Prognostic Impact of ΔTAp73 Isoform Levels and Their Target Genes in Colon Cancer Patients

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Abstract

**Purpose:** Cumulative data support the role of ΔTAp73 variants in tumorigenic processes such as drug resistance. We evaluate the impact of TP73 isoforms and their putative target genes ABCB1, HMGB1, and CASP1 on the survival of colon cancer patients and the correlation between their expressions.

**Experimental Design:** We determined in 77 colon cancer patients the expression of ΔEx2p73, ΔEx2/3p73, ΔNp73, TAp73, ABCB1, HMGB1, and CASP1 by quantitative real-time reverse transcriptase-PCR. Tumor characteristics, disease-free survival, and overall survival (OS) were examined in each patient. Functional experiments were carried out to check whether ectopic expression of ΔNp73 modifies the proliferation, drug resistance, migration, and invasion properties of colon tumor cells and the expression of ABCB1, HMGB1, and CASP1.

**Results:** Positive correlations were observed between the expression levels of ΔTAp73 variants and HMGB1. Furthermore, a trend was observed for ABCB1. Overexpression of ΔEx2/3p73 and ΔNp73 isoforms was significantly associated with advanced stages (P = 0.04 and P = 0.03, respectively) and predicted shortened OS (P = 0.04 and P = 0.05, respectively). High levels of ABCB1 and HMGB1 were associated with shorter OS (P = 0.04 and P = 0.05, respectively). Multivariate analysis showed that, in addition to the tumor stage, ABCB1 and HMGB1 had independent relationships with OS (P = 0.008). Ectopic expression of ΔNp73 was associated with an increase in proliferation and drug resistance.

**Conclusions:** The positive correlation between ΔTAp73 variants and HMGB1 and ABCB1 expression supports them as TP73 targets. The fact that upregulation of ΔTAp73 isoforms was associated with shortened OS, increase in proliferation, and drug resistance confirms their oncogenic role and plausible value as prognostic markers. ABCB1 and HMGB1, putative ΔTAp73 target genes, strongly predict OS in an independent manner, making clear the importance of studying downstream TP73 targets that could predict the outcome of colon cancer patients better than ΔTAp73 variants themselves do. *Clin Cancer Res; 17(18): 6029–39.* ©2011 AACR.

Introduction

TP73, a member of the p53 family, is expressed in multiple variants. TAp73 isoforms (full-length) have tumor-suppressor potential (1), whereas ΔTAp73 variants (ΔEx2p73, ΔEx2/3p73, ΔNp73, and ΔNCp73), lacking the transactivation domain, show oncogenic properties (2–7). TP53 and TP73 share significant structural and functional homology (8), although some evidence shows that their roles differ in human tumorigenesis. The 2 genes are activated through different pathways after DNA damage, and are capable of inducing cell-cycle arrest and cell death. Unlike TP53, inactivating mutations of TP73 are extremely rare in human tumors (9). Moreover, although TP73 can activate some TP53-responsive genes to varying degrees, such as those induced after DNA damage (10, 11), recent analyses showed that p73 has its own set of target genes (11, 12), indicating unique and overlapping functions for this family. Further complexity is revealed by the fact that the members of the TP53 family can transactivate common target genes but through the recognition of distinct binding elements (11). In addition, several reports have indicated that ΔNp73 acts downstream from TP53 and TAp73 as a transcriptional negative regulator that...
Translational Relevance

The tumor-suppressor and/or oncogenic functions of TP73 isoforms have been intensely debated recently. The publication of an article in 2010 on the specific role of ΔTAp73 in knockout mice strongly supports their role as oncogenes in the tumorigenic process. Thus, there is currently increasing interest in unraveling the mechanisms that underlie the oncogenic potential of ΔTAp73 isoforms. Our report is the first that shows the prognostic value of ΔTAp73 variants and their target genes involved in drug resistance in colon cancer patients. The positive correlation found in our colon cancer series between ΔTAp73 variants and HMGB1 and ABCB1 expression supports them as TP73 targets in vivo. The upregulation of these 2 genes after ectopic expression of ΔNp73 in colon tumor cells also sustains this statement. The fact that ΔTAp73 isoforms are associated with shortened overall survival (OS) and with increase in proliferation and drug resistance confirms their oncogenic role and plausible value as prognostic markers. ABCB1 and HMGB1 strongly predict OS in an independent manner, making clear the importance of studying downstream TP73 targets that could predict the outcome of colon cancer patients better than ΔTAp73 themselves do.

