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Evidence that \( p53 \)-Mediated Cell-Cycle-Arrest Inhibits Chemotherapeutic Treatment of Ovarian Carcinomas

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Gene expression profiles of malignant tumors surgically removed from ovarian cancer patients pre-treated with chemotherapy (neo-adjuvant) prior to surgery group into two distinct clusters. One group clusters with carcinomas from patients not pre-treated with chemotherapy prior to surgery (C-L), while the other clusters with non-malignant adenomas (A-L). We show here that although the C-L cluster is preferentially associated with \( p53 \) loss-of-function (LOF) mutations, the C-L cluster cancer patients display a more favorable clinical response to chemotherapy as evidenced by enhanced long-term survivorships. Our results support a model whereby \( p53 \) mediated cell-cycle-arrest/DNA repair serves as a barrier to optimal chemotherapeutic treatment of ovarian and perhaps other carcinomas and suggest that inhibition of \( p53 \) during chemotherapy may enhance clinical outcome.


INTRODUCTION

Ovarian cancer is the most deadly of gynecologic malignancies and the fourth leading cause of all cancer deaths of women in the United States [1]. Because the disease is essentially asymptomatic early in its progression, approximately 70% of all ovarian cancers are not diagnosed until advanced stages (FIGO stage III or IV) when long-term prognosis is poor (<20% long-term survival) [2]. The current standard treatment for patients with advanced ovarian cancer is cytoreductive surgery followed by platinum/taxane combination therapy [3]. While this treatment can be effective in the short-term, 80% of patients relapse within 5 years. The failure of current therapies to significantly improve the long-term survival is believed to be due primarily to the development of chemotherapy resistance, e.g. [4,5].

In recent years, significant effort has focused on the identification of molecular markers that can predict the likely response of ovarian cancer patients to chemotherapeutic treatments with the ultimate goal of developing optimal treatments for individual patients. An experimental approach successful in predicting the outcome of chemotherapy treated patients is gene expression profiling [e.g. 6–8]. Several such profiling experiments have been carried out on ovarian tumor samples removed from patients prior to chemotherapy treatment [e.g. 9, 10]. Collectively, these studies indicate that gene expression profiling of ovarian and other cancers holds significant promise, not only as prognostic indicators of clinical outcome, but as a means of identifying specific molecular abnormalities that may underlie various manifestations of the disease.

Here, we report on a gene expression profile analysis of ovarian carcinoma samples obtained after neo-adjuvant chemotherapy (carboplatin/taxol), samples from primary surgical resections, and non-malignant ovarian adenoma tissues (Table 1). Our results demonstrate that the gene expression profiles of the primary carcinomas and non-malignant adenomas cluster into two distinct groups. The neo-adjuvant treated patient samples cluster with either the primary carcinoma samples or with the non-malignant adenomas. The neo-adjuvant samples that clustered with the primary carcinomas were preferentially associated with LOF mutations in the \( p53 \) gene and displayed an expression profile characteristic of a highly proliferative state. Comparison of our expression profiles with the previously established “Ovarian Cancer Prognostic Profile” (OCPP) [6] demonstrated a significant overlap in profiles, and predicted a more favorable outcome for patients whose samples clustered with the primary carcinomas. Survivorship profiles of patients involved in our study were found to be consistent with this prediction. Our findings indicate that \( p53 \) mediated cell-cycle-arrest/DNA repair serves as a barrier to optimal chemotherapeutic treatment of ovarian and perhaps other carcinomas and suggest that inhibition of \( p53 \) during chemotherapy may enhance the long-term survivorship of ovarian cancer patients.

RESULTS

Gene expression profiles of ovarian carcinomas from neo-adjuvant patients cluster into two groups

Unsupervised clustering of the expression profiles of all of the genes detected on the Affymetrix HG_U95Av2 GeneChip microarrays was performed on ovarian adenomas (AD) and carcinomas from neo-adjuvant (CC) and untreated (CA) patients. This initial unsupervised analysis was performed using average linkage of Euclidian distance on all 9,106 probe sets in which the signal from at least one sample exceeded an arbitrary threshold.

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The resulting clustering pattern (Figure 1A) divided the samples into two main groups. The carcinomas (CA) and adenomas (AD) from patients not receiving chemotherapy formed two distinct and separate clusters, while the neo-adjuvant treatment carcinomas (CC) were divided equally between these two groups. These two groups were designated “carcinoma-like” (C-L) and “adenoma-like” (A-L) respectively. These two main clusters were very robust and were not changed if the samples were

<table>
<thead>
<tr>
<th>Cluster</th>
<th>Sample</th>
<th>Malignant Potential</th>
<th>Histological Information</th>
<th>Stage/Grade</th>
<th>Age at surgery</th>
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</table>
re-ordered, or if the samples were clustered using alternative metrics such as Manhattan city-block, uncentered correlation, or Spearman Rank correlation.

