Relationship between p21 Expression and Mutation of the p53 Tumor Suppressor Gene in Normal and Malignant Ovarian Epithelial Cells

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ABSTRACT

In many cell types, p53-mediated growth inhibition is dependent on induction of p21, which is an inhibitor of cyclin-dependent kinases that are required for cell cycle progression. Failure of mutant p53 proteins to transactivate p21 may lead to uncontrolled proliferation. Because many ovarian cancers have mutations in the p53 gene, we examined p21 levels in normal and malignant ovarian epithelial cells to determine whether p21 expression is dependent on wild-type p53. Normal ovarian epithelial cells and two ovarian cancer cell lines with wild-type p53 expressed readily detectable levels of p21, whereas in p53 null and mutant cell lines, expression of p21 was diminished strikingly. A correlation between the status of the p53 gene and p21 expression also was noted in 23 primary epithelial ovarian cancers. Normal levels of p21 RNA were seen in 4/7 (57%) cancers with wild-type p53, whereas 14/16 (88%) cancers with mutant p53 had reduced p21 expression (P < 0.05). In addition, we found that γ-irradiation of normal and malignant ovarian epithelial cells with wild-type, but not mutant, p53 resulted in induction of p21. These data are suggestive that induction of p21 is a feature of p53-mediated growth inhibition in normal ovarian epithelial cells. Conversely, mutation of the p53 gene in ovarian cancers usually is associated with decreased p21 expression. The lack of an absolute correlation between p21 expression and the status of the p53 gene in ovarian cancers is consistent with other studies that have suggested that p21 may also be regulated by p53-independent pathways.

INTRODUCTION

Most cancers that arise in the ovaries are found to have spread throughout the peritoneal cavity at diagnosis, and ovarian cancer is the fourth leading cause of cancer deaths in women in the United States. Although a small fraction of ovarian cancers arise because of inherited mutations in the BRCA1 gene (1), it is thought that acquired alterations in several different oncogenes and tumor suppressor genes are responsible for more than 90% of cases. In this regard, amplification of the HER-2/neu and c-myc genes are a feature of some sporadic ovarian cancers (2). Inactivation of the p53 tumor suppressor gene is the most common alteration described thus far in ovarian cancers, however (3, 4). Mutation and overexpression of p53, usually in concert with deletion of the other wild-type p53 allele, occurs in 50% of advanced stage III/IV cases (5) and 15% of early stage I/II cases (6).

It is thought that wild-type p53 normally acts to restrain inappropriate cellular proliferation (7). In addition, p53 expression is increased after DNA damage due to ionizing radiation (8, 9). Growth arrest in the G1 phase of the cell cycle allows for DNA repair prior to replication, but if repair is inadequate, p53 can trigger apoptosis. Conversely, if p53 has been inactivated, apoptosis may not occur appropriately, allowing survival of cells that have undergone DNA damage. The biological activity of p53 protein is dependent on its ability to bind to transcriptional regulatory elements in DNA. The search for critical genes regulated by p53 led to the discovery of the p21 (CIP1/WAF1) gene (10, 11). A consensus p53-binding site is located 2.4 kb upstream of the p21 coding sequence and confers p53-dependent transcriptional regulation on a heterologous reporter gene (10). Transcription of p21 is 50-fold lower in fibroblasts from p53-null mice compared to fibroblasts from normal mice (12). In addition, transcription of p21 is induced 10-fold after irradiation in myeloid leukemia cells with functional p53, whereas induction of this gene is not seen in those lacking functional p53 (12). The subsequent discovery that p21 acts as an inhibitor of cdk3 provides a functional link between p53 and cell cycle control (11, 12).

This paradigm of regulation of p21 expression by p53 is well accepted based on studies performed in various immortalized cell lines. In some cases, molecular alterations observed initially in cancer cell lines have not been found when the corresponding type of primary cancer has been examined, however. Confirmatory studies in various types of primary normal and malignant cells represent a critical step toward establishing the relevance of hypotheses generated in cell lines. Because many primary human epithelial ovarian cancers have mutations in the p53 gene, we examined p21 levels in normal and malig-

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The abbreviations used are: cdk, cyclin-dependent kinase; FBS, fetal bovine serum; TGF, transforming growth factor.
nant ovarian epithelial cells to determine whether p21 expression correlates with the status of the p53 gene.

 MATERIALS AND METHODS

 Cell Culture. Ovarian cancer cell lines OVCA 420, 429, 432, and 433 were established and maintained in modified Eagle's medium with 10% heat-inactivated FBS as described previously (13). The SKOV3 ovarian cancer line was obtained from the American Type Culture Collection and maintained in RPMI supplemented with 10% FBS. Primary monolayer cultures of ovarian epithelial cells were established from surgical specimens of normal ovaries as described previously (14, 15). Briefly, the surface of the ovary was scraped gently, and the epithelial cells were then plated in a 1:1 mixture of MCDB 105/M199 medium supplemented with 15% heat-inactivated FBS and epidermal growth factor (10 ng/ml). Cells were cultured at 37°C in 5% CO₂ and 95% humified air.

