correction. We used PRISM for all statistical analyses (Version 8.4.0)(455). For Kaplan-Meier survival analysis, we used the Kaplan-Meier plotter online tool (6) for correlation of VEGFA mRNA expression levels with overall survival (OS) in $n=1656$ ovarian cancer patients.

Results

We mined published microarray data (2, 3) to identify differentially expressed genes in epithelial ovarian cancer and specifically in high-grade serous ovarian cancer (HGSC), the type of ovarian cancer responsible for 70-80% of deaths resulting from the most lethal gynecologic malignancy.

VEGFA is differentially expressed in ovarian tumors from women diagnosed with HGSC

We identified VEGFA as among the genes whose expression was most different when comparing primary HGSC tumors to normal fallopian tube tissue (2) (Chart 1). When sorting all of the transcripts measured by microarray based on change in expression between HGSC and the normal fallopian tube, in this data set, VEGFA ranked 241 out of 40481 total transcripts (Chart 1), equating to 99.4% differential expression. Differential expression of VEGFA in HGSC tumors was statistically significant (Chart 1; $p=3.25E-05$).

We analyzed a second microarray dataset (3) generated using normal ovarian tissues and tumors

from women diagnosed with epithelial ovarian cancer (EOC) to determine whether differential expression of VEGFA could be observed in tumors from a different group of patients, which included HGSC tumors.

We found that VEGFA was differentially expressed in epithelial ovarian cancers broadly (Chart 2). When sorting all of the transcripts measured by microarray based on change in expression between tumors from patients with epithelial ovarian cancers and the normal ovary, VEGFA ranked 416 out of 29088 total transcripts (Chart 2), equating to 98.6% differential expression. Differential expression of VEGFA in EOC was statistically significant (Chart 2; $p=4.54E-06$).

VEGFA is expressed at significantly higher levels in HGSC when compared to the normal fallopian tubes.

We then extracted exact mRNA expression levels for the differentially expressed VEGFA transcript from both normal fallopian tube tissue and from epithelial ovarian tumors. VEGFA was expressed at significantly higher levels in high-grade serous ovarian cancers when compared to the normal fallopian tube (Figure 1; $p=0.0065$). We calculated a mean fold change of 1.60 in VEGFA expression when comparing HGSC tumors to normal fallopian tissue, as VEGFA was expressed at 7.29 ± 1.03 arbitrary units (AU) in the fallopian tubes but at 11.69 ± 0.79 AU in tumors of the ovary.

VEGFA tumor expression is correlated with survival outcomes in patients with ovarian cancer.

We performed Kaplan Meier survival analysis (6) to evaluate whether VEGFA tumor expression correlated with survival outcomes in patients with ovarian cancer. VEGFA primary tumor expression was correlated with overall survival (OS) in patients with ovarian cancer, in the lower quartile, in the lower tertile, in the upper tertile and in the upper quartile (Figure 2).

VEGFA expression was a negative prognostic indicator in patients with ovarian cancer, in the lower quartile, though median OS data do not reflect this. While median OS was 45 months for ovarian cancer patients with low tumor expression of VEGFA, median OS was 45.38 months for ovarian cancer patients with high tumor expression of VEGFA (Chart 3). Correlation of OS with VEGFA tumor expression in patients with ovarian cancer, in the lower quartile, trended towards statistical significance (Figure 2: log rank p-value: 0.096; hazard ratio: 1.14 (0.98-1.32)).

VEGFA primary tumor expression was not correlated with overall survival in patients with ovarian cancer, in the lower tertile (Figure 2: log rank p-value: 0.12; hazard ratio: 1.12 (0.97-1.28)), in the upper tertile (Figure 2: log rank p-value: 0.99; hazard ratio: 1 (0.87-1.15)), and in the upper quartile (Figure 2: log rank p-value: 0.92; hazard ratio: 0.99 (0.86-1.15)).

Thus, we found using published microarray data (2, 3) that VEGFA was among the genes most differentially expressed in tumors from women with high-grade serous carcinomas, and in epithelial ovarian cancer broadly. VEGFA expression was significantly higher in HGSC tumors when compared to the normal fallopian tubes, and VEGFA tumor expression was correlated with overall survival in patients with ovarian cancer.

Discussion

Transcriptional profiling of HGSC in a Cancer Genome Atlas integrated genomic analysis classified HGSC into four subtypes based on gene clustering: immunoreactive, differentiated, proliferative, and mesenchymal (7). We sought to describe the transcriptional landscape of epithelial ovarian cancers in an unbiased fashion by using published microarray data from primary tumors of women diagnosed with HGSC compared to transcriptome data from normal ovarian and fallopian tube tissue (2,

3). In both datasets analyzed (2, 3), VEGFA was among the genes whose expression changed most significantly when comparing normal gynecological tissue to ovarian tumors, from women with epithelial ovarian cancer as well as specifically from women with HGSC. VEGFA may be a molecule of relevance in understanding transformation or disease progression in human epithelial ovarian cancer.

References

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Rank: 241
Probe ID: A_23_P81805
p-value: 3.25E-05
t: -6.8168036
B: 2.778
Gene: VEGFA
Gene name: vascular endothelial growth factor A

Chart 1: VEGFA is differentially expressed in high-grade serous ovarian carcinomas (HGSC).

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

Rank: 416
Probe ID: 8119898
p-value: 4.54E-06
t: -5.2207437
B: 4.0428477
Gene: VEGFA
Gene name: vascular endothelial growth factor A

Chart 2: VEGFA is differentially expressed in epithelial ovarian cancers, including high-grade serous ovarian carcinomas (HGSC).

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

Figure 1: VEGFA is expressed at significantly higher levels in HGSC tumors when compared to normal fallopian tube.

The mRNA expression of VEGFA in normal fallopian tube tissues (left) and in the primary tumors of patients with HGSC (right) is represented with mean mRNA expression level marked and the result of a statistical test evaluating the significance of difference in VEGFA expression between the normal fallopian tube and primary tumors from patients with HGSC, a *p*-value, listed above.

Figure 2: VEGFA tumor expression correlates with overall survival in patients with ovarian cancer.

Depicted in this Kaplan-Meier plot is the probability of overall survival (OS) for $n=1656$ patients, in the lower quartile (top left), in the lower tertile (top right), in the upper tertile (bottom left), and in the upper quartile (bottom right), based on primary tumor expression of VEGFA (low and high). 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 VEGFA 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.

Lower quartile

Low VEGFA expression: 45 months

High VEGFA expression: 45.38 months

Chart 3: Overall survival is generally superior in ovarian cancer patients with high tumor expression of VEGFA, though median OS data do not reflect this.

The median overall survival of $n=1656$ ovarian cancer patients based on stratification into low or high tumor expression of VEGFA is listed in this chart, in the lower quartile.