To identify a signature of genes that were significantly different between the A-L and C-L group, we performed supervised analysis using the Significance Analysis of Microarrays (SAM) software [11]. Using thresholds of 2-fold change and <1% False Discovery Rate (FDR), 1,527 probe sets corresponding to 1,334 unique genes were found to be significantly (p < 0.05) different between the C-L and A-L sample groups (Figure 1B). A heat map giving the names of each of the 1,527 probe sets is available in the supplementary material (Figure S1).

To independently test the validity of the differential expression patterns determined by microarray, we measured the expression patterns of 3 representative genes in 4 tissue samples using quantitative real-time polymerase chain reaction (qRT-PCR). In all cases, the qRT-PCR results of the analyses confirmed the differences detected in the microarray studies (Figure 2).

**Gene Ontology (GO) analysis identifies functional differences between the C-L and A-L groups**

To determine if the 1,334 genes significantly altered between C-L and A-L groups were enriched for specific biological functional categories, we analyzed this gene set for enrichment in GO functional annotations using GOstat [12]. Several functional categories were significantly (p < 0.05) over-represented in this gene set relative to the total GO categories available on the U95Av2 GeneChip (Table 2). Most notable were biological functions involved in the cell cycle, cellular proliferation, cell cycle checkpoints, stress response, DNA damage, and apoptosis. In general, the C-L group demonstrated increased expression of...
genes involved in nucleosome assembly, including histone genes, suggestive of a higher proportion of cells in S phase.

**Predictive models accurately distinguish between the C-L and A-L sample groups**

To determine if we could use the expression profiles from these samples to identify sets of genes that would be predictive of the C-L and A-L sample clusters, we used both K-nearest neighbor leave-one-out cross validation (KNNxVal) and KNN randomized four-fold cross validation methods. For both methods, we built models using sets of the 30 genes to predict whether “unknown” samples partitioned to one group or the other. Using the KNNxVal approach, we built 43 models and correctly predicted the sample class in 42/43 (99%) of the cases. For the KNN approach, the samples were randomly divided into training sets of 29 cases, and test sets of 14 cases. Models were built using the 29 cases in the training sets and subsequently used to predict the grouping (class) of the 14 test cases. For these models, the class of the predicted samples was correctly determined in 95% of the cases. Because many predictor models were generated (43 KNNxVal and 4 KNN models), we identified the 37 most predictive genes as those that were used in at least two of the KNNxVal models and were used in at least one of the KNN models. The expression profiles, identities, fold changes, and the number of models in which these probe sets were used, are presented in Figure 3.

Prediction of CC samples into C-L and A-L clusters was also achieved with 100% accuracy by support vector machine (SVM) analysis using GenePattern software.

**Altered biological pathways characterize the C-L and A-L groups**

To investigate biological pathways possibly affected by the highly predictive genes, we performed Ingenuity Pathway Analysis (IPA) (http://www.ingenuity.com/) on the set of the 37 most predictive genes used in our predictive models (see above). A number of pathways were found to be affected by the genes that were predictive between the C-L and A-L groups (Figure 4). Among the most significant pathways was the death receptor apoptosis pathway (p<0.01). Figure 5 shows a simplified canonical Death Receptor Pathway, with genes increased in the C-L group colored in red, and genes decreased in C-L group colored in green.

![Figure 2. qRT-PCR validation of microarray results.](image_url)

The expression patterns of BCL2, BAX and CCND1 in 4 tissue samples were determined using quantitative RT-PCR. In all cases, the qRT-PCR results of the analyses confirmed the differences detected in the microarray studies.

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**Table 2. GO annotations significantly enriched in genes altered between A-L and C-L groups.**

<table>
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<tr>
<th>GO</th>
<th>Significant Genes</th>
<th>Total Genes</th>
<th>P-value</th>
<th>GO as name</th>
</tr>
</thead>
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<td>470</td>
<td>2.02E-18</td>
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</tr>
<tr>
<td>GO:0000786</td>
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<td>18</td>
<td>2.89E-09</td>
<td>nucleosome assembly</td>
</tr>
<tr>
<td>GO:007155</td>
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<td>381</td>
<td>2.89E-09</td>
<td>cell adhesion</td>
</tr>
<tr>
<td>GO:0006950</td>
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<td>621</td>
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<td>response to stress</td>
</tr>
<tr>
<td>GO:007051</td>
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<td>16</td>
<td>0.00192</td>
<td>spindle organization and biogenesis</td>
</tr>
<tr>
<td>GO:0000074;</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>GO:0007049</td>
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<td>320</td>
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<td>GO:0008632</td>
<td>13</td>
<td>29</td>
<td>0.00872</td>
<td>apoptotic program</td>
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</table>

The p-value for GO significance was computed with GOSTat (12) using the Benjamini FDR correction for multiple testing and the HG_U95Av2 gene collection for comparison. Significant genes indicates the number of genes significantly altered between A-L and C-L tumors with the given GO annotation. Total genes indicates the total number of genes with that GO annotation on the HG_U95Av2 GeneChip.

