Differential expression of F-box and leucine rich repeat protein 22 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 F-box and leucine rich repeat protein 22, FBXL22, as among the genes whose expression was most different in epithelial ovarian cancer as compared to the normal fallopian tube. FBXL22 expression was significantly lower in high-grade serous ovarian tumors relative to normal fallopian tube. These data indicate that expression of FBXL22 is perturbed in epithelial ovarian cancers broadly and in ovarian cancers of the HGSC subtype. FBXL22 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 F-box and leucine rich repeat protein 22, FBXL22, as among the most differentially expressed in HGSC tumors of the ovary and in epithelial ovarian cancer broadly. FBXL22 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 $n=8$ 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 FBXL22 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).

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.

FBXL22 is differentially expressed in ovarian tumors from women diagnosed with HGSC

We identified FBXL22 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, FBXL22 ranked 77 out of 40481 total transcripts (Chart 1), equating to 99.8% differential expression. Differential expression of FBXL22 in HGSC tumors was statistically significant (Chart 1; $p=1.14E-06$).

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 FBXL22 could be observed in tumors from a different group of patients, which included HGSC tumors.

We found that FBXL22 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, FBXL22 ranked 7981 out of 29088 total transcripts (Chart 2), equating to 72.6% differential expression. Differential expression of FBXL22 in EOC was statistically significant (Chart 2; $p=5.58E-02$).

FBXL22 is expressed at significantly lower levels in HGSC when compared to the normal fallopian tubes.

We then extracted exact mRNA expression levels for the differentially expressed FBXL22 transcript from both normal fallopian tube tissue and from epithelial ovarian tumors. FBXL22 was expressed at significantly lower levels in high-grade serous ovarian cancers when compared to the normal fallopian tube (Figure 1; $p=0.0007$). We calculated a mean fold change of 0.74 in FBXL22 expression when comparing HGSC tumors to normal fallopian tissue, as FBXL22 was expressed at 7.62 ± 0.26 arbitrary units (AU) in the fallopian tubes but at 5.62 ± 0.26 AU in tumors of the ovary.

Thus, we found using published microarray data (2, 3) that FBXL22 was among the genes most differentially expressed in tumors from women with high-grade serous carcinomas, and in epithelial ovarian cancer broadly. FBXL22 expression was significantly lower in HGSC tumors when compared to the normal fallopian tubes.

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 (6). 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), FBXL22 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. FBXL22 may be a molecule of relevance in understanding transformation or disease progression in human epithelial ovarian cancer.

References

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Rank: 77
Probe ID: A_32_P334875
p-value: 1.14E-06
t: 9.1017129
B: 5.93432
Gene: FBXL22
Gene name: F-box and leucine rich repeat protein 22

Chart 1: FBXL22 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: 7981
Probe ID: 7984152
p-value: 5.58E-02
t: -1.9644249
B: -4.6840714
Gene: FBXL22
Gene name: F-box and leucine rich repeat protein 22

Chart 2: FBXL22 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: FBXL22 is expressed at significantly lower levels in HGSC tumors when compared to normal fallopian tube.

The mRNA expression of FBXL22 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 FBXL22 expression between the normal fallopian tube and primary tumors from patients with HGSC, a *p*-value, listed above.