Materials and Methods

Patients, tumor samples, and nucleic acid extraction

The present study, approved by the research ethics board of the Puerta de Hierro Majadahonda University Hospital (Madrid, Spain), was based on a consecutive series of 77 patients undergoing surgery for colorectal cancer between January 2001 and January 2003. All colon cancer patients were considered sporadic cases because no clinical antecedents of familial adenomatous polyposis (FAP) were reported and those with clinical criteria of hereditary non-polyposis colorectal cancer (Amsterdam criteria) were excluded. Both normal and tumor tissue samples were obtained sequentially, immediately after surgery, snap-frozen in liquid nitrogen, and stored at −80°C until further processing.

All tumors were histologically examined by a pathologist to confirm the diagnosis of colon cancer, verify the presence of tumor, select those samples with at least 75% tumor tissue, and establish the pathologic stage.

RNA was extracted from approximately 30 mg of colon tumor and normal tissue samples using the RNeasy Mini Kit (Qiagen Inc.). After extraction, RNA was quantified spectrophotometrically.

Real-time PCR

mRNA levels were detected in the normal and tumor counterpart samples by a relative quantification approach in which the amount of the targets is expressed in relation to the geometric average of the 3 reference housekeeping genes, as described in detail elsewhere (20). The relative concentrations of the target and the reference genes were calculated by interpolation, using a standard curve of each gene plotted from a serial dilution of a cDNA prepared from the RNA of an individual expressing the specific analyzed gene. The expression level of the target gene in a patient was calculated as a ratio: target in tumor tissue to target in normal tissue (T:N). For the synthesis of the first-strand cDNA, 400 ng of RNA was reverse-transcribed, using...
the Gold RNA PCR Core Kit (Applied Biosystems) according to the manufacturer’s instructions. Random hexamers were used as primers for cDNA synthesis.

Real-time PCR (quantitative PCR) was carried out in a Light Cycler apparatus (Roche Diagnostics) using the Light Cycler-FastStart DNA Master SYBR Green 1 Kit (Roche Diagnostics). Each reaction was carried out in a final volume of 20 μL containing 2 μL of the cDNA product sample, 0.5 μmol/L of each primer, and 1 reaction mix including FastStar DNA polymerase, reaction buffer, deoxyribonucleotide triphosphates, and SYBR green.

Thermal cycling for all genes was initiated with a denaturing step at 95°C for 10 minutes and then subjected to 40 cycles of PCR (denaturing at 94°C for 10 seconds, annealing at a different temperature for each gene—67°C for 5 seconds for ABCB1, 58°C for 5 seconds for HMGB1, and 62°C for 4 seconds for CASP1—and elongation at 72°C for 5 seconds, in which fluorescence was acquired). At the end of the PCR cycles, melting curve analyses were conducted, followed by sequencing, to validate the generation of the specific PCR product expected.

Primer sets for ΔEx2p73, ΔEx2/3p73, ΔNp73, and TAp73 and the conditions for each reaction have been described elsewhere (20). Primer pairs for ABCB1, HMGB1, and CASP1 were designed using Primer Express version 2.0 (Applied Biosystems). The following primers were used:

ΔEx2p73: forward, 5′CTAAGCACTATATGCATCTGGCC3′; reverse, 5′CTCTGCCAGCTCACTCACTCC3′; ΔEx2/3p73: forward, 5′ACCCAGATGCTTCAGTCAACTTC3′; reverse, 5′TGCCATATCTTCAAATTTTCCTTTC3′; ΔNp73: forward, 5′AGTTACCTGGCAGGCCGT3′; reverse, 5′TGGAAAGGAAGAAAGTACTCCTTGA3′; TAp73: forward, 5′CTATGCACTATATGCATCTGGCC3′; reverse, 5′CTCTGCCAGCTCACTCACTCC3′.

