Delineation of a FOXA1/ERα/AGR2 Regulatory Loop That Is Dysregulated in Endocrine Therapy–Resistant Breast Cancer

Tricia M. Wright, Suzanne E. Wardell, Jeff S. Jasper, James P. Stice, Rachid Safi, Erik R. Nelson, and Donald P. McDonnell

Abstract
Tamoxifen, a selective estrogen receptor (ER) modulator (SERM), remains a frontline clinical therapy for patients with ERα-positive breast cancer. However, the relatively rapid development of resistance to this drug in the metastatic setting remains an impediment to a durable response. Although drug resistance likely arises by many different mechanisms, the consensus is that most of the implicated pathways facilitate the outgrowth of a subpopulation of cancer cells that can either recognize tamoxifen as an agonist or bypass the regulatory control of ERα. Notably in this regard is the observation here and in other studies that expression of anterior gradient homology 2 (AGR2), a known proto-oncogene and disulfide isomerase, was induced by both estrogen (17β-estradiol, E2) and 4-hydroxytamoxifen (4OHT) in breast cancer cells. The importance of AGR2 expression is highlighted here by the observation that (i) its knockdown inhibited the growth of both tamoxifen-sensitive and -resistant breast cancer cells and (ii) its increased expression enhanced the growth of ERα-positive tumors in vivo and increased the migratory capacity of breast cancer cells in vitro. Interestingly, as with most ERα target genes, the expression of AGR2 in all breast cancer cells examined requires the transcription factor FOXA1. However, in tamoxifen-resistant cells, the expression of AGR2 occurs in a constitutive manner, requiring FOXA1, but loses its dependence on ER. Taken together, these data define the importance of AGR2 in breast cancer cell growth and highlight a mechanism where changes in FOXA1 activity obviate the need for ER in the regulation of this gene.

Implications: These findings reveal the transcriptional interplay between FOXA1 and ERα in controlling AGR2 during the transition from therapy-sensitive to -resistant breast cancer and implicate AGR2 as a relevant therapeutic target. Mol Cancer Res; 12(12); 1829–39. ©2014 AACR.

Introduction
Approximately 40,000 women die from breast cancer each year, making it the leading cause of early mortality in women (1). Most breast cancers are estrogen receptor alpha (ERα)-positive and recognize estrogens as mitogens. Therefore, not surprisingly, strategies that interfere with ERα action have emerged as frontline therapies for the treatment and prevention of breast cancer. Specifically, ERα can be effectively targeted at the level of (i) receptor activity, using selective ER modulators (SERM), such as tamoxifen and selective ER degraders (SERD) or (ii) ligand availability, using aromatase (cyp19) inhibitors. However, close to 60% of ERα-positive tumors exhibit intrinsic resistance or rapidly acquire resistance to endocrine interventions (especially in the metastatic setting), requiring the subsequent use of largely ineffective cytotoxic therapies (2–4). Unfortunately, it has been difficult to predict de novo resistance to endocrine therapy and/or assess the likelihood of early relapse. Some progress in this regard was made with the development of the HoxB13/IL17RB gene predictor (5), although clinically this test has not been widely used and its utility remains unclear. Thus, there is an unmet medical need to define the fundamental processes underlying endocrine resistance with a view to developing mechanism-based diagnostic tests to assess likely drug responses and to identify new approaches to mitigate the impact of resistance.