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C-L group samples are associated with p53 LOF mutations

Cisplatin is a DNA damaging agent that is expected to trigger p53-dependent cell cycle arrest and apoptosis in tumors with wild-type p53 tumor suppressor function. Several of the GO categories enriched for genes that differed between the C-L and A-L expression profile groups relate directly to p53 function. For example, cell cycle regulation, stress response, DNA repair, and apoptosis are all profoundly influenced by the status of p53 [13,14]. Downstream targets of p53 that were altered between these groups were identified using Ingenuity Pathway Analysis software. A summary of the observed mRNA fold change between the C-L and A-L samples of genes recognized as downstream transcriptional targets of p53 is given in Table 3. Of the downstream targets altered between the C-L and A-L groups, 16/23 (70%) displayed changes in gene expression consistent with a loss of p53 function in the C-L group. Since we detected no significant difference in p53 expression among the samples examined in this study, we explored the possibility that p53 LOF (loss-of-function) mutations were preferentially associated with the C-L group. Tissue samples from both the A-L and C-L cluster groups were assayed for immunohistochemical staining using a p53 antibody (Figure 6). Positive staining has been previously employed as an indicator of p53 mutations [26]. In our study, 4 out of the 6 positively staining samples were correlated with p53 LOF mutations (see below) while 11 out of the 16 negatively staining samples were correlated with no or functionally equivalent mutations (Table 4). Direct testing for p53 LOF mutations was carried out by DNA sequencing. cDNA was synthesized from mRNA isolated from 14 CC, 5 CA and 6 AD samples. Regions of the p53 gene (exons 5-10) previously associated with LOF mutations [27,28] were amplified using PCR and sequenced (Table 4). Consistent with previously published results [29], we found that about half of ovarian cancer samples from patients not pre-treated with chemotherapy prior to surgery are associated with p53 LOF mutations. In contrast, only 1 of the 6 AD samples we examined was associated with known p53 LOF mutations. The 7 CC samples clustering within the A-L group had either no mutations or were associated with functionally silent mutations in p53 gene. Remarkably, 6 of the 7 tested CC samples whose expression profiles clustered within the C-L group were associated
with missense or non-sense mutations and 5 of these have previously been associated with loss of p53 function. Analysis of the correspondence of p53 LOF mutations with the C-L and A-L clusters was significant (p = 0.006 by Fisher’s Exact Test). These results support the hypothesis that the functional status of p53 is a major distinguishing characteristic between the neo-adjuvant (CC) samples clustering in the C-L and A-L groups.

The C-L group profile predicts a more favorable prognosis

Previous expression profiling studies of ovarian tumors have examined the overall survival (“Ovarian Cancer Prognostic Profile” or OCPP) [6] and the chemotherapeutic response (“Chemotherapeutic Response Profile” or CRP) [10] of ovarian
cancer patients. To determine if these previously reported signatures could be used to make predictions regarding the C-L and A-L groups, we looked for overlap between OCPP and CRP with genes whose expression was significantly different between the C-L and A-L groups. While we found a few genes that overlapped with the CRP set including PDGFRα and RB1, the overlap between gene lists was not statistically significant (p = 0.05). This lack of overlap may be due to the fact that all of the neo-adjuvant patients appeared to respond to chemotherapy clinically. For example, the tumors of all chemotherapy treated patients were similarly reduced in size and all treated patients displayed an equivalent reduction in levels of CA 125 prior to surgery (Table 5).

Also relevant is the fact that there was no significant difference in the age of patients in the C-L and A-L group (Table 1). In addition, our microarray analysis was conducted after chemotherapy treatment, and thus subsequent to any differential selection imposed by the neo-adjuvant treatment. In this regard, it is relevant to note that none of the untreated cancer patient samples (CA) clustered within the A-L group, indicating that the cell composition of the neo-adjuvant cancer patient samples (CC) displaying the A-L group expression pattern was most likely selectively amplified in response to the chemotherapy.

In contrast, when the list of genes altered between our C-L and A-L sample groups was compared to the OCPP, we observed a significant overlap (p = 0.005 by hypergeometric distribution; Table 6). Interestingly, 21/23 (91%) of the overlapping genes displayed changes in expression predictive of a favorable outcome for the C-L group of samples.

