ABCG2/BCRP gene expression is related to epithelial–mesenchymal transition inducer genes in a papillary thyroid carcinoma cell line (TPC-1)

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Abstract

Tumor malignancy is associated with the epithelial–mesenchymal transition (EMT) process and resistance to chemotherapy. However, little is known about the relationship between the EMT and the multidrug-resistance gene in thyroid tumor progression. We investigated whether the expression of the ABCG2/BCRP gene is associated with ZEB1 and other EMT inducer genes involved in tumor dedifferentiation. We established a subpopulation of cells that express the ABCG2/BCRP gene derived from the thyroid papillary carcinoma cell line (TPC-1), the so-called TPC-1 MITO-resistant subline. The most relevant findings in these TPC-1 selected cells were a statistically significant upregulation of ZEB1 and TWIST1 (35- and 15-fold change respectively), no changes in the relative expression of vimentin and SNAIL1, and no expression of E-cadherin. The TPC-1 MITO-resistant subline displayed a faster migration and greater invasive ability than parental cells in correlation with a significant upregulation of the survivin (BIRC5) gene (twofold change, \( P < 0.05 \)). The knockdown of ZEB1 promoted nuclear re-expression of E-cadherin, reduced expression of vimentin, N-cadherin, and BIRC5 genes, and reduced cell migration (\( P < 0.05 \)). Analysis of human thyroid carcinoma showed a slight overexpression of the ABCG2/BCRP at stages I and II (\( P < 0.01 \)), and a higher overexpression at stages III and IV (\( P < 0.01 \)). SNAIL1, TWIST1, and ZEB1 genes showed higher expression at stages III and IV than at stages I and II. E- and N-cadherin genes were upregulated at stages I and II of the disease (ninefold and tenfold change, respectively, \( P < 0.01 \)) but downregulated at stages III and IV (fourfold lower, \( P < 0.01 \)). These results could be a promising starting point for further study of the role of the ABCG2/BCRP gene in the progression of thyroid tumor.
Introduction

Most patients with papillary or follicular thyroid tumors present survival rates close to 90% 10 years after diagnosis (Hundahl et al. 1998). However, between 2% and 11% of these tumors develop aggressive behavior, with local recurrence or metastases at diagnosis or during follow-up, significantly reducing the survival rate (Cooper et al. 2009). The molecular mechanisms and the type of cells involved in the dedifferentiation processes in these tumors are complex and largely unknown. One group of cells that is known to be implicated in the development of these tumors and resistance to chemotherapy is cancer stem cells (CSCs; Mimeault & Batra 2006, Dalerba et al. 2007, Akunuru et al. 2012). These cells possess stem-cell-like properties and share the expression of several stem cell markers (Li et al. 2013). However, their role in thyroid tumors is inconclusive (Lin 2011).

One stem cell marker detected in thyroid glands is the Prominin 1 (PROM1), also known as CD133. This marker, identified both in human cell lines and in biopsies from patients with thyroid cancer, contributes to radioresistance and maintenance of the undifferentiated status of the tumors (Friedman et al. 2009, Todaro et al. 2010, Ke et al. 2013). Another stem marker detected in thyroid cancer is nestin. Nestin is also known to be a marker of neuroepithelial stem or progenitor cells in the brain, and to be related to malignancy in some solid cancers (Krupkova et al. 2010). In the thyroid, nestin has been identified in differentiated thyroid tumors, but its expression does not relate to malignant characteristics of these tumors (Yamada et al. 2009).

In 2007, Hoshi et al. identified a cell population which expresses the ABCG2/BCRP gene in the thyroid gland (Hoshi et al. 2007). This gene, referred to as the breast cancer resistance protein, is implicated in protection against several xenobiotics, in chemoresistance, and maintenance of the regenerative capacity of adult tissue. However, little is known about its physiological role in the thyroid gland (Krishnamurthy & Schuetz 2006, Robey et al. 2007, Thomas et al. 2008, Fatima et al. 2012).

