Loss of Coordinated Androgen Regulation in Nonmalignant Ovarian Epithelial Cells with BRCA1/2 Mutations and Ovarian Cancer Cells

Andreas Evangelou, Michelle Letarte, Igor Jurisica, Mujahid Sultan, Kathleen J. Murphy, Barry Rosen, and Theodore J. Brown

Cancer and Blood Research Program, The Hospital for Sick Children [A. E., M. L.]; Division of Reproductive Science, The Samuel Lunenfeld Research Institute, Mt. Sinai Hospital [A. E., T. J. B.]; Divisions of Cancer Informatics [I. J., M. S.] and Gynecology Oncology [K. J. M., B. R.], Ontario Cancer Institute/Princess Margaret Hospital, University Health Network; and the Departments of Zoology [A. E., T. J. B.], Obstetrics and Gynecology [M. L., T. J. B.], Computer Science [I. J.], Medical Biophysics [M. L., I. J.], and Immunology [M. L.], University of Toronto, Toronto, Ontario MSG 1X5, Canada

ABSTRACT

Epidemiological studies have implicated androgens in the etiology/progression of epithelial ovarian cancer. Because normal and malignant ovarian epithelial cells are growth inhibited by transforming growth factor (TGF-β), we tested the ability of 5α-dihydrotestosterone (DHT) to modulate this response and the expression of TGF-β receptor types I and II. Cells derived from the ovarian surface epithelium of women undergoing oophorectomy (n = 7) for nonovarian indications or with a germ-line BRCA1 or 2 mutation (n = 9), and from the ascitic fluid of patients with primary ovarian cancer (n = 8) were cultured with and without DHT. Cell proliferation after TGF-β1 or vehicle treatment was determined, and transcripts for TGF-β receptors were measured by quantitative reverse transcription-PCR. As low levels of androgen receptor were observed in the current study, we also measured transcript levels for steroid receptor coactivators SRC-1, ARA70, and AIB1. TGF-β1 inhibited growth in 12 of 13 cultures tested, and DHT generally reversed this effect, demonstrating that androgens can block TGF-β-induced growth inhibition in both malignant and nonmalignant ovarian epithelial cells. Transcripts for TGF-β receptors, SRC-1, and ARA70 were found to be coordinately regulated by androgen in control cells, but not in either malignant or BRCA1/2-positive cell cultures. These findings raise the possibility that by modulating steroid receptor coactivator expression, androgen might affect other hormonal responses and contribute to the initiation of ovarian cancer.

INTRODUCTION

Despite the introduction of diverse and powerful chemotherapeutic agents, the survival rate for epithelial ovarian cancer has changed little over the past 20 years. In 2000 alone, ovarian cancer was diagnosed in 30,000 North American women and caused 15,400 deaths (1, 2). At the current time, a family history of ovarian or breast cancer is associated with the greatest increase in risk (3). Mutations in BRCA1 and BRCA2 genes account for the majority of inherited predisposition to this disease, with carriers of germ-line mutations having an estimated lifetime risk of 28% and 21%, respectively, for developing ovarian cancer (4, 5).

Numerous studies indicate that the ovarian steroid milieu may influence the initiation or progression of epithelial ovarian cancer and support a role for androgens (reviewed in Ref. 6). The majority of ovarian cancer is diagnosed after menopause, when the balance of ovarian steroid production shifts from estrogens to androgens. Women with high serum androgen levels (pre- or postmenopausal) or polycystic ovarian disease (associated with anovulation and overproduction of ovarian androgens) have an increased risk of developing ovarian cancer (7, 8). Ovarian epithelial cells and up to 95% of ovarian epithelial tumors express AR3 (9–12), indicating that these cells are directly responsive to androgens.

