Identification of TACC1, NOV, and PTTG1 as new candidate genes associated with endocrine therapy resistance in breast cancer

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Abstract

Cross-resistance to molecules used in endocrine therapy is among the main challenges in the treatment of estrogen receptor-α (ERα) positive breast cancer. In this study, we used two different cell models of resistance to anti-estrogens: MVLN/CL6.7 cells and VP229/VP267 cells selected after exposure to tamoxifen respectively in vitro and in vivo to characterize a phenotype rarely observed, i.e. acquisition of cross-resistance to the pure ER antagonist fulvestrant. As MVLN/CL6.7 cells and VP229/VP267 cell lines are original and valuable models of cross-resistance to tamoxifen and fulvestrant, we examined candidate genes using a RTQ-PCR strategy to identify new biomarkers of endocrine resistance. Out of the 26 candidate genes tested, 19 displayed deregulation of expression at the basal level in at least one of the two resistant cell lines. Eight genes (TACC1, NOV, PTTG1, MAD2L1, BAK1, TGFβ2, BIRC5, and CCNE2) were significantly overexpressed in samples from ER-positive breast cancer patients who relapsed after tamoxifen treatment (n=24) compared with samples from patients who did not (n=24). Five genes (TACC1, NOV, PTTG1, BAK1, and TGFβ2) were correlated with significantly shorter relapse-free survival (univariate analysis). Finally, we identified TACC1 and a three-gene expression signature (TACC1, NOV, and PTTG1) as independent prognostic markers (multivariate analysis). Aberrant mRNA and protein levels of TACC1, NOV, and PTTG1 were also observed under tamoxifen and/or fulvestrant exposure in resistant CL6.7 cells compared with their respective control MVLN cells. In conclusion, our data identify TACC1, NOV, and PTTG1 as promising new markers that could be used in the clinical management of ER-positive breast cancer patients.

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Introduction

Breast carcinoma, the most common female cancer, is currently undergoing an alarming increase. Breast cancer growth is regulated by estrogen, which acts by binding to the estrogen receptor α (ERα). ERα is routinely used as a prognostic and predictive marker in the management of breast cancer patients, in particular to identify patients who may respond to endocrine therapy. The selective estrogen receptor modulator tamoxifen (Tam) which aims to block the ERα has been the mainstay of hormonal therapy in both early and advanced breast cancer patients for approximately three decades (EBCTC Group 1998, Gradishar 2005). However, Tam is only partially effective because of intrinsic or acquired tumor resistance. Approximately, 40% of patients with ER-positive breast cancer will not respond to Tam (de novo resistance). Moreover, long-term follow-up and clinical trials have demonstrated that up to 62% of cancers initially responsive to endocrine therapy subsequently escape control with the patient requiring salvage surgery (Horobin et al. 1991, Fennessy et al. 2004). In general, Tam-resistant tumors respond to second-line endocrine therapy, suggesting that resistance is not attributable to the loss of or alterations in ERα, and that tumor growth may involve functional ERα signaling (Howell et al. 1995, Osborne 1998). New endocrine therapies have recently emerged, in particular with the selective estrogen receptor down-regulator (SERD) fulvestrant (ICI 182,780). The mechanism of action of this ER antagonist is different from that of Tam, as binding of fulvestrant to ER induces destabilization and degradation of the
receptor. Moreover, Tam only blocks the transcriptional activating function AF2 of ER, and thus only partially inactivates ER-regulated transcription (Tzulerman et al. 1994, McDonnell et al. 1995), while fulvestrant blocks both AF1 and AF2 functions of ER, resulting in complete abrogation of the transcription of ER-regulated genes (Wakeling et al. 1991, Dowsett et al. 2005). Two phase III trials have demonstrated that fulvestrant is as efficient as anastrozole, a third-generation aromatase inhibitor, in second-line treatment for postmenopausal women with advanced-stage Tam-resistant breast cancer (Dodwell & Pippen 2006). Recent clinical trials have also shown that in patients with advanced breast cancer progressing on prior endocrine therapy with Tam or an aromatase inhibitor, fulvestrant produces a clinical benefit in respectively 43% and 30% of the patients (Howell et al. 2002, Osborne et al. 2002, Perey et al. 2007). These clinical data underline not only the importance of fulvestrant in the therapeutic arsenal against ER+ breast cancers, but also suggest that in a subset of patients who have developed resistance to first-line endocrine therapy (with Tam or aromatase inhibitors), cross-resistance to fulvestrant can also occur.

In in vitro-established resistant breast cancer cells, Tam-resistant cells selected under Tam exposure are usually sensitive to fulvestrant (Parisot et al. 1999, Kilker et al. 2004, Martin et al. 2005, Shaw et al. 2006), whereas resistant cell lines established under fulvestrant selection are commonly cross-resistant to Tam (Lykkesfeldt et al. 1995, Brunner et al. 1997, Fan et al. 2006a, Shaw et al. 2006). Few studies have reported a decreased sensitivity of Tam-resistant breast cancer cells or xenografts to fulvestrant (Lykkesfeldt et al. 1994, Naundorf et al. 2000), but none, to our knowledge, has demonstrated the total abrogation of fulvestrant response. In this study, we fully characterized for the first time the endocrine resistance developed by two cellular models of acquired Tam resistance: in vitro-selected Tam-resistant CL6.7 cells (Badia et al. 2000) and in vivo-selected Tam-resistant VP267 cells (McCallum & Lowther 1996). Strikingly, we found that, while selected under Tam exposure, CL6.7 and VP267 cells also acquired cross-resistance to fulvestrant, characterized by a total abrogation of the SERD’s response. Thus, the combination of CL6.7 and VP267 cells represents a good cellular model for the genomic screening of molecular markers of endocrine resistance with potential clinical relevance. The recent development of effective tools for investigating gene-expression profiles has already led to the identification of new diagnostic and prognostic markers. These tools include cDNA arrays (van ’t Veer et al. 2002, van de Vijver et al. 2002, Ma et al. 2004, Frasor et al. 2006) and real-time quantitative RT-PCR (RTQ-PCR). While cDNA array allows the screening of a large number of genes at a time, RTQ-PCR is an alternative approach that has already proved useful for the identification of molecular markers. Indeed, RTQ-PCR is an accurate, sensitive and reproducible technique more suitable for detecting small variations in gene expression and weakly expressed genes (Bieche et al. 2004). While this technique allows the quantitative measurement of only a small number of selected candidate genes, it has already been successfully used in several studies aimed at identifying markers associated with endocrine therapy resistance (Bieche et al. 2004, Paik et al. 2004, Tozlu et al. 2006).