**Proliferation, migration, invasion, and drug resistance experiments**

The colon cancer cells HCT116 were obtained from the American Type Culture Collection and maintained in Dulbecco’s Modified Eagle Medium (DMEM; Lonza Group Ltd). Cells were seeded in triplicate and transiently transfected with a pcDNA plasmid encoding ΔNp73 or the empty vector (kindly provided by Dr. Marín, Instituto de Biomedicina, Universidad de León, Spain), using Lipofectamine 2000 (Invitrogen) according to the manufacturer’s instructions. At 24, 48, 72, and 96 hours posttransfection, different fractions were kept to preserve cells and isolate RNA and/or protein. RNA samples were submitted to a DNase treatment for evaluation of the levels of ΔNp73, HMGB1, ABCB1, and CASP1. Proliferation was evaluated by 3 different approaches: First, cell density was assessed with a cell-counter apparatus (Digital Bio). Second, 2 × 10⁴ colon cells were seeded in quadruplicates in 96-well E-plates to carry out an MTT cell proliferation assay (Cayman Chemical Company). At 24, 48, and 72 hours posttransfection, MTT reagent was added and absorbance was measured on a microplate reader at 570 nm (Multiskan Ex; Thermo Scientific). The RT-CES microelectronic cell sensor system (ACEA) was used for analysis. Cells were placed on the reader in the incubator for continuous recording of impedance (every 10 minutes for 96 hours) as reflected by cell index (47). Cells were transfected when attached (15 hours after seeding), and impedance changes are shown 12 hours after transfection (after 27 hours of the beginning of the process).

For drug resistance experiments, HCT116 cells were treated with 100 μmol/L oxaliplatin for 36 hours. Subsequently, floating and adherent cells were trypsinized and checked for viability by flow cytometry using the Annexin V–FITC Apoptosis Detection Kit (BD Pharmingen). Specifically, cells were resuspended in 1 × binding buffer at a concentration of 1 × 10⁶ cells/mL. Two hundred microliters of the cell suspension was transferred to a 5-ml polypropylene tube, and 5 μL each of propidium iodide (PI; 50 μg/mL stock) and Annexin V–fluorescein isothiocyanate (FITC) was added simultaneously. Cells were mixed and incubated at room temperature for 15 minutes in the dark. Cells were analyzed within 30 minutes.

HCT116 cells were cultured on 8.0-μm pore Transwells (Corning Inc.) previously covered with either 0.5% gelatin for migration assays or with Matrigel matrix (125 μg/mL; BD Biosciences) for invasion assays. Before culture, cells were labeled with Cell Tracker Green (CMFDA C2925; Invitrogen). After several time points, from 8 to 72 hours, cells adhering to the lower surface of the filter were recovered by trypsinization and counted by fluorescence with the Wallac Plate Reader (Ex: 485 nm; Em: 535 nm; Perkin Elmer Life Science) by interpolating using a standard curve.

**TP53 analysis**

TP53 immunophenotypic analysis in the colon tissue samples was conducted according to standard procedures, with overnight incubation in the presence of the c1801 mouse monoclonal antibody (Oncogene Sciences). Immunodetection was carried out with peroxidase-labeled streptavidin biotin (LSA; DAKO) using diaminobenzidine chromogen as substrate. All immunostaining was done using the TechMate 500 (DAKO) automatic immunostaining device. The c1801 mouse monoclonal antibody was used because of its ability to detect up to 89% of TP53 point mutations (48). Tissue samples exhibiting definitive nuclear (or nuclear and cytoplasmic) staining in more than 10% of the epithelial cells were considered positive for TP53. Cases displaying no nuclear staining were considered negative.