AR is a ligand-activated nuclear transcription regulatory factor that acts by binding to response elements in the regulatory region of target genes where it interacts with transcription factors to modulate gene expression. Steroid receptor coactivators, of which SRC-1 has been best studied, act as bridging proteins between the receptor and the transcription initiation complex (13, 14) and enhance the transactivational activity of the receptor in part via direct or indirect acetylation of histones (15, 16). Two steroid receptor coactivators have been reported to be up-regulated in ovarian cancer. AIB1 (amplified in breast cancer 1), which enhances ER-dependent transactivation, was amplified in 25% of sporadic ovarian cancer (17, 18) and ARA70 (AR-assOCIating protein 70), which has a predilection for AR, was up-regulated in ovarian carcinomas examined by in situ hybridization (19). Increased expression of ARA70 or AIB1 in steroid-sensitive cells could significantly magnify their steroid response pattern, thereby altering growth regulation and contributing to the development or progression of malignancy.

Additional support for a role of androgen in ovarian cancer came from the study of a polymorphic region in the AR NH2-terminal domain, consisting of a variable number of CAG repeats. A shorter CAG repeat tract, which correlates with increased transactivational activity of the receptor (20), is associated with an earlier onset (by 7 years) of both sporadic and familial ovarian cancer (21).

One mechanism by which androgens might influence the growth of ovarian cancer cells is by modulating their sensitivity to TGF-β, a potent inhibitor of epithelial cells, including malignant and nonmalignant ovarian cells (22–24). Decreased expression or mutations in TGF-β receptor type I and/or II (TβR-I and TβR-II) have been observed in various malignancies, which render the cells unresponsive to the growth inhibitory effects of TGF-β (25–27) and may contribute to cancer initiation or progression. The vast majority of ovarian cancer cells isolated from patient ascites were growth-inhibited by TGF-β in culture (22–24) indicating an intact signaling cascade and suggesting that mechanisms to suppress the actions of TGF-β must exist in vivo. That androgen exposure might represent one such mechanism is supported by our previous work. We showed that treatment of HEY and SKOV-3 ovarian cancer cell lines with DHT, a nonaromatizable androgen, down-regulated the expression of TGF-β receptors (28).

To determine the effect of androgens on modulation of growth and TGF-β receptor expression, cultures of cells derived from the ovarian surface epithelium of women undergoing oophorectomy for nonovarian indications (OSE), or with a confirmed germ-line BRCA1 or BRCA2 mutation (OSEb), and from the ascitic fluid of patients with primary ovarian cancer were maintained in the presence or absence of 10 nM DHT, to mimic in vivo contact with androgen. Because these cells expressed low amounts of AR, levels of transcripts for the
coactivators ARA70, SRC-1, and AIB1 were also measured. Our results show that androgens modulate the growth response to TGF-β1 in both malignant and nonmalignant ovarian epithelial cells, and after the expression of TβRI and TβRII, as well as the coactivators studied. The expression of TβRI, TβRII, ARA70, and SRC-1 was coordinately regulated by androgen in OSE cultures but not in OVCAS cultures. Remarkably, this coordinate regulation was also lost in OSEb cultures. These findings suggest that altered androgen responses may occur in the ovarian epithelium of some patients with BRCA1 or 2 mutations and play a role in ovarian carcinogenesis.

MATERIALS AND METHODS

Patients and Cell Cultures. Cell cultures were derived from surgical material obtained over an 18-month period from 24 patients. Clinical information on these patients is summarized in Table 1. The mean patient age was 59.6 ± 6.3, 53.9 ± 3.0, and 63.6 ± 4.2 years (+SE) for OSE, OSEb, and OVCAS patients, respectively. The majority of patients were postmenopausal, 7 were premenopausal, and 1 OVCAS patient (OVCAS-27) was perimenopausal (Table 1).

OSE cultures were derived from patients with nonmalignant ovaries who were undergoing surgery for uterine/cervical tumors or for a dermatomy. Eight OSEb samples were obtained from women undergoing prophylactic oophorectomy because of a confirmed germ-line BRCA1 or BRCA2 mutation. The following germ-line mutations were detected: 6174delT (OSEb-7), 49 Post Prophylaxis/breast adenocarcinoma

Five OSEb samples were obtained from women undergoing prophylactic oophorectomy because of a confirmed germ-line BRCA1 or BRCA2 mutation. The following germ-line mutations were detected: 6174delT (OSEb-7), 49 Post Prophylaxis/breast adenocarcinoma