In two previous genomic studies, we had identified by cDNA arrays new genes demonstrated as estrogen-modulated or associated with agonist activity of 4-hydroxy-tamoxifen (OH-Tam) and hyper-response to 17 β-estradiol (E2) in OH-Tam-resistant breast cancer cell lines (Vendrell et al. 2004, 2005). With the aim to identify gene expression deregulation associated with resistance to Tam and fulvestrant, we selected from these studies 26 candidate genes whose biological functions are associated with cell proliferation, transformation, apoptosis, DNA repair, and DNA replication. We analyzed by RTQ-PCR the expression of the 26 candidate genes in CL6.7 and VP267 cells. Genes with a deregulated expression in resistant cells were then selected to be explored in a series of 48 ER+ breast tumor samples from postmenopausal patients, who relapsed after primary surgery and adjuvant endocrine therapy (n=24) or did not (n=24).

Materials and methods

Cell-proliferation analysis

MVLN, CL6.7, CL6.8, VP229, and VP267 cells were grown as described previously (Demirpence et al. 1993, McCallum & Lowther 1996), then purged for 4 days in DMEM without Phenol Red and supplemented with 3% steroid-depleted, dextran-coated, charcoal-treated FCS (DCC medium). The cells were then treated (with media changed every two days) in the absence or the presence of E2 (Sigma, Saint Louis, MO, USA), OH-Tam (Sigma) or fulvestrant (Tocris, Ellisville, MO, USA). Proliferating cells were analyzed using the cell proliferation ELISA, 5-bromodeoxyuridine (BrdU) colorimetric kit (Roche) as previously described (Vendrell et al. 2005).

Western blot

Cell extract preparation and western blot analysis were performed as previously described (Vendrell et al. 2004). ERz and NOV antibodies were purchased from Santa Cruz Biotechnology (Santa Cruz, CA, USA).
TACC1 antibody from Upstate (Lake Placid, NY, USA), PTTG1 antibody from Zymed Laboratories (San Francisco, CA, USA) and α-tubulin antibody from Sigma.

**Breast tumor samples**

Samples from primary breast tumors were obtained from women operated on at the Centre René Huguenin (St Cloud, France) between 1980 and 1994. Informed consent was obtained from all patients and the study was approved by the ethics committee of the institution. A set of 48 ER+ breast tumor samples was used in this study; the tumors were taken from patients treated with primary surgery followed by adjuvant Tamoxifen alone: thirty-nine (81.2%) underwent a mastectomy and nine (18.8%) had breast-conserving surgery. Twenty-four patients relapsed under Tam treatment and developed metastases (‘Relapse’ group) and 24 patients did not (‘No relapse’ group). Standard prognostic factors are shown in Table 1.

**Table 1** Characteristics of the 48 ER+ tumors taken from patients treated with primary surgery followed by adjuvant Tam alone, and who relapsed or did not relapse under Tam treatment and developed metastases (‘Relapse’ group) and 24 patients did not (‘No relapse’ group). Standard prognostic factors are shown in Table 1.

**Statistical analyses**

Gene-expression levels in subgroups of breast tumor samples were compared using the Kruskal–Wallis test. Differences between groups were judged significant at a confidence level greater than 95% (P<0.05). To visualize the capacity of a molecular marker to discriminate between two populations (in the absence of an arbitrary cut-off value), we summarized the data in a receiver operating characteristic (ROC) curve (Hanley & McNeil 1982). ROC curves plot sensitivity (true positives) on the y-axis against one specificity (false positives) on the x-axis, considering each value as a possible cut-off. The area under curve (AUC) was calculated and used as a single measure of the discriminatory capacity of each molecular marker. When a molecular marker has no discriminative value, the ROC curve lies close to the diagonal and the AUC is close to 0.5. Conversely, when a marker has strong discriminative value, the ROC curve comes closest to the AUC of 1.
upper left-hand corner (or to the lower right-hand corner) and the AUC is close to 1.0 (or 0). Hierarchical clustering was performed using the GenANOVA software (Didier et al. 2002). Relapse-free survival (RFS) was defined as the interval between diagnosis and detection of the first relapse (local and/or regional recurrence, and/or distant metastasis). Survival distributions were estimated by the Kaplan–Meier method (Kaplan & Meier 1958) and the significance of differences between survival rates was ascertained by using the log-rank test (Peto et al. 1977). Cox’s proportional hazards regression model (Cox 1972) was used to assess prognostic significance.

**Immunohistochemical and RTQ-PCR analyses of breast tumor samples**

Ten ER+ frozen breast tumors from patients diagnosed at Centre Léon Bérard were obtained from the Biological Resource Centre of Centre Léon Bérard, (French agreement number: DC-2008-99) after approval by the institutional review board and ethics committee, with fully informed patient consent. Paraffin-embedded breast tumors were fixed in 10% formalin and inserted in tissue microarray blocks. The blocks containing invasive carcinoma were sectioned at a thickness of 4 μm. After deparaffinization and rehydration, endogenous peroxidases were blocked by incubating the slides in 5% hydrogen peroxide in sterile water. The slides were then incubated with a protein blocking agent (Immunotech, Marseille, France) for 10 min at room temperature. For heat-induced antigen retrieval, tissue sections were boiled in a water bath at 97°C for 50 min either in 10 mM high pH buffer (Dako, Trappes, France) for anti-NOV antibody or in citrate buffer (Dako) for anti-PTTG1 antibody. The slides were then incubated at room temperature for 30 min with the anti-NOV goat polyclonal antibody (Santa Cruz) or for 1 h with the anti-PTTG1 polyclonal rabbit antibody (Zymed). Both antibodies were diluted using an antibody diluent solution (Dako) at 1/800 (anti-NOV antibody) or at 1/600 (anti-PTTG1 antibody). After rinsing in PBS, the slides were incubated with a biotinylated secondary antibody bound to a streptavidin–peroxidase conjugate (LSAB+ Kit, Dako). Bound antibody was revealed by adding 3,3-diaminobenzidine. Sections were counterstained with hematoxylin. The slides were analyzed independently by the pathologist and the technician who assessed both the percentage of stained cells and the staining intensity (0 = none, 1+ = low, 2+ = intermediate, 3+ = high) in infiltrative carcinomatous cells. The tumors were then stratified according to a score established by multiplying the percentage of stained cells by the intensity. The cut-off values chosen to classify the tumors into the ‘low protein expression’ group or the ‘high protein expression’ group were determined after a pre-observation performed on a larger set of breast tumors (n=80, data not shown). As three levels of intensity could be observed for NOV immunostaining and only two for PTTG1 immunostaining, the staining score had to be at least 100 for NOV and at least 40 for PTTG1 to belong to the ‘high protein expression’ group.