 Primary Ovarian Cancers. Twenty-three snap-frozen samples of epithelial ovarian cancer were obtained from patients who underwent primary surgery at Duke University Medical Center from 1985 to 1993. The disease was staged in accordance with the International Federation of Gynecologists and Obstetricians staging system for ovarian carcinoma. The tissues were frozen in liquid nitrogen immediately after extirpation, and the presence of viable cancer was confirmed by histological analysis. In the tissues selected for this study greater than 90% of the sample comprised malignant cells. Sixteen of the 23 cases had been shown previously to overexpress mutant p53 protein by immunohistochemical analysis (5, 6). In 8 of 23 cases, the precise mutation in the p53 gene also had been identified by DNA sequencing (4). Complete clinical information including survival was abstracted from the hospital chart.

 Cloning CIP1/WAF1. Whole-cell RNA was extracted from tissue culture cells and intact tissue by the method of Chomczynski and Sacci (16). Forward (ACTCAGAGGAG-GCCCATGT) and reverse (TTCCTGTGGGCGGATTAGGG) primers were designed based on the published cDNA sequence of p21 to include the entire coding sequence (12). Whole-cell RNA from normal mammary epithelial cells was reverse transcribed using random hexamers, and p21 cDNA was amplified by the PCR. A product of the anticipated size was obtained and cloned into the EcoRV site of Bluescript SK (Stratagene, La Jolla, CA). Sequencing of the cloned product confirmed the identity of the p21 cDNA.

 Northern Analysis. Ten μg of total RNA from each source was separated electrophoretically on a 1% formaldehyde/agarose gel and transferred to a nylon membrane. Membranes were hybridized overnight at 65°C with 2 × 10⁶ cpm of a labeled probe to the human p21 gene. Washing was performed at 65°C in 0.2× SSC (1× SSC, 0.15 m NaCl–0.015 m sodium citrate) and 0.1% SDS. The intensity of the p21 bands present in the resulting autoradiographs was quantitated using laser densitometry. Expression of p21 was corrected for relative loading of each lane as determined by densitometric scanning of the 28S RNA.

 Radiation Treatment and Western Analysis. Subconfluent cells were exposed to γ-irradiation (0, 3, and 7 Gy). Six h after irradiation, the cells were lysed and protein was extracted according to the method of Li et al. (17). Aliquots of protein (100 μg) were electrophoresed on a 12.5% SDS-polyacrylamide gel and transferred onto a nitrocellulose membrane. After incubating with blocking buffer (PBS, 5% nonfat dry milk, and 0.1% Tween 20), the membrane was probed with a mouse antihuman p53 monoclonal antibody (Ab-2; Oncogene Science, Manhasset, NY) and detected using goat antimouse IgG-horse radish peroxidase conjugate. The reaction was visualized with a chemiluminescent substrate solution using the enhanced chemiluminescence kit (Amersham, Arlington Heights, IL) and exposed to Kodak X-OMAT film for 3 min at room temperature. The membrane was probed and assayed in the same manner for p21 and B-actin using rabbit anti-human polyclonal antibody for p21 (PharMingen, San Diego, CA) and mouse anti-human monoclonal antibody for B-actin (Oncogene Science, Manhasset, NY).

 RESULTS

 The coding sequence of the p21 gene was isolated by reverse transcription and subsequent PCR amplification of RNA derived from normal ovarian epithelial cells. An amplification product of the expected size was obtained and cloned. Sequencing of the cloned product confirmed that this was the p21 gene. All hybridizations were performed using this cloned cDNA as probe. Total cellular RNA was prepared from immortalized and primary epithelial ovarian cancers. Northern blot hybridization of these RNAs with the p21 probe revealed a single band of 2.1 kb (Figs. 1 and 2). The level of p21 transcript varied widely. Detectable p21 message was present in primary monolayer cultures of normal ovarian epithelial cells. In three immortalized
Fig. 2  Northern analysis of p21 (CIP1) in primary ovarian cancers with mutant or wild-type (WT) p53 genes. Lanes 1 and 2 (positive control), OVCA 429 and OVCA 433, which have normal p53 genes. Lanes 3 and 4 are blank. Lanes 5–15, primary ovarian cancers with mutant p53 genes; in all cases, p21 expression is decreased by greater than 75% compared to OVCA 433. Lanes 16–20, ovarian cancers with wild-type p53 genes. Although p21 expression is reduced in Lanes 16, 17, and 20, p21 expression in Lanes 18 and 19 is normal.