![Figure 5. Apoptosis pathway with genes displaying increased expression (colored red) and decreased expression in carcinoma-like samples (colored green). Carcinoma-like samples had higher expression of pro-apoptotic genes such as BAX, BID, CASP8, and cIAP2. Adenoma-like samples had higher Bcl-2 expression than carcinoma-like samples.](image1)

**Table 3. Changes in expression of known p53 target genes between A-L and C-L group tumor samples.**

<table>
<thead>
<tr>
<th>Target Gene</th>
<th>p53 effect</th>
<th>Fold change Including CC</th>
<th>Fold change CA/AD only</th>
<th>Consistent with p53 mutation</th>
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<td>Repressed</td>
<td>3.0</td>
<td>2.9</td>
<td>Y</td>
<td>[14]</td>
</tr>
<tr>
<td>HMMR</td>
<td>Repressed</td>
<td>2.6</td>
<td>3.8</td>
<td>Y</td>
<td>[14]</td>
</tr>
<tr>
<td>RB1</td>
<td>Repressed</td>
<td>2.5</td>
<td>3.7</td>
<td>Y</td>
<td>[16]</td>
</tr>
<tr>
<td>PCNA</td>
<td>Repressed</td>
<td>2.1</td>
<td>3.0</td>
<td>Y</td>
<td>[17]</td>
</tr>
<tr>
<td>ID2</td>
<td>Induced</td>
<td>−2.1</td>
<td>−3.0</td>
<td>Y</td>
<td>[14]</td>
</tr>
<tr>
<td>PPM1D</td>
<td>Induced</td>
<td>−2.2</td>
<td>−2.0</td>
<td>Y</td>
<td>[18]</td>
</tr>
<tr>
<td>CAV1</td>
<td>Induced</td>
<td>−2.6</td>
<td>−3.5</td>
<td>Y</td>
<td>[19]</td>
</tr>
<tr>
<td>GSTM1</td>
<td>Induced</td>
<td>−3.1</td>
<td>−5.1</td>
<td>Y</td>
<td>[20]</td>
</tr>
<tr>
<td>FDXR</td>
<td>Induced</td>
<td>−3.1</td>
<td>−6.8</td>
<td>Y</td>
<td>[21]</td>
</tr>
<tr>
<td>COL14A1</td>
<td>Induced</td>
<td>−3.9</td>
<td>−15.6</td>
<td>Y</td>
<td>[20]</td>
</tr>
<tr>
<td>FHL2</td>
<td>Induced</td>
<td>−4.3</td>
<td>−6.0</td>
<td>Y</td>
<td>[22]</td>
</tr>
<tr>
<td>PEG3</td>
<td>Induced</td>
<td>−6.3</td>
<td>−39.3</td>
<td>Y</td>
<td>[23]</td>
</tr>
<tr>
<td>SLPI</td>
<td>Induced</td>
<td>−6.7</td>
<td>9.0</td>
<td>N</td>
<td>[20]</td>
</tr>
<tr>
<td>S100A2</td>
<td>Induced</td>
<td>5.1</td>
<td>5.2</td>
<td>N</td>
<td>[24]</td>
</tr>
<tr>
<td>IRF5</td>
<td>Induced</td>
<td>2.8</td>
<td>2.5</td>
<td>N</td>
<td>[25]</td>
</tr>
<tr>
<td>AKAP12</td>
<td>Repressed</td>
<td>−2.9</td>
<td>−3.2</td>
<td>N</td>
<td>[14]</td>
</tr>
<tr>
<td>ENG</td>
<td>Repressed</td>
<td>−3.7</td>
<td>−7.4</td>
<td>N</td>
<td>[14]</td>
</tr>
<tr>
<td>H53ST1</td>
<td>Repressed</td>
<td>−6.5</td>
<td>−9.1</td>
<td>N</td>
<td>[14]</td>
</tr>
</tbody>
</table>

Sixteen of 23 p53 target genes (69.6%) were altered in a manner consistent with a loss of p53 function in ovarian carcinomas.

![Figure 6. p53 immunohistochemical staining of a serous papillary adenocarcinoma (sample CA99) displaying strong diffuse p53 immunoreactivity. Intense staining of tumor cells is typically associated with the presence of point mutational damage in p53 exons 5–8 (magnification X 400).](image2)
Table 4. Summary of immunohistochemistry staining (IMMUNO HIS) and mutations found in the p53 gene in tumor samples from patients not pre-treated with chemotherapy prior to surgery (A) and neo-adjuvant treated patients (B).