The same 10 breast tumor samples were disrupted using the TissueLyser (Qiagen) and total RNA was extracted using the RNeasy Mini Kit (Qiagen) according to the manufacturer’s recommendations. Total RNA was subsequently quantified on a Nanodrop ND-1000 spectrophotometer (Nanodrop Technologies, Wilmington, DE, USA), and RNA integrity was checked using the BioAnalyzer 2100 (Agilent Technologies). RTQ-PCR for NOV and PTTG1 was performed as described above. For each gene, the 10 ER+ breast tumors were divided into two groups: samples with ‘low mRNA expression level’ (lower than the median mRNA level) and those with ‘high mRNA expression level’ (higher than the median mRNA level).

**Results**

The CL6.7 cell line developed a phenotype of OH-Tam resistance similar to that of the previously characterized CL6.8 cells

MVLN is an ER+, hormone-responsive, and OH-Tam-sensitive breast carcinoma cell line derived from MCF-7 cells (Demirpence et al. 1993). Six-month exposure of MVLN cells to OH-Tam allowed the emergence of several OH-Tam-resistant (OTR) but still estrogen-dependent cellular clones (Badia et al. 2000). We have previously characterized the phenotype of OTR CL6.8 cells, defined by an agonist activity of OH-Tam and hypersensitivity to E2 (Vendrell et al. 2005). The OTR CL6.7 cell line remains to be characterized.

One of the mechanisms possibly involved in endocrine therapy resistance is an alteration in the expression of ERα and/or ERβ (Johnston et al. 1995, Speirs et al. 1999). We found that, as previously observed for OTR CL6.8 cells (Vendrell et al. 2005), ERα protein expression was decreased in OTR CL6.7 cells when compared with MVLN cells, and this decrease was more pronounced in CL6.7 than in CL6.8 cells (Fig. 1A).

Investigation of ESR1/ERα mRNA levels by RTQ-PCR (Table 2) demonstrated no difference in the ESR1/ERα gene expression level between CL6.7 and MVLN cells (−1.2-fold), suggesting that the down-regulation of ERα expression in CL6.7 cells mainly occurs at a post-transcriptional level. On the contrary, ESR1/ERα gene expression was decreased in the CL6.7 cell line when compared with MVLN (−2.4-fold, data not shown). ESR2/ERβ mRNA level was 1000-fold lower than ESR1/ERα mRNA and no difference in expression was observed, either between OTR CL6.7 and MVLN cells
developed by the CL6.7 cell line also exhibits a hyper-response to E2 evidenced by the earlier detection of E2 stimulation in CL6.7 cells (day 3) than in the MVLN cell line (day 5), and by a significantly greater amplitude of proliferation under E2 treatment in OTR cells than in MVLN cells (Fig. 1C), similarly to what was previously observed for CL6.8 cells (Fig. 1C and Vendrell et al. 2005). The phenotype of OH-Tam resistance developed by CL6.7 cells was characterized under OH-Tam exposure by the loss of the cytostatic activity of the molecule that is detectable in MVLN cells and the occurrence of a strong stimulation of CL6.7 cell proliferation (estrogen-like effect; Fig. 2A). This phenotype was very close to the one developed by OTR CL6.8 cells (Fig. 2A and Vendrell et al. 2005). Taken together, these observations indicate that the OTR CL6.7 and CL6.8 cellular clones obtained from MVLN cells using the same selection process (6-month 200 nM OH-Tam treatment) developed a similar resistance phenotype defined by agonist activity of OH-Tam and hypersensitivity to E2.

**OTR CL6.7 cells, but not OTR CL6.8 cells, developed cross-resistance to fulvestrant**

As fulvestrant may be used as second-line therapy following Tam resistance, we investigated the proliferation response of MVLN, CL6.7, and CL6.8 cells under 100 nM fulvestrant exposure for 1, 3, 5, and 8 days (Fig. 2B). Fulvestrant treatment completely abolished the proliferation of MVLN cells detectable from the third day of treatment. Fulvestrant was also able to inhibit the proliferation of the CL6.8 cell line in a time-dependent manner, but with different kinetics. Indeed, after 3 and 5 days of treatment, CL6.8 cells were significantly less sensitive to the inhibition of cell proliferation induced by fulvestrant than MVLN cells (P<0.01), but after 8 days of treatment the inhibitory action of the drug was similar in both cell lines (Fig. 2B). More surprisingly, CL6.7 cells developed total resistance to the compound, as no cytostatic activity of fulvestrant could be observed after any exposure time. The patterns of cell growth observed after exposure to both E2 and fulvestrant for 5 days were identical to those obtained on fulvestrant alone (Fig. 2C), suggesting that in CL6.7 cells, fulvestrant is still able to prevent the E2 stimulation of cell proliferation, but is unable to exert its cytostatic activity. As fulvestrant is known to bind to ERα and to induce the degradation of the receptor via the proteasome (Dauvois et al. 1992, Fan et al. 2003), the loss of fulvestrant-induced ERα degradation in CL6.7 cells would be an obvious explanation for the development of resistance to this molecule. As shown in Fig. 2D, fulvestrant treatment is able to induce a decrease in ERα protein expression in MVLN and CL6.8 cells, as expected, but also in the fulvestrant-resistant CL6.7 cell line. This suggests that...
other unknown mechanisms are involved in the development of resistance to this SERD by CL6.7 cells.

**In vivo**-selected VP cell lines are another breast cancer cell model of cross-resistance to Tam and to fulvestrant

The VP229 cell line was established from a primary breast tumor removed before any pharmacological treatment, whereas VP267 was derived from the same patient after a local recurrence following Tam treatment (McCallum & Lowther 1996). These cells represent another interesting cellular model because they were selected *in vivo* under Tam treatment, but they are still not fully characterized. We explored ERz expression in the two VP cell lines, and we found a down-regulation in VP267 cells compared with VP229 cells, both at the mRNA level (−2.9-fold, Table 2) and at the protein level (Fig. 3A). *ESR2/ERz* mRNA levels were 1000-fold lower than *ESR1/ERα* mRNA levels and no difference in expression was noted between VP229 and VP267 cells (Table 2). The functionality of ERz was shown by the induction of *TFF1* (pS2) gene expression under E2 stimulation in VP229 and VP267 cell lines (+49.1-fold and +13.1-fold respectively, Fig. 3B). ER-driven transcriptional activity was assessed by a gene reporter assay using an ERE-luciferase reporter gene; E2 induced the up-regulation of luciferase activity by approximately fourfold in VP229 cells and a weak but reproducible 1.7-fold up-regulation in VP267 cells (data not shown). Finally, E2 was capable of stimulating the proliferation of both VP229 and VP267 cells, but to a lesser extent in VP267 cells (Fig. 3C). Taken together, these data suggest that VP cell lines express a

### Table 2. Genes differentially expressed at the basal level in the CL6.7 cell line compared with the MVLN cell line, and in the VP267 compared with the VP229 cells