**Clinicopathologic parameters**

The following parameters were obtained from the medical records of the 77 patients: age, tumor size, tumor location, lymph node metastases, pathologic stage, histologic grade, and vascular invasion (VI). Pathologic stage was assessed by the tumor-node-metastasis (TNM) classification. Presence of lymph node metastases was evaluated by optical microscopy. No other immunohistochemical or molecular techniques were used. No patient received chemotherapeutic treatment before undergoing surgery.
Patient follow-up
Clinical follow-up after diagnosis and surgery was based on periodic visits (every 3 months during the first year, every 6 months during the second year, and then yearly until relapse, in our medical oncology department, complemented by other periodic controls in health centers of our hospital), clinical and biochemical tests, and computed tomography scans. In addition, an ultrasonic study was done when liver function was impaired. OS and disease-free survival (DFS) were the study endpoints. OS was defined as the period from time of diagnosis until death. DFS was defined as the interval between diagnosis and first recurrence.

Statistical analysis
As the values of gene expression (T:N ratio) displayed nonnormal distribution (Kolmogorov–Smirnov test, Lilliefors’ correction), the data were normalized by log_{10} transformation. For the same reason, we used the geometric, rather than the arithmetic, average of the T:N ratio to describe the gene expression data.

Expression of TP73 isoforms, ABCB1, CASP1, and HMGB1 was divided into bicentiles and tertiles. The DFS analysis did not include the patients with pathologic stage IV disease. OS distribution was estimated by the Kaplan–Meier method (49), and differences between groups were tested using the log-rank test (50). Cox proportional hazard univariate and multivariate analyses were also conducted, including relative risk and 95% confidence intervals (CI). Finally, the Cox proportional risk regression model was fitted to data to estimate the independent prognostic importance of OS and DFS and confuser variables were analyzed (51). The basic assumptions of the model were evaluated (proportional hazards).

For statistical study of quantitative variables in the proliferation assays, the mean and SD were calculated. Student t-test was conducted to compare mean values of mock and ΔNp73 cells.

All P values were 2-sided, and values less than 0.05 were considered to indicate statistical significance. Analyses were conducted using the Statistical Package for Social Sciences version 14 (SPSS v.14).

Results
Association between TP73 isoform levels and tumor stage
Pathologic stage is the prognostic factor that has most clearly shown practical use in colorectal cancer. In a previous report of a series of 113 colorectal cancer patients, we found an association between tumor stage and expression levels of ΔEx2/3p73 and ΔNp73 isoforms (20). Our current series of 77 patients is included in the aforementioned report, and we posited whether this association was maintained. ΔEx2/3p73 expression was significantly higher in stage IV (P = 0.04), with geometric averages of 0.24 for stage I, 0.25 for stage II, 0.16 for stage III, and 7 for stage IV. ΔNp73 levels increased in parallel with stage (P = 0.03). The geometric average expressions were 0.009, 0.27, 0.36, and 5.33 in stages I, II, III, and IV, respectively.

Correlation between expression of TP73 variants and prognosis
The follow-up period of our series was the interval between surgery and the time of last medical appointment or death. As of October 2009, the series had been followed for a median of 70 months (range of follow-up, 3–104 months). During this period, 19 recurrences (24.3%) were recorded and 21 patients (27%) died. Description of the number of recurrences and deaths in the different categories for each variable is shown in Table 1.

Disease-free survival
The Kaplan–Meier and univariate analyses were conducted to determine the influence of stage and TP73 isoform levels on DFS. No statistical associations were observed between TP73 variant levels and DFS. As expected, tumor stage correlated in both statistical approaches with DFS (P = 0.002 and P = 0.02 for Kaplan–Meier and univariate analyses, respectively). Patients at stage III had a 5-year DFS rate of 59.6% (95% CI, 36.3–82.9); patients at stage II, 76.4% (95% CI, 57.6–95.2); and those at stage I, 100%. In the multivariate analysis, the pathologic stage was seen as a statistically supported factor in DFS prediction (P = 0.015).