<table>
<thead>
<tr>
<th>CLUSTER</th>
<th>PATIENT</th>
<th>IMMUNO HIS</th>
<th>MUTATION</th>
<th>ACTIVITY</th>
</tr>
</thead>
<tbody>
<tr>
<td>A-L</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ID159</td>
<td>-</td>
<td></td>
<td></td>
<td>Functional</td>
</tr>
<tr>
<td>ID172</td>
<td>-</td>
<td></td>
<td></td>
<td>Functional</td>
</tr>
<tr>
<td>ID300</td>
<td>-</td>
<td></td>
<td></td>
<td>Functional</td>
</tr>
<tr>
<td>C-L</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>ID132</td>
<td>nd</td>
<td>K139E</td>
<td>LOF</td>
<td></td>
</tr>
<tr>
<td>ID146</td>
<td>-</td>
<td></td>
<td></td>
<td>Functional</td>
</tr>
<tr>
<td>ID159</td>
<td>-</td>
<td></td>
<td></td>
<td>Functional</td>
</tr>
<tr>
<td>ID172</td>
<td>-</td>
<td></td>
<td></td>
<td>Functional</td>
</tr>
</tbody>
</table>

DISCUSSION

Our results indicate that the neo-adjuvant patient samples (CC) that cluster with the untreated cancer samples (i.e., the C-L group), are preferentially associated with LOF mutations in the p53 gene while few such mutations are associated with the CC samples clustering with the non-malignant adenomas (the A-L group). The fact that only one A-L group tumor is associated with a p53 mutation, that the A-L group tumors display reduced BAX expression and increased Bcl-2 levels suggest that they are capable of undergoing cell cycle arrest (G1/S checkpoint) while the majority of those clustering with the malignant carcinomas (C-L group) may not. The C-L group patients display increased expression of genes typically associated with increased proliferation and preferential association with LOF mutations in the p53 gene.

The fact that nearly all of the A-L group tumors are wild-type for p53 implies that they are able to arrest in response to DNA-damage. Cell cycle arrest provides an opportunity for DNA repair, but cells that have accumulated irreparable damage are channeled into the apoptotic pathway [31]. While the DNA repair process is focused on the damage induced by the chemotherapeutic treatment, it does not address the inherited defects that rendered cells malignant in the first place. We hypothesize that at least some of the DNA damaged cells that undergo cell cycle arrest and are successfully repaired, (i.e., not channeled into the apoptotic pathway) may retain the malignant genotype and resume growth after treatment. We hypothesize that it is these cells that may contribute to tumor recurrence.

In contrast, we propose that our C-L group tumors that are associated with p53 LOF alleles proceed through the cell cycle in the presence of significant DNA damage leading to eventual death either by way of a p53 independent apoptotic pathway or by mitotic catastrophe [32]. Consistent with this model, it has been previously shown that loss of p53 function in human ovarian cancer cells results in an increase in cisplatin cytotoxicity with a correlated loss of G1/S checkpoint control [33]. Also consistent is the recent observation that head and neck squamous carcinoma cells mutant for p53 display increased susceptibility to cisplatin-induced apoptosis [34].

One of the evolved objectives of the DNA damage response in biological systems is the repair of the damage and the resumption of cellular growth and replication. In contrast, the clinical
Table 5. CA125 values of chemotherapy treated patients at various time points prior to surgery.

<table>
<thead>
<tr>
<th>CLUSTER (LABEL)</th>
<th>PATIENT (age)</th>
<th>CA 125 Levels (months prior to surgery)</th>
<th>Day of Surgery</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>(5 months)</td>
<td>(4 months)</td>
</tr>
<tr>
<td>C-L</td>
<td>CC187(53)</td>
<td>ND</td>
<td>2347</td>
</tr>
<tr>
<td></td>
<td>CC199(65)</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td></td>
<td>CC255(57)</td>
<td>696</td>
<td>465</td>
</tr>
<tr>
<td></td>
<td>CC259(58)</td>
<td>ND</td>
<td>4626</td>
</tr>
<tr>
<td></td>
<td>CC269(68)</td>
<td>ND</td>
<td>681</td>
</tr>
<tr>
<td></td>
<td>CC272(83)</td>
<td>173</td>
<td>ND</td>
</tr>
<tr>
<td></td>
<td>CC325(64)</td>
<td>ND</td>
<td>2683</td>
</tr>
<tr>
<td>A-L</td>
<td>CC150(65)</td>
<td>10,284</td>
<td>942</td>
</tr>
<tr>
<td></td>
<td>CC286(52)</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td></td>
<td>CC303(44)</td>
<td>ND</td>
<td>ND</td>
</tr>
<tr>
<td></td>
<td>CC311(51)</td>
<td>3576</td>
<td>ND</td>
</tr>
<tr>
<td></td>
<td>CC325(75)</td>
<td>1300</td>
<td>974</td>
</tr>
<tr>
<td></td>
<td>CC326(72)</td>
<td>2450</td>
<td>ND</td>
</tr>
<tr>
<td></td>
<td>CC338(62)</td>
<td>ND</td>
<td>516</td>
</tr>
</tbody>
</table>

The time point most distant from day of surgery reflects the CA 125 value prior to the administration of the first of three to four chemotherapy treatments. The results demonstrate that all patients responded positively to the chemotherapy treatment (ND = not determined).