<table>
<thead>
<tr>
<th>Culture</th>
<th>Patient age</th>
<th>Menopausal status</th>
<th>Reason for surgery/other malignancies</th>
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<tbody>
<tr>
<td>OSE-21+</td>
<td>56</td>
<td>Pre</td>
<td>Cervix mucinous adenocarcinoma</td>
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<tr>
<td>OSE-22</td>
<td>66</td>
<td>Post</td>
<td>Cervix squamous carcinoma-in-situ</td>
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<tr>
<td>OSE-30</td>
<td>54</td>
<td>Post</td>
<td>Cervix recurrent carcinoma-in-situ</td>
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<tr>
<td>OSE-32</td>
<td>43</td>
<td>Pre</td>
<td>Right ovarian dermoid cyst</td>
</tr>
<tr>
<td>OSE-38</td>
<td>66</td>
<td>Post</td>
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</tr>
<tr>
<td>OSE-43</td>
<td>62</td>
<td>Post</td>
<td>Uterine endometriod carcinoma grade 1/3</td>
</tr>
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<td>70</td>
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<td>OSEb-12</td>
<td>61</td>
<td>Post</td>
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<td>46</td>
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<td>Pre</td>
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<td>48</td>
<td>Pre</td>
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<td>43</td>
<td>Post</td>
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</tr>
<tr>
<td>OVCAS-19</td>
<td>80</td>
<td>Post</td>
<td>OC (grade 3 endometrioid)</td>
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<td>60</td>
<td>Post</td>
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<td>44</td>
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<tr>
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<td>51</td>
<td>OC</td>
<td>(grade 3 papillary serous)</td>
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OSEb samples were obtained from women undergoing prophylactic oophorectomy because of a confirmed germ-line BRCA1 or BRCA2 mutation. The following germ-line mutations were detected: 6174delT (OSEb-7), 49 Post Prophylaxis/breast adenocarcinoma

Table 1: Summary of patient clinical data

* OSE, ovarian surface epithelium cases derived from patients with normal ovaries; OSEb, those derived from patients with BRCA1/2 patients; OC, ovarian cancer. FBOC, familial breast/ovarian cancer history; FOC, familial ovarian cancer history; MMMT, mixed malignant Mullerian tumor.

All of the cells were grown in DMEM/F12 medium without phenol red and supplemented with 3% charcoal-stripped fetal bovine serum, 5 μg/ml insulin, 5 × 10−3 m ethanolamine, 5 ng/ml epidermal growth factor, 5 × 10−5 m phosphoethanolamine, 10 μg/ml transferrin, 50 units/ml penicillin, 50 μg/ml streptomycin, and 0.625 μg/ml amphotericin B (Fungizone) at 37°C in a humified 5% CO2 atmosphere. All of the cultures were maintained in the presence or absence of 10 nm DHT (Sigma Chemical Co., St. Louis, MO) added daily. DHT was dissolved in ethanol and diluted with medium to a final ethanol concentration of 0.001%. All of the experiments were carried out with low passage (one to four) cultures.

Flow Cytometry. Cells were washed twice with PBS, detached with 0.25% trypsin-EDTA, and resuspended in 0.1% BSA in PBS (0.1% BSA/PBS). Cells were incubated for 45 min at 4°C with saturating amounts of mAbs to HLA class I (4D6; Ref. 30), MUC-1 (2G3; Ref. 31), or ovarian cancer (Ref. 32, donated by Dr. Alexander Marks, University of Toronto, Toronto, Ontario, Canada); hyaluronic acid receptor CD44 (50B4; Ref. 33), integrin subunits α2 (P166; Telios, La Jolla, CA), α3 (P1B5; Telios), α5 (IB5; donated by Dr. John Wilkins, University of Manitoba, Winnipeg, Manitoba, Canada), and β1 (4B4; Coulter Clone, Fullerton, CA) or control nonimmune murine IgG1. After two washes with 0.1% BSA/PBS, the cells were incubated with FITC-conjugated affinity-purified goat F(ab')2, antimouse IgG (BIOSOURCE International, Camarillo, CA) at 20 ng/ml for 45 min at 4°C in the dark. After washing twice with PBS, cells were stained with propidium iodide to allow for gating of viable cells during analysis by FACScan with CellQuest software (Becton Dickinson, Mountain View, CA). For each cell surface antigen, mean fluorescence intensity and percentage of positive cells were determined by setting the gates such that <5% cells were positive when stained with control nonimmune IgG1.