Overall survival
In the final analysis, the 5-year OS for patients was 57% (95% CI, 43.5–70.5). The tumor stage correlated in the Kaplan–Meier and univariate analyses with OS (P < 0.0001 and P < 0.0001, respectively). Patients at stage IV had a 5-year OS rate of 20% (95% CI, 0–55.1); patients at stage III, 32.4% (95% CI, 10.3–54.5); patients at stage II, 76.7% (95% CI, 62.4–91); and those at stage I, 87.7% (95% CI, 64.6–100). The Kaplan–Meier survival analysis revealed an association between OS and ΔEx2/3p73 expression when its levels were divided into bicentiles (P = 0.038; Fig. 1A). Patients with low ΔEx2/3p73 expression had a 5-year OS rate of 66.8% (95% CI, 47.2–86.4), whereas patients with high levels had a rate of 48.2% (95% CI, 31.1–65.3; Fig. 1B). A trend was observed in OS for the expression of ΔNp73 (P = 0.06). Patients with low expression had a 5-year OS rate of 72.4% (95% CI, 56.9–87.9), whereas patients with high levels had a rate of 39.6% (95% CI, 17.3–61.9).

Correlation between TP73 isoform expression and mRNA levels of drug resistance related genes
Direct correlations were found between the levels of ΔEx2p73, ΔEx2/3p73, and ΔNp73 and HMGB1 expression (Table 2). Similarly, a significant statistical trend was observed between ΔEx2p73, ΔEx2/3p73, and ΔNp73 expression and ABCB1 levels (Table 2). No other correlations were identified.

Correlation between levels of drug resistance related genes and prognosis
Disease-free survival. Kaplan-Meier and univariate analyses were conducted to determine the influence of
ABCB1, CASP1, and HMGB1 levels on DFS. No statistical associations were observed.

**Overall survival.** Patients were divided into bicentiles based on ABCB1, CASP1, and HMGB1 levels. Because no differences between low and high levels were observed for OS, we decided to divide patients into tertiles. Thus, patients presented low, median, or high levels of expression. No association was observed for the expression of ABCB1 ($P = 0.1$). Patients with low expression had a 5-year OS rate of 74.9% (95% CI, 55.7–94.1); patients with

### Table 1. Number of recurrences and deaths in the different categories for each variable

<table>
<thead>
<tr>
<th>Variable</th>
<th>Category</th>
<th>Recurrences ($n = 19/77$)</th>
<th>%</th>
<th>Deaths ($n = 21/77$)</th>
<th>%</th>
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<tr>
<td></td>
<td>II</td>
<td>7/42</td>
<td>16.6</td>
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<tr>
<td></td>
<td>III</td>
<td>9/20</td>
<td>45</td>
<td>9/20</td>
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<tr>
<td></td>
<td>IV</td>
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<td>50</td>
<td>6/6</td>
<td>100</td>
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<td>7/48</td>
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<td>41.4</td>
<td>14/29</td>
<td>48.3</td>
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<td>16</td>
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<td>22</td>
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<td>9/22</td>
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<td>20</td>
<td>1/5</td>
<td>20</td>
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<td>7/53</td>
<td>13</td>
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<td></td>
<td>High</td>
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<td>21</td>
<td>13/39</td>
<td>33</td>
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<td>13/39</td>
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</tr>
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<td>21</td>
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<td>11</td>
<td>4/26</td>
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<td></td>
<td>High</td>
<td>16/51</td>
<td>31</td>
<td>17/51</td>
<td>33</td>
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<tr>
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<td>26</td>
<td>12/38</td>
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<tr>
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<td>High</td>
<td>9/39</td>
<td>23</td>
<td>9/39</td>
<td>23</td>
</tr>
</tbody>
</table>

Abbreviation: LNM, lymph node metastasis.
median levels, a rate of 69.6% (95% CI, 50.8–88.4); and those with the highest levels, a rate of 35.5% (95% CI, 12.6–58.4; Fig. 2A). The Kaplan–Meier graph revealed similar behavior of median- and low-level tertiles (Fig. 2A). Thus, these patients were grouped as described above, and ABCB1 expression was analyzed further with only 2 categories: low and high expression levels of ABCB1.