doi:10.1371/journal.pone.0000441.t005

MATERIALS AND METHODS

Tumor samples and RNA isolation

A set of 43 ovarian tumors was obtained from the Ovarian Cancer Institute (Atlanta): 10 benign serous cystadenomas, 9 adenocarcinomas from patients not pre-treated with chemotherapy prior to surgery (7 serous papillary, Stages II, III and IV; 2 endometrioid, Stages I and III and 24 adenocarcinomas from patients having neo-adjuvant therapy (22 serous papillary, Stages III and IV; 1 endometrioid, Stage III; 1 undifferentiated, Stage III). The average age of the patients participating in the study on the day the samples were collected was 61 (range 41–84). This study was approved by the Institutional Review Boards of Georgia Institute of Technology and Northside Hospital, (Atlanta) from which the samples originally were obtained. Tissue was collected at the time of surgery and preserved in RNAlater (Ambion, Austin, TX) within one minute of collection. Linear polyacrylamide (5 ul) was added to ~50 mg of tumor sample and homogenization was carried out on ice in 1.5 ml Trizol (Invitrogen, Carlsbad, CA) with a polytron homogenizer for 30 seconds. RNA was isolated from crude homogenate according to the manufacturer’s protocols (Trizol) and further enriched using an RNEasy column (Qiagen, Valencia, CA).

Microarray hybridization

Biotinylated target cRNA was generated and cleaned by phenol/chloroform extraction/ethanol precipitation according to established protocols (Affymetrix, Santa Clara, CA). In vitro transcription of the cDNA using the High Yield RNA Transcription Labeling Kit (Enzo, Farmingdale, NY) yielded 50–100 ug of biotin labeled cRNA target. The cRNA was fragmented to a length of 20–200 bp and hybridized to the Affymetrix HG-U95Av2 array for 16 hrs at 45 C. Hybridized arrays were washed, stained and scanned according to established protocols (Affymetrix).

Microarray Data Analysis

Thirteen patient array profiles from our previously published pilot study [40] were combined with 30 previously unpublished arrays for this analysis. Gene expression data from 12,625 probe sets on the HG-U95Av2 GeneChips were normalized, using GCRMA normalization with GeneTraffic Software (Iobion, La Jolla, CA). After data normalization, genes with uniformly low expression were removed from consideration, leaving 9,106 probe sets for analysis using Significance Analysis of Microarrays (SAM 2.23) software [11]. Relevant parameters for the SAM analysis were: Imputation engine, 10-Nearest Neighbor; Number of Permutations, 500; RNG Seed, 1234567; Delta, 1.105; Fold-Change, 2.0; False Discovery Rate<1%. Normalized expression data from the 1,527 significant probe sets were analyzed by a two-dimensional hierarchical clustering using Cluster 3.0 [41] and Java Treeview 3.0 [42]. Both genes and arrays were normalized, median-centered, and hierarchically clustered using unweighted averages and ordered using average Euclidian distance. Analysis of gene sets for enrichment in GO functional annotations, were performed using GOstat [12].
Table 6. Genes displaying significantly altered expression between A-L and C-L samples that overlap with previously published Ovarian Cancer Prognostic Profile (OCPP) [6] or the Chemotherapy Response Profile (CRP) [10].

<table>
<thead>
<tr>
<th>Probe ID</th>
<th>Symbol</th>
<th>Fold Change</th>
<th>Overlap</th>
<th>Favorable</th>
</tr>
</thead>
<tbody>
<tr>
<td>39660_at</td>
<td>DEFB1</td>
<td>15.8</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>1585_at</td>
<td>ERBB3</td>
<td>6.9</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>38143_at</td>
<td>KLK7</td>
<td>5.2</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>36499_at</td>
<td>CELSR2</td>
<td>3.8</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>38160_at</td>
<td>LY75</td>
<td>3.3</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>37956_at</td>
<td>ALDH3B2</td>
<td>3.3</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>40030_at</td>
<td>PRKY</td>
<td>2.5</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>311_s_at</td>
<td>—</td>
<td>2.2</td>
<td>OCPP</td>
<td>No</td>
</tr>
<tr>
<td>36577_at</td>
<td>PLEKH1C1</td>
<td>-2.1</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>33440_at</td>
<td>TCF8</td>
<td>-2.1</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>34320_at</td>
<td>PTRF</td>
<td>-2.5</td>
<td>OCPP</td>
<td>Yes</td>
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<tr>
<td>39066_at</td>
<td>MFA4P</td>
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<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>36119_at</td>
<td>CAV1</td>
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<td>OCPP</td>
<td>Yes</td>
</tr>
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<td>38653_at</td>
<td>PMF22</td>
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<td>OCPP</td>
<td>Yes</td>
</tr>
<tr>
<td>34303_at</td>
<td>FLJ90798</td>
<td>-2.7</td>
<td>OCPP</td>
<td>Yes</td>
</tr>
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<td>34802_at</td>
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<td>OCPP</td>
<td>Yes</td>
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<tr>
<td>1771_s_at</td>
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<td>OCPP</td>
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<td>OCPP</td>
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<td>OCPP</td>
<td>Yes</td>
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<tr>
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<td>CRP</td>
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<td>CRP</td>
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<td>35735_at</td>
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<td>2.1</td>
<td>CRP</td>
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<td>1105_s_at</td>
<td>TRB2V1-1</td>
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<td>CRP</td>
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<td>CRP</td>
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</tr>
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<td>IFIT1</td>
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<td>CRP</td>
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<td>CRP</td>
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<td>4.1</td>
<td>CRP</td>
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</tr>
<tr>
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<td>CRP</td>
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<td>CRP</td>
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<td>SI002A</td>
<td>9.0</td>
<td>CRP</td>
<td>N/A</td>
</tr>
</tbody>
</table>