Although the mechanisms underlying acquired resistance to tamoxifen treatment are multifaceted and diverse, most studies have implicated alterations in kinase signaling pathway activation or epigenetic changes that enable the tamoxifen:ERα complex to activate transcription (4, 6). In addition, several recent studies have described the identification of proto-oncogenes whose expression and/or activities are positively upregulated by endocrine manipulation and which...
alter tamoxifen pharmacology. One such proto-oncogene, the secreted protein AGR2 (anterior gradient homology 2), has been shown to exhibit oncogenic activities in several malignancies, including breast, ovarian, pancreatic, and prostate cancers (7–11). Furthermore, this protein is overexpressed in primary tumors and in cellular models of breast cancer (12–14). Although ERα+ breast cancers, in general, exhibit a low histologic grade, the expression of AGR2 in this tumor subtype is associated with a poorer outcome (8, 12, 15). Furthermore, in primary ERα+ tamoxifen-treated breast cancers, AGR2 overexpression is linked to tamoxifen treatment failure (8). Recently, it was demonstrated that AGR2 is a direct ERα target gene in MCF7 cells. More importantly, however, it was observed that tamoxifen induced the expression of this gene similar to the ERα agonist estradiol (8). Thus, it is possible that although tamoxifen is an effective antagonist on most ERα-responsive genes, its ability to activate AGR2 expression may limit its therapeutic response (7, 8, 16).

In addition to serving as a marker of resistance to endocrine therapy, it is likely that AGR2 itself contributes in a significant manner to tumor biology. However, there is minimal information as to how AGR2 manifests its oncogenic activities. It has been demonstrated that AGR2 has the structural features of a protein disulfide isomerase, although a potential substrate(s) for these activities has yet to be identified. Furthermore, it is not known whether the isomerase activity of this protein is required for its oncogenic functions. Given that it is a secreted protein, it is not surprising that some have considered the possibility that AGR2 may be involved in the folding of the extracellular domains of proteins that influence cell growth and survival (17, 18). Although it has also been shown that the secreted AGR2 protein influences gene expression, it is unclear whether this is accomplished as a consequence of its ability to (i) modulate the activity of some cell surface protein, (ii) bind to and activate a specific “AGR2” receptor, or (iii) function as a direct modulator of an intracellular signaling pathway. Regardless, considering our interest in defining the molecular pharmacology of tamoxifen, we embarked on a study to evaluate the impact of AGR2 expression on the molecular pharmacology of tamoxifen, we embarked on a study to evaluate the impact of AGR2 expression on the therapeutic response (7, 8, 16).

Materials and Methods

Cell culture and treatments

MCF7 and its derivative MCF7 TamR (tamoxifen-resistant) were maintained in DMEM and Ham/F12 Nutrient Mixture (DMEM/F12) with 8% FBS (Gemini), L-glutamine (Invitrogen), and nonessential amino acids (NEAA; Invitrogen). Both cell lines were authenticated by short tandem repeat profiling from ATCC and tested for mycoplasma. MCF7 GPS ER was maintained in DMEM/F12 supplemented with 8% FBS, L-glutamine, and NEAA.

For experiments, cells were plated in media lacking phenol red with 8% charcoal-stripped FBS (CSF; Gemini). Unless otherwise indicated, cells were plated for 48 hours and then treated for 24 hours with 17β-estradiol (E2; Sigma), 4-hydroxytamoxifen (4OHT; Sigma), or ICI182,780 (ICI; Tocris) as indicated and RNA or protein harvested.

Plasmids

The pLenti CMV puro Gal4-DBD (control) and pLenti CMV puro AGR2 plasmids were generated by subcloning Gal4-DBD and AGR2 cDNA into pENTR1a (Invitrogen) and recombining into pLenti CMV puro DEST (Invitrogen).

Gene silencing and overexpression

siRNAs were used to transiently silent ERα (Invitrogen), AGR2 (Invitrogen), and FOXA1 (Sigma) with control siRNAs (sILuc; Invitrogen and Mission Control; Sigma). MCF7 and TamR cells were seeded at 20 × 10³ to 30 × 10⁴ cells per well on a 6-well plate and transfected using DharmaFECT IV (Dharmacon) for 48 to 72 hours, unless otherwise specified.

pLenti CMV puro Gal4-DBD and pLenti CMV puro AGR2 plasmids were cotransfected (FuGENE, Roche Applied Science) with the vsvg, gag-pol, and rev packaging vectors into 293FT cells. The viral supernatants were filtered and supplemented with 8 μg/mL polybrene before infecting MCF7 cells for 2 serial 24-hour periods. Cells were then selected with 1 μg/mL puromycin yielding the MCF7 Gal4 and MCF7 AGR2 cell lines.