<table>
<thead>
<tr>
<th>Gene name</th>
<th>Symbol</th>
<th>CL6.7/MVLN</th>
<th>VP267/VP229</th>
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<tbody>
<tr>
<td>Estradiol receptors</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Estradiol receptor 1 (ERα)</td>
<td>ESR1</td>
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<td>−2.9</td>
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<tr>
<td>Estradiol receptor 2 (ERβ)</td>
<td>ESR2</td>
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<td>−1.4</td>
</tr>
<tr>
<td>Cell proliferation</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Cyclin A2</td>
<td>CCNA2*</td>
<td>1.2</td>
<td>1.2</td>
</tr>
<tr>
<td>Cyclin B2</td>
<td>CCNB2*</td>
<td>4.2</td>
<td>2.6</td>
</tr>
<tr>
<td>Cyclin E2</td>
<td>CCNE2*</td>
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<td>−5.0</td>
</tr>
<tr>
<td>Cyclin-dependent kinase inhibitor 1A (p21, Cip1)</td>
<td>CDKN1A*</td>
<td>1.5</td>
<td>−1.5</td>
</tr>
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<td>Early growth response 2</td>
<td>EGR2*</td>
<td>−2.3</td>
<td>−7.2</td>
</tr>
<tr>
<td>Growth arrest and DNA-damage-inducible, alpha</td>
<td>GADD45A*</td>
<td>2.0</td>
<td>4.4</td>
</tr>
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<td>IRS1</td>
<td>2.4</td>
<td>9.2</td>
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<td>MAD2L1*</td>
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<tr>
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<td>NOV*</td>
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<tr>
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<td></td>
<td></td>
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<td>Tumor necrosis factor</td>
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<td>3.5</td>
</tr>
<tr>
<td>Tumor necrosis factor receptor 1-associated death domain protein</td>
<td>TRADD*</td>
<td>1.9</td>
<td>1.1</td>
</tr>
<tr>
<td>DNA repair and DNA replication</td>
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<td>Breast cancer, type 2</td>
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<td>−1.6</td>
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<tr>
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<td>1.3</td>
<td>−1.6</td>
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<tr>
<td>RAD51 homolog</td>
<td>RAD51*</td>
<td>−1.9</td>
<td>−2.2</td>
</tr>
<tr>
<td>Topoisomerase (DNA) II α 170 kDa</td>
<td>TOP2A*</td>
<td>1.1</td>
<td>2.5</td>
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</table>

The expression values presented are expressed in terms of fold change (FC) values (calculated by dividing the resistant cell line gene-expression value by the one obtained for the corresponding sensitive cell line) and represent means from at least two independent RTQ-PCR measurements. Gene-expression variation was considered significant for FC ≥ 2 or FC ≤ −2. Upregulations and down-regulations are indicated in bold. Asterisks represent genes on which an estrogen-like gene expression signature under OH-Tam treatment was previously demonstrated by Vendrell et al. (2005).
functionally active ERα. We then explored cell response to OH-Tam and fulvestrant using a cell proliferation assay. VP229 cells, selected from a patient before any pharmacological treatment, were sensitive to the cytostatic action of both molecules (Fig. 3C). Strikingly, VP267 cells issued from a tumor recurrence under Tam treatment developed cross-resistance to both OH-Tam and fulvestrant, and these molecules stimulated VP267 cell proliferation to a degree similar to that induced by E2 (Fig. 3C). As observed for MVLN/CL6.7 cells (Fig. 2D), fulvestrant treatment was capable of inducing a decrease in ERα protein expression in both VP229 and VP267 cell lines (Fig. 3D), suggesting again that the loss of fulvestrant-induced ERα degradation was not involved in the development of resistance to this molecule in VP267 cells.

Figure 2 Pharmacological response of MVLN, CL6.7, and CL6.8 cells under OH-Tam and fulvestrant exposure. (A) Proliferative response of MVLN (white bars), CL6.7 (black bars), and CL6.8 (grey bars) cells grown in DCC medium, then treated for 1, 3, 5, or 8 days with vehicle or 200 nM OH-Tam. (B) Proliferative response of MVLN (white bars), CL6.7 (black bars), and CL6.8 (grey bars) cells grown in DCC medium, then treated for 1, 3, 5, or 8 days with vehicle or 100 nM fulvestrant. (C) Proliferative response of MVLN (white bars), CL6.7 (black bars), and CL6.8 (grey bars) cells treated for 5 days with vehicle, 1 nM E2, 100 nM fulvestrant or E2 + fulvestrant. Results are expressed as means ± s.d. from three independent experiments. *P<0.05, **P<0.01 and ***P<0.001 versus the corresponding MVLN treatment according to Student’s t-test. (D) Western-blot analysis of ERα expression in MVLN, CL6.8, and CL6.7 cells under 100 nM fulvestrant (F) exposure as described in the Materials and methods section using anti-ERα antibody. Expression of α-tubulin was used as invariant control.

Figure 3 ERα expression and pharmacological response of VP229 and VP267 cell lines. (A) ERα protein expression was analyzed as described in the Materials and methods section using anti-ERα specific antibody. Expression of α-tubulin was used as invariant control. (B) TFF1 (pS2) gene expression variations (fold change) measured by RTQ-PCR after 4 days of E2 treatment of VP229 and VP267. (C) Proliferative response (BrdU labeling) of VP229 and VP267 cells treated for 5 days with vehicle, 1 nM E2 (white bars), 100 nM OH-Tam (grey bars), or 1 μM fulvestrant (black bars). *P<0.05 versus the corresponding VP229 treatment according to Student’s t-test. (D) Western blot analysis of the expression of ERα in VP229 and VP267 under 100 nM fulvestrant (F) exposure as described in the Materials and methods section using anti-ERα antibody. Expression of α-tubulin was used as invariant control.
Screening of molecular markers associated with endocrine therapy resistance in MVLN/CL6.7 and VP229/VP267 cells

As described above, while selected under Tam exposure, CL6.7, and VP267 cells also acquired cross-resistance to fulvestrant, characterized by a total abrogation of the SERD’s response. Thus, the combination of CL6.7 and VP267 cells represents a good cellular model for the genomic screening of molecular markers of endocrine resistance with potential clinical relevance. To identify deregulation of gene expression associated with resistance to Tam and/or fulvestrant, we selected 26 candidate genes for RTQ-PCR analysis in MVLN/CL6.7 and VP229/VP267 cells. The genes had been identified in our previous studies as estrogen-modulated or associated with agonist activity of OH-Tam and hyper-response to E2 in OTR breast cancer cell lines (Vendrell et al. 2004, 2005). The genes were selected on the basis of the biological function of the encoded proteins: cell proliferation, transformation, apoptosis, DNA repair, and DNA replication.