Fold change is positive if higher in carcinoma-like samples. Favorable indicates whether the directional fold change predicts favorable or unfavorable outcome for the C-L samples.

For K-nearest neighbor (KNN) prediction, the GCRMA normalized microarray data were analyzed with GenePattern 2.0 software [43] and both the KNN cross-validation and KNN class prediction modules were used (KNN = 3). All 9,106 probe sets that had detectable expression were available for inclusion in each model. For these analyses 30 genes (or features) were used for each of the KNN prediction models. In the Leave-one-out cross-validation KNNxVal models, 43 models were generated using 42 samples to predict the class of the sample that was left out. For the four-fold cross validation, the set of 43 samples was randomly divided into a training set of 2/3 of the samples (29 training samples) and a test set of the remaining 1/3 of the samples (14 samples). This random selection was done four times, resulting in four training sets, four test sets, and four KNN models. Thus, four test sets of 14 samples resulted in a total of 56 predictions.

Pathway and Profile Analyses

Lists of probe sets that were predictive by KNN analysis and lists of significantly different genes from SAM analysis were submitted to pathway analysis using Ingenuity Pathway Analysis (IPA) software (http://www.ingenuity.com). This software generates networks of genes using interactions present in the Ingenuity Pathways Knowledge Base that are derived from manually curated and extracted interactions from the published scientific literature. It also identifies overrepresented biological functions and canonical pathways based on the GO annotations of each gene and manually curated canonical pathways. The significance value associated with Functions and Pathways is a measure for how likely it is that a gene list participates in a function. The significance is expressed as a p-value, that is calculated using the right-tailed Fisher’s Exact Test by comparing the number of user-specified genes of interest that participate in a given function or pathway, relative to the total number of occurrences of these genes in all functional/pathway annotations stored in the Ingenuity Pathways Knowledge Base.

Downstream targets of p53 were identified by merging interaction networks identified by IPA and generating all direct transcriptional links from p53 to genes in the network. Relationships were examined manually in the Ingenuity Pathways Knowledge Base to determine if target genes were activated or repressed by p53. All relationships were based on published literature references.

For the gene overlap profile analysis, the intersection of the 115 probes in the OCPP with 1,527 probes significantly different between A-L and C-L samples was determined to include 23 probes. The probability that the intersection of these two groups would include 23 probes given a total of 12,626 probes on the HG-U95Av2 array was computed by the hypergeometric distribution using the R statistical programming language (http://www.R-project.org) and the p-value (p = 0.005) was computed.

Quantitative RT-PCR

Total RNA (2 μg) from ovarian tissue was converted to cDNA using Superscript III (Invitrogen) primed with random hexamers under conditions described by the supplier. cDNA from this reaction was used directly in the qRT-PCR analysis. Gene specific primers for three genes (BAX: Forward 5’ GCTGGTGGGCT- GGATCCAAG 3’, Reverse 5’ TCGAGCCCACCTTCTTCG- CAGA 3’; CCND1: Forward 5’ AGGGTCTGGCGGTCTC- GTG 3’, Reverse 5’ CCGGCTGGGCGATGAACCTACTCT 3’, BCL2: Forward 5’ CTGGTGGAATGT CACG 3’, Reverse 5’ ACAGCCGTGCAGTTTTGTTC 3’) were synthesized (Integrated DNA Technologies, Coralville, IA). The mRNA levels of the three genes were measured in 2 malignant and 2 benign tumor samples on the DNA Engine Opticon 2 System (MJ Research). PCR was performed using the Cybergreen PCR MasterMix (Applied Biosystems) according to the manufacturer’s protocols. Using GAPDH as a control, the expression levels of BAX, CCND1 and BCL2 were calculated according to the 2^-ΔΔCT method [44]. The Ct values of triplicate RT-PCR reactions were averaged for each gene in each cDNA sample. For each tissue sample assayed, the level of gene expression for the gene of interest (BAX, CCND1 and BCL2) was calculated against that of the housekeeping gene (GAPDH). Each Δ Ct value was normalized to
the lowest expressing sample to obtain the ΔΔ Ct value. The standard deviation was calculated for samples within each tissue class.