<table>
<thead>
<tr>
<th>FIGO* stage</th>
<th>Reduced p21 expression no./total (%)</th>
<th>P value*</th>
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<tbody>
<tr>
<td>I/II</td>
<td>2/5 (40%)</td>
<td></td>
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<tr>
<td>III/IV</td>
<td>14/18 (78%)</td>
<td>NS</td>
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<tr>
<td>Histological grade</td>
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<tr>
<td>Well differentiated</td>
<td>5/7 (71%)</td>
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<tr>
<td>Moderately differentiated</td>
<td>10/14 (71%)</td>
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<tr>
<td>Poorly differentiated</td>
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<tr>
<td>Histological type</td>
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<tr>
<td>Serous</td>
<td>7/8 (88%)</td>
<td></td>
</tr>
<tr>
<td>Other</td>
<td>11/15 (73%)</td>
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<tr>
<td>Disease status</td>
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<tr>
<td>No evidence disease</td>
<td>3/6 (50%)</td>
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<tr>
<td>Alive with disease</td>
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<tr>
<td>Dead of disease</td>
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<tr>
<td>p53</td>
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<tr>
<td>Wild-type</td>
<td>3/7 (43%)</td>
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<tr>
<td>Mutant</td>
<td>14/16 (88%)</td>
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*p53, Fédération Internationale des Gynécologues et Obstétristes.
*χ² test.
*NS, not significant.

Table 1  Relationship between p21 expression and other features of primary ovarian cancers

Disruption of cell cycle control is central to the process of malignant transformation. The decision to begin DNA synthesis (S phase) or, alternatively, to arrest in G₁ appears to be one of the main checkpoints in the cell cycle (18). G₁ arrest is dependent on a family of cdk inhibitors including p21, p16, p15, and p25 that interact with cdks, various cyclins, and proliferating cell nuclear antigen (19, 20). Cell cycle progression is characterized by decreased expression of p21, which allows cdks to phosphorylate the Rb (retinoblastoma) protein and other substrates, leading to initiation of DNA synthesis. The hypothesis that p21 expression is requisite for G₁ arrest is also supported by the finding that cells transformed by DNA tumor viruses such as SV40 do not contain the p21 in the cyclin-cdk complex (21) and that transfection of p21 into cancer cells suppresses growth (10). Numerous studies have shown that p53 is an important regulator of p21 transcription (10, 22–24), and it is thought that p21 is the primary effector of the growth-inhibitory effect of p53.

Although the p53 tumor suppressor gene is inactivated because of mutation and/or deletion in approximately half of epithelial ovarian cancers, the other half of these cancers appears to retain functional p53. In cancers with wild-type p53, it is possible that alterations in p21 and other downstream effectors might have the same effect as loss of p53 function, namely, loss of the ability to arrest in G₁. Inactivating mutations in the p21 gene do not appear to be a feature of human cancers, however (25–27).
Consistent with the notion that p21 is transactivated by p53, we found that monolayer cultures of normal and ovarian epithelial cells with wild-type p53 genes expressed readily detectable levels of p21 RNA and protein. Conversely, an ovarian cancer cell line with a missense mutation in the p53 gene and an ovarian cancer cell line in which both copies of the p53 gene have been deleted did not express detectable p21. We were able to detect p21 transcript using PCR in the former cell line, suggesting that the p21 gene is not deleted. Thus, in epithelial ovarian cancer cell lines, there was a close correlation between the status of the p53 gene and expression of p21. These data are consistent with reports that have examined expression of p21 in other types of cancers (28–30).

Prior studies have shown that irradiation-induced cell cycle arrest is associated with a p53-dependent increase in p21 expression in most types of cells (23, 24, 31, 32). Exceptions to this model have been noted, however. For example, in KG human myeloblastic leukemia cells, which lack functional p53, irradiation leads to increased p21 expression by way of mechanisms that appear to be independent of p53 (33). Similar to most other types of cells, however, we found that irradiation increased p21 expression in normal and malignant ovarian epithelial cells with wild-type p53 genes but not in those with mutant or absent p53 genes.

Although convenient to maintain in culture, immortalized ovarian cancer cell lines are not necessarily representative of primary ovarian cancers. In this regard, we have shown previously that although most immortalized epithelial ovarian cancer cell lines are insensitive to the growth-inhibitory effect of TGF-β (13), like normal ovarian epithelial cells, more than 90% of primary ovarian cancers have been found to express normal levels of p21 (34–36). Our findings that three of four primary ovarian cancers with wild-type p53 gene had low levels of p21 also suggests that p53 is not the sole regulator of p21 expression. Inactivation of this pathway may occur downstream from p53 and p21 and may involve cyclins and cdkks (39).

It also appears that proliferation of some ovarian cancers may proceed despite expression of p21. In this study, we found that two of the immortalized ovarian cancer cell lines with relatively high levels of p21 continue to proliferate in monolayer culture. This suggests the possibility that inhibitors of p21 may exist or that other molecular signals may be generated in G1 that allow cells to overcome p21-induced arrest. Recently, it has been reported that p21 can exist in both active and inactive cdk complexes depending on the stoichiometry of the complex components (40). We had previously assayed the downstream targets of p21 specifically, cdk activity and Rb phosphorylation, as an indirect measurement of p21 function in these cell lines (35). Our results indicate that p21 and the cdkks in these cell lines are biologically active. Thus, although p21 may be a key regulator of cell cycle progression, it does appear that it can be circumvented.

REFERENCES

Fig. 3 Western analysis of the effect of γ-irradiation on p53 and p21 expression in normal ovarian epithelial cells (NOSE) with wild-type p53 and malignant ovarian epithelial cells (SKOV3) in which p53 is absent.


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