Knowledge of the molecular mechanisms that control stem cell transformation into stem cell cancer is incomplete. Two of the most important mechanisms identified are the epithelial–mesenchymal transition (EMT) process and the mesenchymal–epithelial transition (MET) induction process. These processes not only maintain normal stem cell phenotypes but also contribute to the development of some types of solid tumors (Klymkowsky & Savagner 2009). Several transcription factors, such as ZEB1, TWIST, and SNAIL1, have been identified as inducers of the EMT/MET processes, and are known to play a role in cancer progression and metastasis (Montserrat et al. 2011). ZEB1 is a master key in these processes. It has been associated with the maintenance of stem cell characteristics through expression of microRNAs and through the inhibition of the sonic hedgehog pathway (Wellner et al. 2009, Tang et al. 2012).

Another gene that is involved in the MET process is BIRC5 (survivin), a member of the apoptosis inhibitor family. BIRC5 (survivin) is highly expressed in fetal tissue and in most human solid tumors. Its expression is abolished in non-tumor cells and mature cells. Detection of BIRC5 (survivin) in tumors derived from human embryonic stem cells, such as teratoma, indicates that it plays a role in the formation of these tumors and their maintenance by transforming normal embryonic stem cells into embryonic cell-like cells (Brabletz et al. 2005, Boidot et al. 2008, Blum et al. 2009). BIRC5 (survivin) has also been shown to be involved in growth arrest, reduced migration, and resistance to chemotherapy- and radiotherapy-induced apoptosis (Tirro et al. 2006, Nabzdyk et al. 2011).

However, the link between the expression of the ABCG2/BCRP transporter gene and genes related to EMT processes in aggressive thyroid tumors is unknown. The aim of the present study was to investigate whether the expression of the ABCG2/BCRP transporter gene is associated with ZEB1 and other EMT-related genes involved in tumor dedifferentiation using a papillary cell line (thyroid papillary carcinoma (TPC-1)) as a cellular model.

Subjects and methods

TPC-1 cell culture and cellular selection

The TPC-1 cell line was provided by Dr Paolo Vigneri (University of Catania, Italy). The short tandem repeat (STR) profiling was carried out using the protocols for the GeneAmp PCR System 2400 Thermal Cycler (Perkin Elmer/Applied Biosystems, Waltham, MA, USA) and the ABI PRISM 310 Genetic Analyzer (Perkin Elmer/Applied Biosystems) according to the manufacturer’s instructions. STR profiles were analyzed using the software package Genemapper 4.1 (Applied Biosystems). The TPC-1 cell line was matched with its STR profiles reported in previous studies (Meireles et al. 2007). This cell line was cultured in RPMI 1640 (w L-glutamine) supplemented with 10% fetal bovine serum and 2% streptomycin/penicillin.

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To enrich the ABCG2/BCRP-positive cells in the TPC-1 cell cultures and to generate a TPC-1 MITO-resistant subline, we used mitoxantrone, a specific substrate of ABCG2/BCRP. Mitoxantrone was diluted to 12 μM in the RPMI (low glucose) basal medium and was added to the culture every 2 days, following the protocol described by Mato et al. (2009). Cell cultures were maintained in 5% CO₂ at 37 °C in a humidified incubator. The surviving cells were then placed in fresh RPMI medium (low glucose; Gibco-BRL) supplemented with 10% FCS and 5% glutamine. Expression of ABCG2/BCRP transporters was confirmed using the qRT-PCR technique before and after cell selection.

**Human thyroid tissue samples**

Thyroid tumor tissue samples (n = 34) were collected from patients undergoing surgery at Hospital de la Santa Creu i Sant Pau (Barcelona, Spain). The study was approved by the Local Ethics Committee and carried out in accordance with the Declaration of Helsinki. Table 1 shows patient data: sex, age at diagnosis, tumor histology, and tumor stage defined by recent international guidelines (Cooper et al. 2009). Diagnosis of underlying disease was verified by histological examination 7 days after surgery.