**Histopathologic and immunohistochemical evaluation**

Histologic slides were studied to confirm histopathologic diagnosis of cancer, and representative formalin fixed, paraffin embedded tissue blocks were selected for p53 immunohistochemical analysis. Three tissue cores measuring 1.0 mm from each block were obtained for tissue microarray (TMA) (Beecher Instruments, Sun Prairie, WI). The TMA slides were deparaffinized through xylene changes and rehydrated in increasing gradations of alcohol. Antigen retrieval was performed using Biocare Medical Decloaking Chamber with DAKO Target Retrieval Solution, pH 6.0. The slides were washed in TBS buffer and loaded onto the DAKO universal autostainer. Slides were blocked in 3% hydrogen peroxide followed by incubation of p53 (clone DO-7, DAKO Corp., Carpinteria, CA) primary antibody at 1:80 dilution for 30 minutes. The DO-7 detects both wild-type and mutant p53 protein. Visualization was achieved utilizing DAKO Envision+ with DAB. The slides were counterstained with hematoxylin and the immunohistochemical staining pattern was assessed using a Nikon microscope. The staining was assayed using a semi-quantitative scoring from 0 to 3+ (0: no staining, 1+: <10% nuclei staining, 2+: 11–50% nuclei staining, 3+: >50% nuclei staining). For the purpose of recording the results, intensity of staining was not taken into consideration, but generally the intensity correlated with the percentage of nuclei staining positive (strongest in 3+ and the weakest in 1+). Samples displaying a ≥ 2+ signal in >50% of cells examined were scored as positive.

**p53 sequence analysis**

RNA samples extracted from adenocarcinomas removed from 14 neo-adjuvant patients, adenocarcinomas from 5 patients not pre-treated with chemotherapy prior to surgery, and benign adenomas from 6 patients were used to synthesize cDNA (SuperScript III,
In vitro), PCR (polymerase chain reaction) amplification was performed to amplify the exons 5-10 of the p53 gene where the majority of the functionally important mutations in human cancer have been mapped [45]. The primer used for the forward direction was 5'-GCA CGT ACT CCC CTG CCC TCA A-3' [55]. The primer used for the reverse direction encompassed the 3' end of exon 10 minus the stop codon, 5'-GTG TGA TGC AGG CCC TTC TGT C-3' [57]. A 760 bp PCR product was generated using the following conditions: 1) 95°C, 5 min; 2) 95°C, 40 sec; 3) 59°C, 40 sec; 4) 72°C, 1 min; 5) repeat steps 2-4 30x; 6) 72°C, 5 min; 7) 4°C hold. Amplified PCR products were cloned into TA vectors using the TOPO TA cloning kit (Invitrogen), and the resulting isolated plasmids analyzed using 1% agarose gels to check for PCR insertions. Sequencing of each PCR reaction was performed in both directions using the M13 Forward and M13 Reverse primers provided with the TOPO TA cloning kit. Each PCR experiment was repeated independently at least twice. DNA sequencing was carried out at the University of Georgia DNA sequencing facility (Athens, GA). Sequences were aligned and analyzed for mutations using MacVector. The functional significance of identified p53 mutations was scored by using the IARC (International Agency for Research on Cancer) TP 53 Mutation Database [http://www-p53.iarc.fr/].

**SUPPORTING INFORMATION**

**Figure S1** Unsupervised hierarchical clustering of the entire gene expression pattern of all 9,106 expressed probe sets detected on the HG-U95Av2 GeneChip in 43 ovarian tumor samples. Samples beginning with AD are adenosomas, with CA are carcinomas, and CC are patients pre-treated with chemotherapy. Samples divided into two major clusters termed adeno-like and carcinoma-like. Found at: doi:10.1371/journal.pone.0000441.s001 (10.15 MB TIF)

**Figure S2** Survivorship data of A-L and C-L group cancer chemo patients (CC) used in the Kaplan-Meier analysis (See Figure 7). Found at: doi:10.1371/journal.pone.0000441.s002 (8.02 MB TIF)

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**Author Contributions**

Conceived and designed the experiments: JM NB. Performed the experiments: SL LM ED. Analyzed the data: JM SL CM NS NB. Contributed reagents/materials/analysis tools: BB. Wrote the paper: JM CM. Other: Co-wrote first draft with Dr. Moreno: JM.

**REFERENCES**