Analysis of the resulting RTQ-PCR data allowed the selection of 19 genes (75%) whose expression was deregulated in at least one of the two resistant cell lines (compared with the sensitive control, Table 2). We identified a variable expression (>twofold) of 14 genes (54%) between CL6.7 and MVLN cells and of 13 genes (50%) between VP267 and VP229 cells. Eight genes were similarly deregulated in the two resistant cell lines (overexpression of CCNB2, GADD45A, IRS1, DAP3, and TNF and underexpression of CCNE2, EGR2, and TGFβ2) and thus might represent common molecular mechanisms developed in vivo or in vitro by breast cancer cells to escape Tam and/or fulvestrant treatment.

In our previous work (Vendrell et al. 2005), we demonstrated that OH-Tam stimulates the proliferation of OTR cells, and that this phenotype is associated with the appearance of an estrogen-like gene-expression signature under OH-Tam treatment (i.e. an OH-Tam agonistic action on E2-regulated genes). This was demonstrated for 19 of the 26 genes studied in the present work (genes indicated by asterisks in Table 2). Interestingly, the expression of 13 out of these 19 genes (68%) was also deregulated at the basal level in VP267 and/or CL6.7 cells (i.e. comparison of resistant cells to their respective sensitive untreated counterparts). Taken together, these observations suggest that the occurrence of Tam-resistance has, for some genes, consequences on their expression either in the absence or under stimulation by the drug, and that the overall gene-expression variation identified in this study could represent molecular markers possibly associated with the development of endocrine resistance in breast cancer cells.

mRNA expression of the 19 candidate genes, ESR1/ERα, and MKI67 in 48 breast tumor samples from patients who relapsed or not under Tam treatment

With the aim to investigate the clinical relevance of the 19 genes identified as associated with endocrine resistance in CL6.7 and/or VP267, we explored their expression levels in 48 ER+ breast tumor samples (Table 1) from postmenopausal women treated with primary surgery followed by adjuvant Tam alone. Twenty-four patients developed acquired resistance to endocrine therapy (‘Relapse’ group), as they relapsed under Tam treatment and developed metastases (at 1-3 to 10-0 years from surgery), while 24 patients did not (‘No relapse’ group). Eight out of the 19 candidate genes (42%) were significantly overexpressed in the ‘Relapse’ group compared with the ‘No relapse’ group ($P<0.05$, Kruskal–Wallis test, Table 3): TACC1, NOV, PTTG1, MAD2L1, BAK1, TGFB2, BIRC5, and CCNE2 (Table 3). The capacity of each of these eight genes to discriminate between breast tumors with and without relapse was then tested by ROC curve analysis, i.e. the overall diagnostic values of the eight molecular markers were assessed in terms of their AUC values (Table 3). TACC1, NOV and PTTG1 emerged as the most discriminating markers of relapse on Tam (with ROC-AUC curve values of 0.899, 0.819 and 0.780 respectively). In the same set of 48 ER+ tumors, we also examined the expression of the ESR1/ERα gene and the MKI67 gene (encoding the proliferation-related Ki-67 antigen) and found that their expression was not significantly different in ER+ breast tumors with or without relapse ($P>0.05$, Kruskal–Wallis test, Table 3), suggesting that the eight candidate genes were associated with outcome independently of proliferation and ERα expression status.

Prognostic significance of TACC1, NOV, PTTG1, MAD2L1, BAK1, TGFB2, BIRC5, and CCNE2

We used univariate analysis (log-rank test) to further study the prognostic value of the eight discriminating genes and to investigate whether their expression level is correlated with prognosis and survival (Table 3). For each gene, the 48 ER+ breast tumors were divided into two equal groups of 24 tumors with ‘low’ (lower than the median mRNA level of the 48 breast tumor samples) and ‘high’ (higher than the median mRNA level of the 48 breast tumor samples) mRNA levels. Univariate analysis showed that a high expression level of TACC1, NOV, PTTG1, BAK1 and TGFB2 was correlated with significantly shorter RFS (Table 3). The TACC1 gene emerged as the strongest prognostic marker ($P=0.000014$, log-rank test, Table 3 and Fig. 4A). No significant prognostic value was associated
Table 3  Statistical analysis of mRNA expression of the 19 candidate genes, ESR1/ERα and MKI67 in 24 ER+ breast tumors with relapse under Tam treatment relative to 24 ER+ breast tumors without relapse

| Genes     | No relapse (n=24) | Relapse (n=24) | P
<table>
<thead>
<tr>
<th></th>
<th></th>
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<th></th>
</tr>
</thead>
<tbody>
<tr>
<td>TACC1</td>
<td>1.0 (0.25–4.56)</td>
<td>3.31 (1.11–17.75)</td>
<td>0.0000021</td>
</tr>
<tr>
<td>NOV</td>
<td>1.0 (0.09–5.52)</td>
<td>2.71 (0.76–6.33)</td>
<td>0.00015</td>
</tr>
<tr>
<td>PTTG1</td>
<td>1.0 (0.26–2.01)</td>
<td>1.44 (0.70–13.95)</td>
<td>0.00087</td>
</tr>
<tr>
<td>MAD2L1</td>
<td>1.0 (0.42–6.22)</td>
<td>2.05 (0.17–6.24)</td>
<td>0.005</td>
</tr>
<tr>
<td>BAK1</td>
<td>1.0 (0.57–4.34)</td>
<td>1.58 (0.76–4.68)</td>
<td>0.0059</td>
</tr>
<tr>
<td>TGFβ2</td>
<td>1.0 (0.05–37.84)</td>
<td>1.88 (0.43–24.54)</td>
<td>0.01</td>
</tr>
<tr>
<td>BIRC5</td>
<td>1.0 (0.15–7.65)</td>
<td>1.99 (0.52–17.51)</td>
<td>0.016</td>
</tr>
<tr>
<td>CCNE2</td>
<td>1.0 (0.42–6.22)</td>
<td>2.05 (0.17–6.24)</td>
<td>0.045</td>
</tr>
<tr>
<td>MKI67</td>
<td>1.0 (0.09–5.52)</td>
<td>1.46 (0.38–8.66)</td>
<td>0.066 (NS)</td>
</tr>
<tr>
<td>CCNB2</td>
<td>1.0 (0.12–5.00)</td>
<td>1.40 (0.52–6.83)</td>
<td>0.068 (NS)</td>
</tr>
<tr>
<td>TOP2A</td>
<td>1.0 (0.15–48.89)</td>
<td>1.22 (0.23–14.94)</td>
<td>0.12 (NS)</td>
</tr>
<tr>
<td>RAD51</td>
<td>1.0 (0.36–4.69)</td>
<td>1.35 (0.34–4.35)</td>
<td>0.18 (NS)</td>
</tr>
<tr>
<td>DAF3</td>
<td>1.0 (0.51–1.84)</td>
<td>1.05 (0.42–2.47)</td>
<td>0.38 (NS)</td>
</tr>
<tr>
<td>GADD45A</td>
<td>1.0 (0.42–3.14)</td>
<td>1.08 (0.58–3.54)</td>
<td>0.39 (NS)</td>
</tr>
<tr>
<td>MYBL2</td>
<td>1.0 (0.14–10.25)</td>
<td>1.09 (0.19–22.92)</td>
<td>0.51 (NS)</td>
</tr>
<tr>
<td>TGFB2</td>
<td>1.0 (0.13–4.69)</td>
<td>1.17 (0.36–2.22)</td>
<td>0.58 (NS)</td>
</tr>
<tr>
<td>TNF</td>
<td>1.0 (0.04–2.96)</td>
<td>0.92 (0.05–16.16)</td>
<td>0.79 (NS)</td>
</tr>
<tr>
<td>BIK</td>
<td>1.0 (0.19–2.22)</td>
<td>1.02 (0.23–3.64)</td>
<td>0.98 (NS)</td>
</tr>
<tr>
<td>EGR2</td>
<td>1.0 (0.19–6.92)</td>
<td>0.86 (0.25–5.01)</td>
<td>0.86 (NS)</td>
</tr>
<tr>
<td>IRS1</td>
<td>1.0 (0.11–4.18)</td>
<td>0.88 (0.33–4.12)</td>
<td>0.68 (NS)</td>
</tr>
<tr>
<td>ESR1/ER α</td>
<td>1.0 (0.08–4.01)</td>
<td>0.55 (0.10–2.18)</td>
<td>0.23 (NS)</td>
</tr>
</tbody>
</table>