**RNA isolation and first strand cDNA synthesis**

Total RNAs obtained from the human tissues and cell lines were isolated using the TRIzol reagent according to the manufacturer’s instructions (Invitrogen). The RNA yield and the ratio of absorbance at 260–280 nm (A260:A280 ratio) were measured using a NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, Montchanin, DE, USA) and the RNA quality was checked by electrophoresis using agarose gels. Total RNA (1 μg) was reverse transcribed using the Transcriptor First-Strand cDNA Synthesis Kit (Roche Applied Science). cDNA samples were stored at −20 °C and diluted with RNase-free water for use as template in real-time PCR analysis.

### Quantitative real-time PCR (qRT-PCR) and RT-PCR

Real-time PCR was conducted using an ABI PRISM 7900HF Sequence Detection System, according to the manufacturer’s protocol (Applied Biosystems). All reactions were carried out using 100 ng of cDNA in a total volume of 50 μl of TaqMan Universal PCR Master Mix (Applied Biosystems) and the predesigned and labeled primer/probe set (Assays-on-Demand Gene Expression assay, Applied Biosystems). The samples were analyzed in duplicate, negative controls were included, and PCR products were verified using dissociation curve analysis immediately after RT-PCR. The GADPH housekeeping gene was used to normalize gene expression data. The relative changes in gene expression were analyzed by the 2^−ΔΔCt method and SDS2.1 and Data Assist V2.1 Software (Applied Biosystems). TaqMan qPCR primers (Applied Biosystems) used in the study were as follows: ABCG2/BCRP (Hs0105379_m1), ZEB1 (Hs01566407_m1), SNAIL1 (Hs00195591_m1), TWIST (Hs003611867_m1), E-cadherin (CDH1) (Hs00178055_m1), N-cadherin (CDH2, Hs00983056_m1), integrin β-binding protein 1 (ITGB1BP1, Hs00178055_m1), ITGB1 (Hs00559595_m1), survivin (BIRC5, Hs0077611_g1), vimentin (VIM, Hs00185584), and GAPDH (4337364F). Commercially available RNA pooled from normal thyroid (636536, Clontech) was used as a control in the real-time PCRs (qRT-PCRs).

### siRNA transfection

siRNA transfection in TPC-1 parental cell lines and in the TPC-1 MITO-resistant subline was carried out using Lipofectamine RNAiMAX transfection reagent (Life Technologies) according to the manufacturer’s protocol. Approximately 4.5 × 10⁴ cells were plated in six-well plates overnight. The next day, the cells were transiently transfected with either 10 nM predesigned siRNA (Stealth Select RNAi) targeting ZEB1 (sc38643) or control siRNA purchased from Invitrogen. The transfected cells were harvested at 24, 48, and 72 h for further analyses. The efficiency of the siRNA transfection showed a significant

<table>
<thead>
<tr>
<th>Table 1</th>
<th>Characteristics of patients with malignant thyroid lesions. Tumor stage defined by the recent international guidelines (Cooper et al. 2009)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean age at diagnosis</td>
<td>59.7 (22-83 years)</td>
</tr>
<tr>
<td>Sex (n)</td>
<td>59.7 (22-83 years)</td>
</tr>
<tr>
<td>Female</td>
<td>30</td>
</tr>
<tr>
<td>Male</td>
<td>4</td>
</tr>
<tr>
<td>Histology</td>
<td>31</td>
</tr>
<tr>
<td>WDTC (papillary)</td>
<td>2</td>
</tr>
<tr>
<td>PTDTC</td>
<td>1</td>
</tr>
<tr>
<td>ATC</td>
<td>13</td>
</tr>
<tr>
<td>Stage (n)</td>
<td>5</td>
</tr>
<tr>
<td>Stage I</td>
<td>6</td>
</tr>
<tr>
<td>Stage II</td>
<td>7 (plus two PTDTC and one ATC)</td>
</tr>
</tbody>
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WDTC, well-differentiated thyroid carcinoma; PTDTC, poorly differentiated thyroid carcinoma; ATC, anaplastic thyroid cancer.
reduction in ZEB1 mRNA expression level \( (P<0.001; \) 
Supplementary Fig. 1, see section on supplementary data
given at the end of this article). Each assay was carried out 
in triplicate in at least three independent experiments.