When OS was analyzed in these 2 groups, a significant difference was observed, because patients with low ABCB1 expression had a 5-year OS rate of 71.8% (95% CI, 58.3–85.3) and patients with high expression, a rate of 35.5% (95% CI, 12.6–58.4; P = 0.03; Fig. 2B).

No correlation was observed, either, for HMGB1 expression (P = 0.1). Patients with low expression had a 5-year OS rate of 69.7% (95% CI, 44.2–95.2); patients with median levels, a rate of 45.2% (95% CI, 24–66.4); and those with the highest levels, a rate of 58.3% (95% CI, 38.5–78.1; Fig. 3A). The Kaplan–Meier graph revealed similar behavior of median- and high-level tertiles (Fig. 3A). Thus, these patients were grouped as above, and HMGB1 expression was analyzed further with only 2 categories: low and high expression levels of HMGB1. When OS was analyzed in these 2 groups, a significant difference was observed, because patients with low HMGB1 expression showed a 5-year OS rate of 69.7% (95% CI, 44.2–95.2) and patients with high expression, a rate of 41% (95% CI, 36.1–65.9; P = 0.04; Fig. 3B).

Correlation between expression of TP73 variants and prognosis depending on TP53 status

Positive TP53 immunostaining (nuclear), suggesting TP53 mutations, was observed in 53 out of 77 colon patients (70%).

Disease-free survival. Kaplan–Meier and univariate analyses were conducted to determine the influence of TP73 isoforms on DFS depending on TP53 status. Patients were divided into bicentiles based on ΔEx2p73, ΔEx2/3p73, ΔNp73, and TAp73 levels. In those cases showing a positive immunostaining for TP53 (suggestive of mutation) a significant difference was observed with regard to ΔEx2/3p73

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**Table 2. Correlations between expression levels of p73 isoforms and HMGB1, ABCB1, and CASP1 for human colon cancer patients**

<table>
<thead>
<tr>
<th></th>
<th>ΔEx2p73</th>
<th>ΔEx2/3p73</th>
<th>ΔNp73</th>
<th>TAp73</th>
</tr>
</thead>
<tbody>
<tr>
<td>HMGB1</td>
<td>P &gt; 0.0001; r = 0.4</td>
<td>P = 0.012; r = 0.28</td>
<td>P = 0.04; r = 0.23</td>
<td>NS</td>
</tr>
<tr>
<td>ABCB1</td>
<td>P = 0.06; r = 0.28</td>
<td>P = 0.08; r = 0.25</td>
<td>P = 0.08; r = 0.25</td>
<td>NS</td>
</tr>
<tr>
<td>CASP1</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
<td>NS</td>
</tr>
</tbody>
</table>

NOTE: P is calculated by analysis of variance; r is the Pearson coefficient.

Abbreviation: NS, no statistically significant correlation.

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![Figure 2.](image-url)
because patients with low ΔE2/3p73 expression had a 5-year DFS rate of 71.2% (95% CI, 51.6–90.8) and patients with high expression, a rate of 88% (95% CI, 64–98; \( P = 0.035 \)). The univariate and multivariate analyses revealed no differences.

**Overall survival.** The Kaplan–Meier analysis revealed a trend when TAp73 levels were divided in quartiles because patients in the first lower quartiles had a 5-year OS rate of 70% (95% CI, 59–88) and patients in the 4th quartile, showing the higher TAp73 expression, a rate of 81% (95% CI, 65–89; \( P = 0.1 \)). The univariate and multivariate analyses revealed no differences.