RNA preparation and qRT-PCR analyses

Total RNA was prepared using the Aurum Total RNA Mini Kit (BioRad). cDNA was synthesized from 0.5 μg total RNA using the BioRad iScript cDNA Synthesis Kit. Quantitative RT-PCR (qRT-PCR) was performed with 2 μL 1:20 diluted cDNA, 0.2 μmol/L primers, and the iQ SYBR Green Supermix (BioRad), the results calculated using the 2^−ΔΔCt method (19) and data normalized to a 36B4 internal control. Primer sequences are available upon request.

Immunoblotting

Cells were lysed in whole-cell extract buffer containing 100 mmol/L Tris-HCl, pH 8.0, 2 mmol/L EDTA, 0.02% SDS, 0.5% Nonidet P-40, 150 mmol/L NaCl, and 1× protease inhibitors (Sigma). Protein samples were separated on a 10% SDS-PAGE, transferred to nitrocellulose membranes, and the following antibodies were used for detection: ERα (D-12, Santa Cruz Biotechnology), AGR2 (Abnova), FOXA1 (Abcam), β-actin (ACTB; Sigma), and cytokeratin 18 (KRT18; Santa Cruz Biotechnology). Appropriate horseradish peroxidase–conjugated secondary antibodies (BioRad) were used and the proteins detected using Western Lightning Plus ECL chemiluminescence reagents (Perkin-Elmer).
Proliferation assay
A total of $30 \times 10^4$ MCF7 and TamR cells were silenced for AGR2 for 48 hours before the proliferation assay. $0.2 \times 10^4$ siAGR2 cells were plated per well on 96-well plates. One plate of MCF7 siAGR2 and TamR siAGR2 was decanted and frozen on day 1 as a control. The remaining plates were treated identically on days 1 and 3 with E2 as specified and harvested on day 5. DNA content was analyzed using FluoReporter assay (Invitrogen) per manufacturer instructions.

Migration assay
Cells were serum starved for 24 hours with DMEM/F12, 0.1% BSA, and 10 mmol/L HEPES. A total of $7.5 \times 10^4$ cells in 100 μL were plated on BD Biocat Control Inserts 8.0 μm (BD Biosciences) in duplicate and migrated toward 8% FBS for 16 hours. Migrating cells were stained with 5% Trypan blue, decanted and frozen on day 1 as a control. The remaining plates were treated identically on days 1 and 3 with E2 as specified and harvested on day 5. DNA content was analyzed using FluoReporter assay (Invitrogen) per manufacturer instructions.

Xenograft tumor analyses
All xenograft procedures were approved by the Duke University Institute for Animal Care and Use Committee (Durham, NC). Ovariectomized estrogenized [0.72 mg/60 days 17β-estradiol (E2)] time-released subcutaneous pellet; Innovative Research of America] nullu mice (~6 weeks of age) were injected with $5 \times 10^6$ MCF7 Gal4 or MCF7 AGR2 into the axial mammary fat pad. Tumors were measured by caliper 3 times per week until tumor volume $[(\ell^2 \times W)/2]$ reached 0.2 cm$^3$. Mice were then randomized for continued treatment with E2 or placebo (E2 withdrawn), with or without tamoxifen cotreatment (injected subcutaneously daily with 0.5 mg/mouse dissolved in corn oil).