NS, not significant.

Kruskal–Wallis Test.

Log-rank test.

ROC, receiver operating characteristics; AUC, area under curve analysis.

Log-rank test.

Median (range) of gene mRNA levels (normalized such that the median of the mRNA levels of the six normal breast samples would equal a value of 1).

Not determined.

With BIRC5, nor with MAD2L1 and CCNE2 although there was a trend toward significance (P=0.065 and P=0.059 respectively, log-rank test, Table 3). Hierarchical clustering of the 48 tumor samples based on the expression of TACC1, NOV and PTTG1 allowed the separation of the samples into two groups (groups A and B) with significantly different outcomes (P<0.05; Fig. 4B): group A (n=24) with good clinical outcome (only 3 out of the 24 samples, i.e. 12.5%, belonged to the ‘Relapse’ group and were misclassified) and group B (n=24) with poor clinical outcome (21 out of the 24 samples of this group, i.e. 87.5%, belonged to the ‘Relapse’ group and were thus correctly classified). The prognostic value of this three-gene expression signature was higher than the prognostic value of TACC1 alone (P=0.000017, log-rank test, Fig. 4C). Finally, using a Cox proportional hazards model, we also assessed the prognostic value for RFS of parameters that were significant or near significant (P<0.1) in univariate analysis, i.e. lymph–node status, macroscopic tumor size (Table 1), and TACC1 alone (Fig. 4A) or the three-gene signature (Fig. 4C). Only the prognostic significance of TACC1 alone and the three-gene signature persisted in Cox multivariate regression analysis of RFS (P=0.0002 and P=0.0001 respectively).

mRNA expression of TACC1, NOV, and PTTG1 in response to OH-Tam or to fulvestrant exposure in the sensitive cell line MVLN and the cross-resistant cell line CL6.7

To further investigate the potential endocrine responsiveness of TACC1, NOV, and PTTG1 gene expression, we analyzed by RTQ-PCR the mRNA levels of the three genes in MVLN and CL6.7 cells after 4 days of E2, OH-Tam or fulvestrant treatment (Fig. 5). Like TFF1/pS2 (Fig. 1B), TACC1, NOV, and PTTG1 responded to E2 in both MVLN and CL6.7 cells (greater than twofold regulation; Fig. 5). The expression of TACC1 and NOV was down-regulated under E2 exposure while PTTG1 mRNA levels were up-regulated. In MVLN cells, none of the variations produced by the pharmacological action of E2 were observed on fulvestrant. On the contrary, fulvestrant seemed to display a ‘reversed’ pharmacology, as treatment induced reproducible up-regulation of TACC1 and NOV gene expression (down-regulated by E2). The OH-Tam signature in MVLN cells was different from that of E2 as NOV and PTTG1 genes did not display any variation.

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of expression. It was also different from that of fulvestrant as no ‘reversed’ pharmacology was observed. Finally, we detected in MVLN cells a partial agonistic action of OH-Tam on the TACC1 gene, evidenced by a down-regulated expression on E2 or OH-Tam treatment. Interestingly, the pharmacological responsiveness to endocrine therapy observed for the three genes in MVLN cells was totally impaired in resistant CL6.7 cells. Indeed, in these cells, OH-Tam treatment had no impact on TACC1 gene expression and the ‘reversed’ pharmacology of fulvestrant observed for TACC1, NOV, and PTTG1 in MVLN cells was also totally abrogated. Taken together these data support the hypothesis that TACC1, NOV, and PTTG1 are candidate molecular markers associated with deregulated endocrine therapy responsiveness.

Figure 4 Prognostic value of TACC1 expression or three-gene (TACC1, NOV, and PTTG1) expression signature. (A) Relationship between RFS and TACC1 expression in a series of 48 ER + breast tumor samples. (B) Dendogram of 48 ER + breast tumor samples from patients who relapsed (R, n=24) or did not relapse (NR, n=24) under Tam treatment, constructed by hierarchical clustering according to the expression of TACC1, NOV, and PTTG1, and allowing the emergence of two groups: group A (n=24) and group B (n=24). Percentage of patients who relapsed (R) in groups A and B are indicated on the right. (C) Relationship between RFS and the three-gene expression signature (TACC1, NOV, and PTTG1) in a series of 48 ER + breast tumor samples. Groups A and B correspond to the groups defined in Fig. 4B.
Concordance between mRNA expression levels and protein expression levels of TACC1, NOV, and PTTG1 in cell lines and breast tumor samples

With the aim to assess the functional relevance of the biomarkers identified in this study, we explored the protein expression levels of TACC1, NOV, and PTTG1 using specific commercially available antibodies. We aimed, first, to explore whether the TACC1, NOV, and PTTG1 gene products are expressed at the protein level, and second, whether mRNA and protein levels are concordant. The data presented in Fig. 6A demonstrate that all the deregulations of expression of TACC1, NOV, or PTTG1 genes identified at the basal level in the resistant CL6.7 or VP267 cell lines, when compared with their respective sensitive cell line (Table 2), were validated by western blot analysis. In OH-Tam- or fulvestrant-treated MVLN and CL6.7 cells, most of the deregulated expression of TACC1, NOV, and PTTG1 observed at the mRNA level (Fig. 5) and associated with aberrant endocrine therapy responsiveness was also validated at the protein level by western blot analysis (Fig. 6B). Taken together, these results demonstrate that in MVLN/CL6.7 and in VP229/VP267 cell lines, there is a very good concordance between deregulations of expression of TACC1, NOV, and PTTG1 at the mRNA level and at the protein level.