Cell Proliferation Assays. Cell proliferation was assessed using a hemocytometer with four replicates per treatment group. Cells maintained in the presence of 10 nm DHT or ethanol vehicle were seeded at 15,000–50,000 cells/well in 24-well plates. TGF-β1 (R&D Systems, Minneapolis, MN), diluted in culture medium, was added every 48 h beginning at time zero, and 10 nm DHT was added every 24 h during the proliferation assays. A dose of 25 pm TGF-β1 was found to be optimal for OVCAS growth inhibition (28). Results are expressed as percentage of control (no DHT or TGF-β1).

Quantitative RT-PCR. Cell cultures were washed in ice-cold PBS and total cellular RNA was isolated using TRIzol Reagent (Invitrogen Corp., Carlsbad, CA) according to manufacturer instructions. The RNA concentration in all of the samples was measured spectrophotometrically in two independent determinations and at three dilutions. cDNAs were generated using Superscript II reverse transcriptase (Life Technologies, Inc., Burlington, Ontario, Canada) and an oligo-dT-primer/primer pair (Pharmacia, Piscataway, NJ).

Quantitative analysis of PCR products was performed according to Murphy et al. (34) with modifications. Selected primers used for amplification of TβRI, TβRII, ARA70, and β-actin cDNA were as reported previously (28, 35). Primers selected for amplification of SRC-1, 5′-TCTGCCTCTGCTA-ACTCTCA-3′ (forward) and 5′-TCAAGGTCAGCTGTAACCTGG-3′ (reverse), and of AIB1, 5′-GGGCAGATTGAACCTATGAA-3′ (forward) and 5′-AGGAGATTCCAAAGAGGGC-3′ (reverse), produced 440 and 320 bp PCR products, respectively. PCR amplification conditions were as described previously (28, 35) with an annealing temperature of 58°C and 28 cycles. Aliquots (20 μl) of the PCR products were fractionated by electrophoresis on
2% agarose gels and detected with SYBRgold (Molecular Probes, Eugene, OR). The gel image was digitized, and the net intensity of each band was analyzed by computer-assisted densitometry using IDImage Analysis Software (Kodak Digital Science, Scientific Imaging Systems, Eastman Kodak Company, Rochester, NY). Data were plotted as the log of densitometric units against the log of equivalent RNA concentration to identify a linear range of exponential amplification. Linear regressions were obtained using SigmaPlot Scientific Graphing Software (version 2.0; Jandel Corporation, San Rafael, CA). The amount of total equivalent RNA estimated from the linear range of amplification after DHT treatment was expressed as a percentage of that measured in cells treated with ethanol vehicle (control). All of the measurements were corrected for β-actin expression.

For detection of AR mRNA, cDNA equivalent to 100 ng of reverse-transcribed RNA was subjected to PCR using an annealing temperature of 64°C, 30 cycles, and primers described previously (28) to yield a 1031-bp PCR product. As a control for the amount of RNA, β-actin was detected in the same cDNA samples, as described above, except that ethidium bromide was used to visualize the PCR products in the agarose gels.

Data Analysis. Data obtained from cell proliferation assays were subjected to ANOVA using SPSS for Windows statistical software (Version 10.0.7; SPSS Inc., Chicago, IL). Additional group comparisons were made using Duncan’s Multiple Range Test at the P < 0.05 level. Quantitative RT-PCR data for the two-dimensional correlation analysis were analyzed by Simple Linear Regression to determine the correlation coefficients using SigmaStat for Windows statistical software (Version 1.0; Jandel Corporation). A pseudocolor matrix was generated using Matlab R12 software (MathWorks Inc., Natick, MA) to display all of the correlations for TγR-I, TγR-II, SRC-1, AIB1, and ARA70 mRNA expression levels within OSE, OSEb, and OVCAS cultures.