Immunocytochemistry
Cytospin slides from cell suspensions of the TPC-1 
parental cell line and TPC-1 MITO-resistant subline were 
immunostained. Samples were then fixed in 4% parafor-
maldehyde and rinsed with PBS solution. They were then 
blocked for 10 min at room temperature in a solution 
containing 1% BSA and 0.2% saponin. The primary 
antibodies and their dilutions were as follows: ZEB1 
(HPA027524, Sigma–Aldrich), vimentin (MAB3400, Milli-
pore, Darmstadt, Germany), and TWIST (sc-6269, Santa 
Cruz Biotechnology, Inc., Dallas, Texas, USA) at 1/100, 
E-cadherin (M3612, Dako, Glostrup, Denmark), 
N-cadherin (M3613, Dako), ITGB1 (610468, Becton 
Dickinson, East Rutherford, New Jersey, USA), SNAIL1 
(sc-10433, Santa Cruz Biotechnology, Inc.) at 1/50, and 
ABCG2/BCRP (AB3380, Abcam, Cambridge, UK) at 
1/1000. All antibodies were diluted with a blocking 
solution (s3022, Dako) and incubated overnight (O/N) at 
4 °C. Biotinylated secondary antibody and peroxidase-
conjugated streptavidin from the Dako Universal LSAB 
Kit (Dako) were added for 20 min each. Finally, sections 
were incubated in 3’3-diaminobenzidine for 5 min, 
followed by hematoxylin counterstaining and mounting. 
Negative controls were prepared by replacing the primary 
antibody with non-immune serum. No signals were 
observed for these samples. The results were visualized 
with a Leica microscope.

Flow cytometry analysis
Subconfluent cells were harvested using trypsin and 
1×10⁶ cells were incubated with the primary antibody 
anti-BCRP, clone 5D3 (MAB4155, Millipore), for 60 min at 
4 °C and washed twice with PBS+2% FCS. FITC-conju-
gated secondary antibody (ab6785, Abcam) was applied 
to the cells for 30 min at 4 °C. Briefly, cells were washed 
twice with PBS+2% FCS, and resuspended in 0.5 ml 
PBS with 10% FCS. Labeled cells were scanned on a 
FACSCalibur Cytometer (Becton Dickinson) and analyzed 
using CellQuest Software (Becton Dickinson), acquiring 
1×10⁶ events. An isotopic control immunoglobulin 
(ab11-4732, eBioscience, San Diego, CA, USA) was used as 
a negative control.

In vitro wound healing assay
TPC-1 parental cells, the TPC-1 MITO-resistant subline, 
and the TPC-1 MITO-resistant subline transfected with 
ZEB1 siRNA were plated at high densities and grown to 
confluence at 90% overnight. The cells were scratched 
with a pipette tip (10 μl) and washed several times to 
remove the cellular debris. Using an inverted microscope, 
the wounds were photographed at 0 h \((t=0)\) and again 
after 16 h of incubation, at the same site, at 37 °C. The 
cultures were incubated with serum-free medium. Image J 
Software (National Institutes of Health, Bethesda, MD, 
USA) was used to analyze photographs. The percentage 
of wound healing was determined based on three measure-
ments of the wound area. Each result is the mean of three 
independent experiments.

Invasion assay
TPC-1 \((2×10⁵)\) in serum-free DMEM was placed in an 
insert made of polycarbonate membrane with 8-μm pores 
and precoated with basement membrane matrix (Cell 
Biolabs, Inc., San Diego, CA, USA) following the manu-
ufacturer’s protocol. The outer chamber was filled with 
500 μl RPMI containing 10% FCS as the chemoattractant. 
The chambers were then placed in an incubator at 37 °C 
with 95% O₂+5% CO₂ for 3 days. The inserts were 
removed, and the noninvading cells were removed using 
cotton-tipped swabs. The cells that traversed the mem-
brane pore and spread to the lower surface of the filters 
were stained with eosin for visualization, and the number 
of cells that penetrated the membrane was determined by 
counting the mean cell number of three randomly 
selected high-power fields \((200×; MOTIC AE31)\). Experi-
ments were carried out in triplicate. The results for 
the TPC-1 MITO-resistant subline alone and transfected 
with ZEB1 siRNA were normalized to the values for TPC-1 
parental cells.