The expression of the three candidate proteins identified above was assessed by immunohistochemistry, using antibodies directed against TACC1, NOV, or PTTG1, in 10 ER+ breast tumor samples. In contrast to stromal cells, specific positive staining was observed in tumor cells using the antibodies directed against NOV or PTTG1 (Fig. 7). For the two proteins, the staining was localized only within the cytoplasm (Fig. 7). Unfortunately, unspecific staining was obtained with the TACC1 antibody used in this study, thus preventing the interpretation of immunohistochemistry data. Finally, when exploring the mRNA and protein expression levels of NOV and PTTG1 in each of the 10 tumor samples, we found that 80% (8/10) and 70% (7/10) respectively, of the tested samples had been correctly classified into the ‘low’ or the ‘high’ expression groups, both at the mRNA and the protein levels. Altogether, these data demonstrate, first, that TACC1, NOV, and PTTG1 gene products are expressed and, secondly, that there is a good concordance between mRNA and protein levels for TACC1, NOV, and PTTG1 in breast cancer cell lines, and at least for NOV and PTTG1 in breast tumor samples.

Discussion

Impressive early results obtained with tamoxifen in the adjuvant setting led clinicians to use tamoxifen as neoadjuvant therapy to avoid surgery in elderly women with ER+ cancer (Horobin et al. 1991). However, long-term follow-up and clinical trials have demonstrated that up to 62% of cancers initially responsive to endocrine therapy subsequently escape control, with the patient requiring salvage surgery (Horobin et al. 1991, Fennessy et al. 2004). With the aim to circumvent the development of endocrine resistance and to delay chemotherapy, several clinical trials have investigated the best sequence of administration of the different molecules available for endocrine therapy as first-, second-, or third-line treatment (Howell et al. 2002, Osborne et al. 2002, Dodwell &
Treatment with the SERD fulvestrant has proven effective upon progression on Tam but, as for Tam treatment in advanced breast cancer, resistance will inevitably occur. The molecular changes associated with fulvestrant resistance are only beginning to emerge, but previous studies have identified several proteins possibly associated with the fulvestrant resistant phenotype in cell lines: EGFR, Erbb2, Erbb3, and Erk (McClelland et al. 2001, Fan et al. 2006a, Frogne et al. 2008), Akt (Frogne et al. 2005), and NFκB (Gu et al. 2002). One study has analyzed global gene expression in Tam-resistant and fulvestrant-resistant MCF-7 cells and suggested that while Tam resistance preferentially alters the expression of genes downstream of ER, fulvestrant resistance is characterized by a strong remodeling of gene expression (Fan et al. 2006a).

As fulvestrant is now approved for second-line treatment after failure of Tam or aromatase inhibitors, the next challenge is identifying molecular changes associated with the development of cross-resistance to fulvestrant and thus valuable cellular models for fulvestrant cross-resistance acquisition are urgently needed. The development of such a phenotype is rarely described, as noted above. Only few studies have reported the decreased sensitivity of Tam-resistant breast cancer cells or xenografts to fulvestrant (Lykkesfeldt et al. 1994, Naundorf et al. 2000), but none, to our knowledge, has demonstrated the total loss of sensitivity to this SERD.

Our data show for the first time that both MVLN/CL6.7 and VP229/VP267 cell lines are valuable cellular models to investigate cross-resistance to endocrine therapy. Indeed, while selected in the presence of OH-Tam (or Tam) alone, CL6.7 and VP267 cells acquired cross-resistance to fulvestrant, characterized by the total loss of fulvestrant response. Our study also demonstrated that such phenomenon can occur under in vitro (MVLN/CL6.7 cells) or in vivo (VP229/VP267
cells) selection. We also showed that acquisition of such phenotype was not due to any loss in ERα functionality or any loss in fulvestrant binding to ERα. Finally, our study also suggests that under the same selection process (OH-Tam selection), the resulting resistant cellular clones can display different endocrine therapy resistance phenotypes, as demonstrated for the two cellular clones CL6.8 and CL6.7 which, while issued from the same selection process (Vendrell et al. 2005), developed different modes of acquisition of resistance to endocrine therapy: OH-Tam resistance only (CL6.8 cells) or cross-resistance to OH-Tam and fulvestrant (CL6.7 cells). This probably reflects the heterogeneity of breast cancer cells in tumors having acquired resistance to first-line Tam endocrine therapy and thus suggests that, in these tumors, cells that will be refractory to fulvestrant second-line therapy are already present after the first selection. This has important clinical consequences because, while the difference between the mechanisms of action of Tam and fulvestrant (Wakeling et al. 1991, Tzukerman et al. 1994, McDonnell et al. 1995, Dowsett et al. 2005) supports the use of fulvestrant as second-line treatment in Tam-resistant patients (Howell et al. 2002, Osborne et al. 2002), cross-resistance to fulvestrant may also occur in Tam-resistant patients. Thus, there is a pressing need for identifying general biomarkers of endocrine therapy resistance to help in the clinical management of such patients.

As MVLN/CL6.7 cells and VP229/VP267 cell lines are original and valuable models of cross-resistance to Tam and fulvestrant, identifying gene expression deregulations in these cell lines would represent a significant step towards the identification of new biomarkers. Of the 26 genes screened by RTQ-PCR, 19 displayed a deregulation of expression in at least one of the two cross-resistant cell lines tested, and two, TGFβ2 and TGFBR2, have also been recently identified in in vitro models of Tam- or fulvestrant-resistance (Fan et al. 2006a). Several genes (CCNB2, CCNE2, EGR2, GADD45A, IRS1, DAP3, TGFβ2, and TNF) which were found similarly deregulated in both resistant cell lines, might represent common molecular mechanisms developed in vivo and in vitro by breast cancer cells to escape Tam and/or fulvestrant treatment. Indeed, all of these genes belong to two functional clusters previously described as associated with poor endocrine response (Paik et al. 2004, Jansen et al. 2005, Chanrion et al. 2008): CCNB2, CCNE2, EGR2, GADD45A, and IRS1 belong to the cell proliferation functional cluster and DAP3, TGFβ2, and TNF to the apoptosis functional cluster. A supporting observation is that CCNB2 has previously been described as part of a 36-gene signature predictive of Tam recurrence (Chanrion et al. 2008).