A BTSVQ method (36) was used to cluster the cultures based on the effects of DHT on TγR-I, TγR-II, SRC-1, AIB1, and ARA70 mRNA expression. This method combines a partitive k-means clustering and a SOM algorithm. Briefly, the quantitative RT-PCR data set was log-normalized and analyzed by BTSVQ. First, we organized cultures into a binary cluster tree by using the quantitative RT-PCR data set was log-normalized and analyzed by the k-means algorithm. Then, we applied SOM to cluster cultures based on their quantized gene expression profiles. Partitive clustering results were cross-verified with the clusters generated by SOMs.

RESULTS

Phenotypic Characterization of Low Passage Ovarian Epithelial Cell Cultures. The epithelial nature of all of the ovarian cell cultures was analyzed by flow cytometry using mAbs 2G3 and M2A, which react specifically with epithelial cell surface MUC-1 and oncofetal antigens, respectively. The mAb 2G3 reacts with a carbohydrate epitope of normal MUC-1 and with hypoglycosylated forms on malignant cells (37–39), whereas mAb M2A, produced against an ovarian epithelial carcinoma cell line, reacts with the monomeric sialoglycoprotein (32). Representative profiles of 2G3 and M2A immunostaining are shown in Fig. 1. All of the OSE, OSEb, and OVCAS cultures tested were positive for 2G3 and M2A surface antigens, confirming their epithelium origin. The level of oncofetal antigen was generally higher than the MUC-1 level, and DHT treatment did not alter their expression. All of the cell cultures analyzed also expressed HLA class I antigen, used as a positive control in the experiments.

The metastatic spread of ovarian cancer cells into the peritoneal cavity is dependent on β1-integrins and CD44 (40, 41). We characterized by flow cytometry the expression of α2–, α3–, α5–, and β1-integrins, and CD44 on the surface of OSE, OSEb, and OVCAS cells maintained in the presence or absence of DHT. Representative profiles are shown in Fig. 1. All of the cultures analyzed expressed high levels of β1-, α2-, and α3-integrins, as well as CD44. However, OVCAS cultures consistently expressed higher levels of α5-integrin than did OSE and OSEb cultures, which showed very low to nondetectable levels of this integrin. These data support previous observations of expression of functional α5β1 integrin on ovarian cancer cells (40, 41). DHT treatment did not affect integrin and CD44 levels in any of the cases studied.

Expression of AR was assessed by RT-PCR in all of the cultures but OSEb-16, -17, and -19. A low level of expression was found in all of the cultures tested, consistent with our previous findings in ovarian cancer cell lines (28). We demonstrated previously that identical results were obtained using sets of primers spanning AR exons 1–4, 4–7, and 1–7, respectively (28), and use routinely the 1031-bp PCR product, corresponding to exons 1–7. This product was detected after staining of the gel with SYBRgold (Fig. 2), a sensitive fluorescent DNA dye, but not with ethidium bromide (data not shown). β-Actin mRNA expression was readily detected with ethidium bromide confirming RNA integrity and efficient reverse transcription in all of the samples.

Reversal of TGF-β1 Growth Inhibition by Androgen. The ability of DHT treatment to reverse the growth-inhibitory effect of TGF-β1 was tested in several cultures of ovarian epithelial cells. In control cultures maintained in the absence of DHT, TGF-β1 inhibited the growth of 5 of 5 OVCAS by 40–50%, of 5 of 6 OSE by 30–60%, and of 2 of 2 OSEb cultures by 40–50% (Fig. 3). Maintenance of the cells in DHT blocked the growth-inhibitory effect of TGF-β1 in 4 of 5 OVCAS, 3 of 5 OSE, and 1 of 2 OSEb cultures (Fig. 3). A significant increase in proliferation by DHT was observed for OSE-30