Statistical analysis
Results are expressed as mean ± S.D. The statistical 
significance was estimated using Student’s unpaired 
t-test. Pairwise comparisons were made using Student’s 
t-test. A two-tailed \( P<0.05 \) was considered statistically 
significant. The analyses were performed using DATA 
ASSIST Software, version 3.01 or GraphPad Prism for 
Windows, version 4.0 (GraphPad Software, San Diego, 
CA, USA).
Results

Establishment and characterization of the TPC-1 MITO-resistant subline compared with the TPC-1 cell line used as a control: relative expression of the ABCG2/BCRP transporter gene and genes related to the EMT process

Stem cell markers analyzed by immunocytochemistry showed a few TPC-1 cells with a weak protein expression for ABCG2/BCRP and nestin, and a high protein level for the CD133 marker. After cell selection, the TPC-1 MITO-resistant cell subline showed an increase in protein expression for ABCG2/BCRP but no changes in protein expression for the other markers tested (Fig. 1A). Immunocytochemistry results for the ABCG2/BCRP gene correlated with a significant increase in the relative expression of mRNA detected for the ABCG2/BCRP gene (eightfold change, \( P < 0.05 \); Fig. 1B) and a higher mean fluorescence intensity measured by flow cytometry (\( P < 0.05 \); Fig. 1C). We also observed a significant increase in expression of the ZEB1 and TWIST genes (35-fold change (\( P < 0.05 \)) and a 15-fold change (\( P < 0.05 \)) respectively) in the same selected cell population. No significant change was observed in SNAIL1 expression in TPC1 or in the TPC-1 MITO-resistant subline (Fig. 2A), indicating a good correlation with the protein levels detected by immunocytochemistry (Fig. 2B). After cell selection, the TPC-1 MITO-resistant cell subline showed an increase in N-cadherin gene expression (twofold change, \( P < 0.01 \); Fig. 3A). The results for N-cadherin gene expression were correlated with protein expression (Fig. 3B). No expression of the E-cadherin gene was observed in the TPC-1 or the TPC-1 MITO-resistant subline (data not shown) and the result for gene expression of E-cadherin was confirmed by immunocytochemical analysis (Fig. 3B). The analysis of ITGB1 and

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**Figure 1**

Characterization of TPC-1 parental cells and the TPC-1 MITO-resistant subline. (A) Representatives images of cell stained for ABCG2/BCRP, nestin, and CD133 in both before and after drug selection (20× magnification). (B) Relative expression levels of mRNA for the ABCG2/BCRP gene. Data are representative of three independent experiments. Data shown represent the mean ± s.d. for three independent experiments for mRNA expression, ***\( P < 0.001 \). (C) Mean intensity of fluorescence (MFI) of TPC-1 parental cells vs the TPC-1 MITO-resistant subline. Bars represent mean ± s.d. from three separate experiments (*\( P < 0.05 \)).
integrin cytoplasmic domain-associated protein 1 molecule (ITGB1BP1) showed significant downregulation of the relative expression in selected cells (twofold lower for both genes) compared with parental cells ($P < 0.05$) (Fig. 4A and B). No significant changes were detected in the relative expression of vimentin at both the mRNA and protein levels (Fig. 4C and D).