### Ectopic expression of ΔNp73 increases proliferation and drug resistance and modifies the levels of HMGB1, ABCB1, and CASP1

We transiently transfected HCT116 colon cancer cells with an expression vector containing ΔNp73 or the empty vector. After 72 hours of transfection, a statistically significant increase in the cell number was observed in those cells ectopically expressing ΔNp73 (Fig. 4A). The MTT cell proliferation assay also confirmed this fact (Fig. 4B). In addition, a significant difference in the initiation and rate of proliferation measured by the cell index and the slope of the curves in the RT-CES system was observed between

| Table 3. Univariate and multivariate analyses of the association between p73 isoforms and MDR1, HMG1, and caspase-1 expression and clinicopathologic characteristics and OS of colon cancer patients |
|-----------------|-----------------|-----------------|-----------------|
| Variable        | Category         | Univariate analysis | Multivariate analysis |
|                 |                  | HR   | 95% CI | \( P \) | HR   | 95% CI | \( P \) |
| Stage           | I vs. II         | 1.6  | 0.19–12.86 | 0.66 | 0.57 | 0.06–5.5 | 0.63 |
|                 | I vs. III        | 8.8  | 1.13–68.5 | 0.037 | 7.18 | 0.86–60.1 | 0.069 |
|                 | I vs. IV         | 75.6 | 7.47–764.8 | <0.0001 | 26.5 | 2.42–289.9 | 0.007 |
| Vascular invasion | Yes vs. no       | 5.13 | 2.23–11.81 | <0.0001 |       |         |       |
| Tumor differentiation | Well vs. poor | 2.29 | 0.83–6.3 | 0.11 |       |         |       |
|                 | Moderate vs. poor | 1.69 | 0.21–13.64 | 0.62 |       |         |       |
| LNM             | Yes vs. no       | 7.23 | 3.19–16.37 | <0.0001 |       |         |       |
| Bicentiles ΔEx2p73 expression | Low vs. high | 1.53 | 0.7–3.35 | 0.28 |       |         |       |
| Bicentiles ΔEx2/3p73 expression | Low vs. high | 2.28 | 1.02–5.1 | 0.044 |       |         |       |
| Bicentiles ΔNp73 expression | Low vs. high | 2.1 | 0.94–4.68 | 0.07 |       |         |       |
| Bicentiles TAp73 expression | Low vs. high | 0.73 | 0.34–1.56 | 0.4 |       |         |       |
| Bicentiles ABCB1 expression | Low vs. high | 2.28 | 1.04–4.99 | 0.04 | 4.5 | 1.48–13.92 | 0.008 |
| Bicentiles HMGB1 expression | High vs. low | 2.61 | 0.99–6.9 | 0.05 | 6.25 | 1.61–24.19 | 0.008 |
| Bicentiles CASP1 expression | Low vs. high | 0.70 | 0.31–1.57 | 0.39 |       |         |       |

**NOTE:** The blank cells correspond to variables that showed no independent relationship to OS in the multivariate analysis. Abbreviation: LNM, lymph node metastasis.
both cells (Fig. 4C). The ectopic expression of ΔNp73 does not compromise the viability of the cells, being in both cell types, with cells overexpressing the isoform and the control variant in the range of 95% to 98%.

Cells expressing the ΔNp73 vector showed 30% higher viability after oxaliplatin exposure than those transfected with the mock vector (Fig. 5). Oxaliplatin did not modify the endogenous levels of ΔNp73. No modification in migration and invasion was detected.

Ectopic expression of ΔNp73 led to a 6- to 20-fold increase in its mRNA levels compared with the mock vector. This increase was accompanied by an upregulation in the mRNA levels of ABCB1 and HMGB1 of 2- to 8-fold. No modifications in CASP1 levels were detected.