Fig. 1. Representative flow cytometry profiles of MUC-1, M2A oncofetal antigen, CD44, and integrins on ovarian epithelial cells from a control (OSE-38), a patient with a BRCA1 mutation (OSEb-41), and from ascites of a patient with ovarian cancer (OVCAS-27), maintained in the presence (heavy lines) or absence (dotted lines) of 10 nM DHT. HLA class I antigen staining defines the region of positive cells. The gate was set using isotype control IgG1 such that <5% cells fell within the positive gate. Cells were analyzed immediately using propidium iodide to allow for gating of viable cells.
Correlation between Androgen-induced Modulation of TGF-β Receptors and Steroid Receptor Coactivators in OSE, OSEb, and OVCAS Cultures. In view of the multiple effects of DHT observed on TGF-β receptors and AR coactivators, the percentage of changes in mRNA levels were subjected to linear regression analysis. In OSE cultures, the change in expression of TβR-I was significantly correlated with that of TβR-II (Fig. 6). However, this correlation was not observed in OSEb or OVCAS cultures. In addition, changes in SRC-1 mRNA levels correlated with changes in TβR-II and ARA70 in OSE cultures (Fig. 6). Again, these correlations were not observed in OSEb and OVCAS cultures. These results suggested that TGF-β receptors and the AR coactivators ARA70 and SRC-1 were coordinately regulated by androgen in OSE but that this normal mechanism was lost in OSEb and OVCAS.

To visualize the complex pattern relating the effects of DHT on TGF-β receptor and steroid receptor coactivator gene expression, a pseudocolor matrix of correlation values was constructed (Fig. 7A). An intriguing pattern developed between the different groups of patients. The effects of DHT on the expression levels of all of the genes except AIB1 were highly correlated in OSE cultures but not in OVCAS cultures. Interestingly, OSEb cultures displayed a pattern similar to OVCAS and distinct from OSE cultures. This suggests that ARA70, SRC-1, TβR-I, and TβR-II are coordinately regulated by androgen in nonmalignant ovarian epithelial cells, and that this coordination is lost in malignant cells and in ovarian epithelial cells with a predisposition to malignant transformation.

To determine how individual cultures are distributed relative to one another based on their altered expression of AIB1, ARA70, SRC-1, TβR-I, and TβR-II in response to DHT, a BSVQ method of data clustering was used (36). A tree-structured visualization revealed that, with few exceptions, OSE and OVCAS cultures partitioned to separate arms of the tree (Fig. 7B). OSEb cultures partitioned with both 4. Androgen-induced Modulation of Steroid Receptor Coactivators ARA70, SRC-1, and AIB1. Several coactivator proteins have been identified that can interact with steroid receptors to increase their transcriptional activity, including ARA70, SRC-1, and AIB1. We examined the effect of DHT on the levels of mRNA for these steroid receptor coactivators. A summary of these results is shown in Table 2, and representative experiments are illustrated in Fig. 5. In general, the levels of ARA70 and AIB1 mRNA expression in controls were ~2-fold higher in OVCAS than in OSE or OSEb cultures, whereas levels of SRC-1 did not appear to change significantly between these groups.

DHT reduced ARA70 and SRC-1 mRNA levels in 3 OVCAS and AIB1 mRNA in 5 OVCAS to ~60% of control values. In contrast, DHT up-regulated the expression of AIB1 mRNA by ~3-fold in OVCAS-34. In OSE cultures, treatment with DHT down-regulated the expression of ARA70, SRC-1, and AIB1 mRNA levels in 3 cultures to ~60% of control. ARA70 mRNA was increased ~2-fold in 2 cases, whereas SRC-1 mRNA was increased 4-fold in OSE-32, and AIB1 mRNA was increased 2-fold in OSE-30. For the OSEb cultures, DHT treatment increased ARA70 mRNA >2-fold in OSEb-23, SRC-1 mRNA by 2.7-fold in OSEb-41, and AIB1 mRNA by 2–6-fold in 3 cases.
OSE and OVCAS cultures, 3 clustered tightly with 5 of the OVCAS cultures, whereas the remainder clustered with the OSE cultures (Fig. 7B).

A pseudocolor distance matrix shown in Fig. 7C was used to visualize the partitioning of individual OSEb cultures relative to OSE and OVCAS using a SOM algorithm. OSEb cultures partitioned as three distinct groups. One group of 3 OSEb cultures (OSEb-7, -12, and -14) were indistinguishable and clustered with 2 OSE cultures (-30 and -36), and less closely with OSEb-45 and OVCAS-24 cultures. The 3 OSEb cultures with BRCA2 mutations (7, 17, 16) did not partition as a distinct group.