Effects of silencing of the ZEB1 gene on EMT-related genes in the TPC-1 MITO-resistant cell subline

The effects of silencing of the ZEB1 gene at 48 h on EMT-related genes resulted in a significant induction of E-cadherin gene expression (eightfold change, $P < 0.001$) and nuclear localization of E-cadherin protein in 35% of cells (Fig. 5A and B). In contrast, vimentin gene expression showed significant downregulation at 24 h (twofold change, $P < 0.05$) and an even higher downregulation at 48 h (fourfold change, $P < 0.001$), although some expression remained (Fig. 5C and D). After silencing of the ZEB1 gene for 24 h, analysis of ABCG2/BCRP gene expression showed a significant upregulation (twofold change, $P < 0.01$). However, a significant reduction in ABCG2/BCRP gene expression was noted at 48 and 72 h, although some expression remained (fourfold lower, $P < 0.05$; Fig. 6A). A significant downregulation at 24 h was observed in N-cadherin gene expression (fourfold lower, $P < 0.05$) and was maintained at 48 and 72 h (Fig. 6B). Significant upregulation of ITGB1 gene expression was detected at 48 and 72 h (twofold change and 2.5-fold change, $P < 0.01$, respectively; Fig. 6C). The ITGB1BP1 (ICAP1) molecule interacted with ITGB1 and had a low level of expression in the TPC-1 MITO-resistant cell subline at 24 and 48 h. This molecule exhibited high upregulation at 72 h (12-fold change, $P < 0.05$; Fig. 6D).

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in the TPC-1 MITO-resistant subline (twofold change, \(P < 0.05\); Fig. 7A). The ability to close a wound, analyzed by wound-healing assays, showed a statistically significantly faster migration in the TPC-1 MITO-resistant subline cells than in the TPC-1 parental cell line (40% closure of wound area) \((P < 0.05)\) (Fig. 7B). The wound healing effects after silencing the \(ZEB1\) gene showed statistically significant downregulation of \(BIRC5\) gene expression at 48 and at 72 h of transient transfection (fourfold change, \(P < 0.05\); Fig. 7C). The faster cell migration observed in the TPC-1 MITO-resistant subline was reverted after knock-down of the \(ZEB1\) gene, \(P < 0.05\) (Fig. 7D). The TPC-1 MITO-resistant subline showed higher ability to invade a reconstituted ECM than the TPC-1 parental cell line at 92 h of cell culture \((P < 0.05; \text{Fig. 8})\).

**Relative expression of mRNA ABCG2/BCRP transporter, and EMT-related genes in human thyroid carcinoma tissues**

The analysis of gene expression carried out in a cohort of 34 patients with different stages of the disease (see Table 1) showed a statistically significant upregulation in the relative expression of the \(ABCG2/BCRP\), \(SNAIL1\), \(TWIST1\), and \(ZEB1\) genes compared with control tissue \((P < 0.05)\). These results correlated with the stage of the tumors (Fig. 9A, B, C and D). The analysis of E- and N-cadherin genes showed a statistically significant upregulation for both genes (tenfold change and 11-fold change respectively \((P < 0.05))\) in patients with stages I and II of the disease. In contrast, downregulation (fourfold change) was statistically significant for both genes in patients with stages III and IV disease. (Fig. 9E and F).

**Discussion**

In this study, we identified for the first time, to our knowledge, cells positive for ABCG2/BCRP, nestin, and CD133 in a papillary cell line (TPC-1). However, we did
not detect changes in gene expression for nestin or CD133 genes after enriching the cell culture with cells that expressed the ABCG2/BCRP gene, indicating that more than one cell population has a pluripotent capacity in TPC-1. Furthermore, we observed, for the first time, a relationship between the increase in expression of the adult stem marker ABCG2/BCRP gene, a member of the ATP-binding cassette transporters and EMT inducer genes, TPC-1 MITO-resistant subline transfected with siRNA control was used as a control.

Figure 5
Effect of knockdown of ZEB1 on EMT inducer genes (E-cadherin and vimentin). (A) qRT-PCR analysis showed a significant increase in the expression of the mRNA for the E-cadherin gene (***P<0.001).

(B) Representative image of cells positively stained for E-cadherin protein showing nuclear. The arrows indicate staining at 48 h of ZEB1 silencing (20× magnification). (C) qRT-PCR analysis showed a significant reduction of expression at 24 and 48 h of silencing of ZEB1 for vimentin mRNA (**P<0.01 and ***P<0.001).

(D) Representative image showed a reduction of expression of protein at 48 h of silencing of ZEB1 (20× magnification).