In a well-defined cohort of 48 relapsing or non-relapsing ER+ postmenopausal breast cancer patients treated with primary surgery followed by adjuvant Tam alone, we found that 8 out of the 19 genes selected on cross-resistant breast cancer cells (TACC1, NOV, PTTG1, MAD2L1, BAK1, TGFβ2, BIRC5, and CCNE2) were significantly overexpressed in the group of patients who relapsed under Tam treatment (P<0.05, Kruskal–Wallis test). Interestingly, 3 out of these 8 are mitotic checkpoint genes (TACC1, PTTG1, and MAD2L1).
BIRC5 also belongs to the 21-gene Tam recurrence signature described by Paik and colleagues (Paik et al. 2004), and CCNE2 to the 70-gene prognostic signature identified by van ’t Veer et al. (2002).

In the present work, multivariate analysis demonstrated that TACC1 alone and the three-gene expression signature TACC1, NOV, and PTTG1 were independent prognostic markers (log-rank test, Cox multivariate analysis). The transforming acidic coiled coil 1 (TACC1), which emerged as the strongest prognostic marker, is a putative oncogene located within a breast cancer amplicon found on human chromosome 8p11 (Still et al. 1999) which we have previously identified as a new estrogen-regulated gene (Vendrell et al. 2004). The TACC1 protein is involved in mitotic checkpoint regulation through stabilization of microtubules in the growing spindle; and interacts with the Aurora A/STK6 kinase (Conte et al. 2003). TACC1 can transform fibroblasts (Still et al. 1999), and recent work has shown that it promotes transformation and mammary tumorigenesis through positive regulation with the Ras and PI3K signaling pathways (Cully et al. 2005), both also involved in the development of Tam resistance (for review, Moy & Goss 2006). More interestingly, high levels of amplification of the 8p11 region (encoding the TACC1 gene) have been significantly associated with reduced survival duration or distant recurrence in breast cancer (Chin et al. 2006). NOV (neuroblastoma overexpressed gene), which encodes a negative regulator of cell proliferation, can be involved in tumorigenesis (Scholz et al. 1996). In a previous work, we have identified NOVs as a new estrogen-regulated gene (Vendrell et al. 2004) and also a gene on which Tam exerts an estrogen-like activity in Tam-resistant breast cancer cells (Vendrell et al. 2005).

Several studies have reported an association between low expression levels of NOV and progression of adenocortical tumors (Martinere et al. 2001), renal cell carcinoma (Niu et al. 2005), and poor breast cancer prognosis (Jiang et al. 2004). In this study, we show that high expression levels of NOV are associated with endocrine therapy cross-resistance in CL6.7 cells (Table 2) and endocrine therapy resistance in breast tumor samples (Table 3). Further investigations are needed to explain this specific point. Finally, PTTG1 (pituitary tumor-transforming gene 1, also called Securin) encodes a regulatory protein that plays a central role in mitotic checkpoint control, chromosome stability, the p53 pathway and DNA repair. PTTG1 negatively regulates the transcriptional activity and related apoptotic activity of p53, which explains the strong transforming capability of this protein when it is over-expressed (Bernal et al. 2002). In a previous work, we have demonstrated that PTTG1 gene expression is associated with hypersensitivity to E2 and agonist-like activity of Tam in Tam-resistant breast cancer cells (Vendrell et al. 2005). Recently, two single-nucleotide polymorphisms in the PTTG1 gene have been associated with increased risk of breast cancer (Lo et al. 2007). Furthermore, increased expression of PTTG1 has been correlated with poor prognosis in glioma patients and in hepatocellular carcinoma (Fujii et al. 2006, Genkai et al. 2006).

Taken together, these data provide evidence that TACC1, NOV, and PTTG1 genes are new biomarkers associated with endocrine therapy resistance in breast cancer. None of these three genes belongs to the 21-gene Tam recurrence signature described by Paik and colleagues (Paik et al. 2004), to the gene expression signature that predicts the clinical outcome of breast cancer patients treated with tamoxifen (Jansen et al. 2005), to the two-gene signature described by Ma and colleagues (Ma et al. 2004), or to the predictive gene expression signature of Tam recurrence defined more recently by Chanrion and colleagues (Chanrion et al. 2008). Fan et al. (2006b) have compared the predictions derived from five gene expression profiling studies and suggested that, even though there is little gene overlap between the different studies using different algorithms, the outcome predictions are similar and probably track the same phenotype. This suggests that although there is no overlap between the present study and other published studies, the three genes selected here may still be compatible. The supporting argument is that these three genes belong to a functional cluster (proliferation/transformation) present in previously published classifiers (van ’t Veer et al. 2002, Paik et al. 2004, Jansen et al. 2005, Chanrion et al. 2008).

In conclusion, the identification of more specific new markers to better predict breast cancer outcome and response to endocrine therapy appears fundamental and clinically useful, as it would allow personalizing the patient’s treatment. Genomic approaches based on large-scale experiments have been successfully used in breast cancer tumors to identify prognostic markers such as aberrant gene expression signatures or genomic alterations associated with Tam failure (Ma et al. 2004, Paik et al. 2004, Jansen et al. 2005, Han et al. 2006, Chanrion et al. 2008). An alternative approach is based on the exploration of a limited number of candidate genes by RTQ-PCR. This technique, which focuses on a small number of genes, has already proved useful for the identification of candidate gene expression signatures with prognostic significance. Using RTQ-PCR, Paik and colleagues have been able to identify a 21-gene signature that could predict recurrence of tamoxifen-treated breast cancer (Paik et al. 2004). In this study, we selected candidate genes identified by previous cDNA array experiments and we explored by RTQ-PCR their expression in cellular models of endocrine therapy cross-resistance and in breast tumor samples. We were able to identify TACC1, NOV, and PTTG1 as prognostic markers associated with endocrine therapy resistance in breast tumor samples. Future work on a larger cohort is needed to validate their prognostic value but also their
predictive value for fulvestrant response in patients developing resistance to first-line Tam treatment. Moreover, as aromatase inhibitors may replace Tam for first-line therapy in postmenopausal women, investigating the expression of these new biomarkers in aromatase inhibitor-resistant breast tumor samples would be very informative, as it would allow to delineate the overlap between expression signatures of resistance to ER-ligands (Tam and fulvestrant) and to aromatase inhibitors. Encouraging results have been obtained, since we have shown a good correlation between the mRNA and protein levels of TACC1, NOV, and PTTG1 in cell lines and/or breast tumor samples, suggesting that they could be considered as candidate protein markers for immunohistochemical analysis. The present work is thus a first step towards the identification of new biomarkers associated with endocrine resistance that could be used in the clinical management of ER+ breast cancer patients.

Declaration of interest

All co-authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research report.

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