**DISCUSSION**

Our results demonstrate that androgens can suppress the growth inhibitory actions of TGF-β1 in most ovarian cell cultures tested, indicating that this may be a normal regulatory effect of androgens that persists in the cancer cells. Androgen levels are high in follicular fluid and in the ovarian stroma (42, 43). Thus, ovarian epithelial cells would normally be exposed to the paracrine action of androgens at ovulation, when the expelled follicular fluid bathes the surrounding ovarian surface, or as these cells form deep invaginations leading to inclusion cysts within the ovarian stroma. These inclusion cysts, which are thought to be normally short-lived, have been implicated as the primary site of origin for epithelial ovarian cancer (44, 45). Therefore, androgen-induced suppression of growth-inhibitory signals could contribute to the persistence of these cells within the stroma and the development of ovarian cancer.

TGF-β signaling requires the combined action of TβRI and TβRII, and occurs principally through SMAD 2/3 mediated pathways (46) and to some degree via mitogen-activated protein kinase pathways (47). Maintenance of ovarian cell cultures in DHT was capable of either decreasing or increasing transcript levels for these receptors. Furthermore, the loss of TGF-β-induced growth suppression was not always associated with a down-regulation of the receptors (e.g., OSE-32), suggesting that androgen effects on downstream members of the signaling cascade or opposing signaling pathways may be involved.

With the exception of a single culture, DHT treatment did not alter growth in the absence of TGF-β. This finding is consistent with that of Karlan et al. (48), who reported a lack of effect of androgen on growth of OSE cells. However, two recent studies reported androgen-stimulated DNA synthesis in low-passage OSE cultures (12, 49). The differences in the studies likely reflect the various growth conditions, treatment paradigms, and/or methods of measuring proliferation. In the present study, cultures were maintained continuously in medium supplemented with charcoal-stripped fetal bovine serum, epidermal growth factor, and supplemented with charcoal-stripped fetal bovine serum, epidermal growth factor.
growth factor, insulin, and either DHT or ethanol vehicle. These conditions were chosen to reflect more closely the in vivo situation and test the ability of androgen to block TGF-β-induced growth inhibition.

The most striking findings of this study were the coordinate regulation by DHT of ARA70, SRC-1, and TβR-I, and TβR-II transcripts in OSE cultures, and the loss of this coordination not only in malignant cells, but also in OSEb cells with a genetic predisposition to malignant transformation. That androgen could regulate the expression of several steroid coactivators was unexpected. Although it has been shown that androgens modulate ARA70 mRNA expression in prostate cancer cell lines (50), its effect on AIB1 and SRC-1 has not been reported previously. However, nucleotide sequences consistent with androgen (and estrogen) response elements are present in the 5 kb immediately upstream of the coding regions of these coactivators and of TGF-β receptors, as determined using MatInspector v. 2.0 software for transcription factor binding site prediction (51), raising the possibility of direct regulation of these genes by AR.

What can be the influence of BRCA1 or BRCA2 breast/ovarian susceptibility genes in androgen regulation of TGF-β receptors and steroid receptor coactivators? The structurally distinct proteins encoded by BRCA1 and BRCA2 have both been implicated in DNA repair and homologous recombination, cell cycle checkpoint progression, and transcription (52, 53). Although expression of the remaining wild-type allele is usually lost in tumor cells, mutation in only one BRCA allele is sufficient to predispose a carrier to breast and/or ovarian cancer. Decreased expression of BRCA1 has been shown to increase the proliferation of malignant and nonmalignant breast mammary cells (54), whereas overexpression led to decreased growth of both breast and ovarian cancer cells (55). BRCA1 has also been implicated in transcriptional regulation by steroids. Interaction of BRCA1 with ER inhibited signaling pathways involved in ER-mediated growth (56, 57), whereas interaction with AR increased the transactivational activity of this receptor in prostate cancer cell lines (58, 59). Interestingly, the cultures bearing confirmed BRCA2 mutations in this study did not cluster separately from those bearing BRCA1 mutations, suggesting that the observed altered androgen responses were not BRCA1 protein-specific and, therefore, not because of altered coactivator function of BRCA1. Nevertheless, it remains possible that the disruption of coordinated androgen responses in OSEb cultures results from other regulatory factors that are present in BRCA heterozygotes that affect normal hormonal mechanisms.