Bars represent mean ± S.D. from three separate experiments. The TPC-1 MITO-resistant subline transfected with siRNA control was used as a control.

Figure 6
Effect of knockdown of ZEB1 on the relative expression of mRNA for ABCG2/BCRP, N-cadherin, ITGB1, and ITGB1BP1 at 24, 48, and 72 h.
(A) Knockdown of ZEB1 resulted in upregulation of ABCG2/BCRP gene expression at 24 h (**P<0.01). This increment was decreased at 48 and at 72 h, a reduction of expression was detected (***P<0.001).
(B) Downregulation of N-cadherin was detected at 24 h of ZEB1 silencing (***P<0.001) and was maintained at 48 and 72 h (**P<0.01).

(C) The relative mRNA expression of ITGB1 showed an upregulation at 24 h (**P<0.05), 48 h (**P<0.001), and 72 h (**P<0.001).
(D) The relative mRNA expression of ITGB1BP1 gene showed an upregulation of gene expression at 72 h (**P<0.001). Bars represent mean ± S.D. from three separate experiments. The TPC-1 MITO-resistant subline transfected with siRNA was used as a control.
in TPC-1 and in papillary thyroid tumors. Although there is evidence that the EMT process generates CSCs, the connection between the specific genes involved in this process and the radioresistance observed in thyroid tumors has not been clearly established (Visvader & Lindeman 2008, Singh & Settleman 2010, Chu et al. 2013, Lan et al. 2013). Recent research using anaplastic thyroid cancer as a model has confirmed an association

Figure 7
Analysis of survivin (BIRC5) gene expression, cellular migration in TPC-1 parental cells, and the TPC-1 MITO-resistant subline transfected with siRNA ZEB1. (A) The relative mRNA expression of survivin gene showed upregulation in selected cells (TPC-1 MITO-resistant subline cells; twofold change, *P < 0.05). (B) The wound-healing assay showed significantly faster migration in the TPC-1 MITO-resistant subline compared with TPC-1 parental cells (*P < 0.05). The images were obtained by phase-contrast microscope (×100). (C) Transient ZEB1 knockdown resulted in downregulation of BIRC5 gene expression at 48 h (***P < 0.001) and at 72 h (****P < 0.0001). (D) The wound-healing assay showed a significant decrease in the closed wound area in the TPC-1 MITO-resistant subline transfected with siRNA ZEB1 compared with the TPC-1 MITO-resistant subline transfected with siRNA control (*P < 0.05). Phase-contrast microscope images (×100). Bars represent mean ± S.D. from four separate experiments.

Figure 8
Transwell invasion ability of TPC-1 parental cells and TPC-1 MITO-resistant subline cells. (A and B) The ability to invade surrounding extracellular matrix was analyzed at 48, 72, and 92 h of cell culture in complete medium. The TPC-1 MITO-resistant subline cells showed a high capacity for invasion at 92 h (*P < 0.05) compared with TPC-1 parental cells used as a control. Bars represent mean ± S.D. from four separate experiments.
between the stem-like phenotype and chemotherapy resistance, indicating that the multidrug transporter system is responsible for this chemotherapy effect (Zito et al. 2008, Davies et al. 2011, Carina et al. 2013). Our results indicate that the cell subpopulation identified in TPC-1 expresses the ABCG2/BCRP gene, possibly contributing to the malignant progression of these tumors. This cell subpopulation also showed upregulation of expression of the BIRC5 gene, faster cellular migration, and greater ability for invasion when the selected cells (TPC-1 MITO-resistant subline) were compared with the parental cell line (TPC-1). These results are consistent with those reported for pancreatic cancer (Arumugam et al. 2009, Wellnet et al. 2009, Palena et al. 2011). It was of interest to note that this effect could be reverted when the ZEB1 gene was knocked down in the selected cells. In these selected cells, the transient silencing of the ZEB1 gene produced a downregulation of ABCG2/BCRP and BIRC5, and reduced cell migration in vitro. These results indicate that ABCG2/BCRP, ZEB1, and BIRC5 genes are linked and could play a role in the more aggressive behavior observed in some well-differentiated papillary tumors.