Discussion

Although several studies have linked the upregulation of specific TP73 isoforms with poor tumor prognosis parameters (20), little information is available on the impact of the altered expression of TP73 variants on patient survival. ΔNp73 overexpression is associated with shorter survival in patients with neuroblastoma (27), medulloblastoma (28), and lung (26), hepatocellular (30), and cervical squamous cell carcinomas (29). In addition, ΔEx2/3p73 variant upregulation is associated with survival in patients with low-grade glioma (31). In our colon cancer patient series, we observed that overexpression of ΔNp73 leads to an increase in the cell-proliferation rate compared with the mock HCT116 cells (*, \( P < 0.001; **, \ P < 0.0001 \)). C, significant difference in the initiation and rate of proliferation measured by the cell index and the scope of the curves in the RT-CES system (**, \( P < 0.0001 \). P value was calculated taking the different cell-index measurements in the exponential cellular growth phase).
isms involved in the simultaneous regulation of target genes by TP53, TAp73, and ΔNp73 isoforms and the putative feedback among them to obtain solid conclusions from the cancer patient studies. Lastly, it is interesting to note that both TAp73 and ΔTAp73 forms were found to be upregulated in a significant number of our colon tumors. It is possible that the presence of ΔTAp73 variants, even at low levels, completely suppresses the transactivation activity of TAp73, with the consequent elimination of essential TAp73 antitumorigenic function. Furthermore, at the protein level, ΔTAp73 isoforms have been described to be more stable than those of TAp73, in terms of what can contribute to promote a cellular oncogenic context (2, 13).

The use of compounds that can increase the stability of TAp73 variants, such as netrin-1 (53), could diminish this tumorigenic environment.

The association of the overexpression of ΔTAp73 isoforms with shorter survival could be due to some putative TP73 target genes being involved in drug resistance, invasiveness, and other stages of the tumorigenesis process. ABCB1, HMGB1, and CASP1, among others, have been described as TP73 targets (35–38). These previous data are supported by the fact that the ectopic expression of ΔNp73 in our cellular system induces the upregulation of ABCB1 and HMGB1. In our study, direct statistical correlation was found between expression of ΔEx2p73, ΔEx2/3p73, and ΔNp73 and HMGB1 levels. Furthermore, a direct trend was observed between the same variants and ABCB1 expression levels. This supports the possible positive regulation of HMGB1 in ABCB1 by the ΔTAp73 forms in vivo in colorectal carcinomas. In a larger colon cancer patient series, the correlation between ABCB1 and ΔTAp73 variants might reach statistical significance. Although TP73 has been described as regulating CASP1 expression, no such direct correlation between CASP1 levels and TAp73 expression was found in our set of patients (38).

In addition, ABCB1 and HMGB1 overexpression was associated with shorter OS of patients. In the multivariate analysis including clinicopathologic parameters of the tumors and the levels of TP73 variants, ABCB1, HMGB1, and CASP1, we observed that, in addition to tumor stage, ABCB1 and HMGB1 expression were also strong, independent predictors of OS. These data underline the importance of identifying the specific targets downstream of ΔTAp73 isoforms, which might have an oncogenic function and could be stronger than TP73 variants themselves in predicting patient outcome. As such, they could be used as prognostic markers in the clinical setting. Little is known about the relevance of ABCB1 and HMGB1 to the outcome of cancer patients, although the fact that upregulation of ABCB1 and HMGB1 has been associated in a few reports with poor prognosis of cancer patients sustains our hypothesis (44–46). Remarkably, the finding that the ectopic expression of ΔNp73 increases the proliferation rate and confers resistance to oxaliplatin to colon cancer cells strengthens the oncogenic potential of this specific isoform and its involvement in specific tumorigenesis processes. As previously reported by other groups (54, 55), the exposure of the cells to oxaliplatin did not modify the endogenous levels of TP73 variants. It is possible that those tumors already expressing high levels of ΔNp73 can show resistance to the treatment; in addition, the oxaliplatin action could gradually select the cells overexpressing this putative oncogenic p73 variant, resulting in a resistant tumor.

As cumulative data support the oncogenic role of ΔTAp73 isoforms (14, 56), the mechanisms and targets underlying these functions are currently of great interest. In this article, we present original data with regard to the impact of specific TP73 variants in the outcome of colon cancer patients. In addition, we found that putative ΔTAp73 isom forms are independent prognostic markers of OS. Specifically, upregulation of ABCB1 and HMGB1 predicts, in a strong, independent manner, the OS of patients diagnosed with colon cancer. Further experiments are needed to identify specific targets of ΔTAp73 isoforms that carry out an oncogenic role and could be used as clinical markers of relapse.
Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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References


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Prognostic Impact of ΔTAp73 Isoform Levels and Their Target Genes in Colon Cancer Patients

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