Whereas as a group, OSEb cells responded more like cultures of malignant cells than OSE cells, cluster analysis indicated that there is heterogeneity in this group. Interestingly, three OSEb cultures partitioned strongly with the malignant cell cultures (Fig. 7, B and C), whereas the remaining OSEb cultures partitioned loosely with OSE

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*Internet address: http://www.gsf.de/biodv/matinpector.html.
cultures. This is perhaps not surprising given that only a third of women with BRCA mutations develop epithelial OVCAS. Although it is generally accepted that specific BRCA1/2 mutations influence the risk of ovarian cancer, little is known of the penetrance of specific mutations. Thus, it is presently difficult to speculate on whether these three cases represent patients within the OSEb cohort most likely to develop ovarian cancer. However, one of these cases (OSEb-7) contained a BRCA2 mutation within the ovarian cancer cluster region (nucleotides 4075–6503), which is associated with the greatest risk of ovarian cancer (60).

The modulation of ARA70, AIB1, and SRC-1 by DHT represents a mechanism whereby androgen can modify sensitivity to itself as well as to other steroids. ARA70 has been shown to interact with PRs and ERs (61). SRC-1 and AIB1 interactions have been best characterized for ER, but also occur with multiple members of the steroid hormone receptor superfamily, including AR and PR (62–64). ERα and β expression has been reported in ovarian cancer tumor specimens as well as in OSE (11, 65), and estradiol has been shown to stimulate growth of both malignant and nonmalignant ovarian epithelial cells (49). OSE cells and most ovarian tumors also express PR (11, 66). Progesterone in micromolar quantities has been shown to induce apoptosis in two immortalized ovarian cancer cell lines (67). The modulation of multiple steroid receptor coactivators by androgen suggests a mechanism whereby androgen could modify responses to estrogens, progestins, and possibly other nuclear receptor ligands. Through such action, androgen could alter the cancer-promoting or protective effects of these steroids.

The study of androgen effects on ovarian epithelial cells requires the use of cultured cells, which represents a more controllable but somewhat artificial environment. The inherent limitations of the use of cell cultures include the removal of various endocrine and paracrine factors secreted from multiple cell types present in vivo and changes in cell-cell interactions that occur in vivo.
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In the extracellular microenvironment, and likely altered production of specific matrix proteins, and integrin binding and cell signaling. Although the possibility that the androgen responses of ovarian epithelial cells in vivo may differ from those observed in vitro, our studies clearly reveal novel and interesting differences between malignant and nonmalignant cells, which should provide insight in both disease processes and hormone effects. The derivation of cultures from patient material was not always successful: 60% of ascites and 50% of ovarian surface scrapings yielded growing cells. Thus, potential bias introduced to the study through the removal of nonproliferating cultures cannot be excluded. However, differences were found between OSE and OSEb cultures, which are both derived by the same procedures. Exclusion of OVCAS-16 and OVCAS-33, a rare poorly differentiated epithelial type cancer and a recurrent case, respectively, because they differ from the other OVCAS, did not alter the outcome of the study.

In summary, our results demonstrate that androgens regulate the growth of ovarian epithelial cells in vitro by preventing inhibition by TGF-β1 and coordinately modulate TGF-β receptors and steroid receptor coactivators in these cells. This coordinated effect of androgen was lost in tumor cells and in some cells bearing a BRCA1/2 mutation, raising the possibility that altered androgen response may influence the predisposition to cancer or reflect a consequence of regulatory changes brought about by both ovarian carcinogenesis and BRCA heterozygosity.

REFERENCES


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Loss of Coordinated Androgen Regulation in Nonmalignant Ovarian Epithelial Cells with BRCA1/2 Mutations and Ovarian Cancer Cells

Andreas Evangelou, Michelle Letarte, Igor Jurisica, et al.