Other markers that we studied in TPC-1 cells were E- and N-cadherin. These genes belong to transmembrane protein families and are involved in cell-adhesion. We found no expression of the E-cadherin gene in the TPC-1 cell line or in the TPC-1 MITO-resistant subline. However, the N-cadherin gene was increased in expression in TPC-1 MITO-resistant cells. Other authors have described a relationship between the loss of expression of the E-cadherin gene and the metastasic process. The role of expression of N-cadherin gene in carcinomas is controversial (Hazan et al. 2004, Li et al. 2010, Shih & Yamada 2012). In our study, we observed that transient ZEB1 silencing in the TPC-1 MITO-resistant subline promoted increased expression of E-cadherin with a nuclear localization, and downregulation of N-cadherin. This result supports the observation that E-cadherin can translocate to the nucleus and participate in the regulation of Wnt-dependent genes (Kuphal & Behrens 2006).

We also analyzed integrin transmembrane receptors, ITGB1 and integrin β1-binding protein 1 (ICAP1), genes involved in the progression of malignancy, chemoresistance, morphogenesis, terminal cellular differentiation, and maintenance of the progenitor population in adult tissue (De Toni et al. 2006, Piwko-Czuchra et al. 2009, Wu et al. 2009, Ju et al. 2010, Shiraki et al. 2011). ICAP1 is considered to be the most specific ligand for the ITGB1 cytoplasmic domain and is involved in cellular processes such as cellular adhesion and migration (Fournier et al. 2002, Brunner et al. 2011). In selected cells, we found that both ITGB1 and ICAP1 genes were downregulated, but the ZEB1 silencing gene was able to promote an up-expression in both. Further research is needed, nevertheless, to

**Figure 9**

Gene expression of EMT inducer genes (ZEB1, SNAIL1, and TWIST1). E-cadherin, N-cadherin, and ABCG2/BCRP from human thyroid carcinoma (papillary tumors and poorly differentiated/anaplastic tumors). (A, B, C and D) The relative mRNA expression of ABCG2/BCRP, SNAIL1, TWIST1, and ZEB1 showed a higher increase in expression in tumors from patients with aggressive stages (III and IV) in comparison with those with the more benign stages (I and II). (E and F) The relative mRNA expression of E- and N-cadherin genes showed a significant increase in expression in tumors from patients with benign stages (I and II), in contrast a decrease in expression of both genes was detected in tumors from patients with more aggressive stages (III and IV). Data shown represent the mean ± S.D.
clarify the relationship between these genes and the ABCG2/BCRP gene.

Another novel finding in our study is that high increase in expression of the ABCG2/BCRP, SNAIL1, TWIST1, and ZEB1 genes in poorly differentiated thyroid carcinoma, anaplastic carcinoma, and papillary thyroid tumors correlated with more aggressive disease stages. However, in agreement with published results, reduced expression of the E- and N-cadherin genes at stages III and IV also correlated with more aggressive stages. Studies in larger series and with a longer follow-up will be needed, however, to demonstrate whether these two genes can be considered as biomarkers of poor prognosis for papillary thyroid carcinoma.

In summary, we found that the expression of the ABCG2/BCRP gene was associated with ZEB1 and other EMT-inducer genes involved in papillary thyroid tumor dedifferentiation. These results could be a promising starting point for improving understanding of the role of these cells in tumor progression, and a new tool for designing innovative therapeutic strategies.

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**Supplementary data**

This is linked to the online version of the paper at [http://dx.doi.org/10.1530/JME-14-0051](http://dx.doi.org/10.1530/JME-14-0051).

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**Declaration of interest**

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

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**Author contribution statement**

E M and was responsible for supervision the experiment, analysis of the gene expression, statistical analysis of all data, and prepare the manuscript. A M, J I P, C G, and E L were responsible for collection of all human samples and clinical-histological studies. O B for setting up of the experiment and technical supported. A L responsible for the supervision of experiments and prepare the manuscript.

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