Bioinformatics analyses
Forest plot. To query the prognostic significance of our 4OHT-induced genes, we assembled a meta-set of patients with breast cancer from 25 publicly available datasets, which included 4,885 patients. The Affymetrix microarray data (HGU133plus2 and HGU133A) were downloaded from GEO, normalized with RMA (20), and batch corrected using the COMBAT algorithm within R yielding only the probe sets common between the two platforms. Clinical data samples were removed. Each tumor was then classified into tumor subtypes using the PAM50 (21) gene modules in Genetu. Genes identified as being induced by 4OHT were then ranked according to significance and the top 25 were submitted to the R package surcormp (22) to calculate concordance index scores for each gene and plotted.

AGR2 correlation network. Data from The Cancer Genome Atlas (TCGA-BRCA; ref. 23) were downloaded and compiled locally. The RNA-Seq data composed of 961 patient samples at the time of download and Spearman correlation were computed for every gene present with respect to AGR2 or ESR1. Clustering analysis of the top correlating genes of AGR2 indicated distinct groups and the package DiffCorr (24) from R (25) was used to derive the differential correlation metric of (AGR2 – ESR1). In addition, mRNA expression from 921 cell lines was downloaded from CCLE (26) and Spearman correlation was similarly obtained. Top AGR2 correlating genes from TCGA data ($R > 0.50$) were inputted into Cytoscape (27) with TCGA Spearman values indicated by node color and CCLE Spearman values indicated by node size. The associated table lists the top factors and is ranked by the differential correlation metric.

Statistical analysis
Migration, qPCR, and transfection data are represented as mean ± SEM. Tumor growth data were analyzed by either 2-way ANOVA (non-repeated measures) followed by a Bonferroni t test or by Kaplan–Meier survival analysis.

Results
The ERα target gene AGR2 is constitutively expressed in models of tamoxifen-resistant ERα$^+$ breast cancer
Previously, we identified a set of genes whose expression in MCF7 cells was positively upregulated by 4OHT and whose induction by other SERMs reflected the relative agonist activity of the compound tested (28). Analysis of the prognostic significance of these genes in luminal A cancers revealed that the expression of PTGES and AGR2 was among the most significantly associated with poor outcome (Fig. 1A). Because previous clinical data suggest that PTGES has no major effect on breast cancer susceptibility or survival among those with invasive breast cancer (29), we chose to focus on AGR2. AGR2 is a proto-oncogene whose expression is shown to be induced by 17β-estradiol (E2) in several cancers of epithelial origin (7, 8, 16). Furthermore, there is considerable interest in using AGR2 as a potential biomarker of drug resistance in breast cancer (17, 18). Given these data, we decided to evaluate the extent to which AGR2 contributes to the pathobiology of ERα$^+$ breast cancer and influences the response of these cancers to tamoxifen.

We have developed a cellular model of tamoxifen resistance (TamR) from an MCF7 xenograft tumor continually treated with tamoxifen in vivo until the onset of resistance. In contrast to TamR models developed by continuously treating cells with tamoxifen in vitro (30, 31), the cell line derived from the corresponding TamR tumors retains both ERα expression and a robust ERα-dependent transcriptional program. This model has been shown to be very predictive of the human disease and has been used in the development of several endocrine agents for breast cancer (refs. 16, 32; unpublished results). With some exceptions, the ERα dependence of genes was conserved in MCF7 and TamR cells (ref. 16; data not shown). However, several genes showed constitutively higher expression in TamR than in the parental MCF7. Of relevance to this work is the observation


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that in parental MCF7 cells, the expression of AGR2 was induced following treatment with E2 or 4OHT but was inhibited by concomitant treatment with the pure anti-estrogen ICI 182,780 (ICI; Fig. 1B). Interestingly, AGR2 levels (both mRNA and protein) were expressed at a high constitutive level in TamR cells and this expression was not influenced by treatment with E2, 4OHT, or ICI (Fig. 1B and C). Several other ERα target genes such as KRT13 were also expressed in a constitutive manner in the TamR cells, although their expression was inhibited by ICI (data not shown). Furthermore, it was demonstrated that the expression of AGR2 and other tamoxifen-responsive genes, including KRT13, was induced by tamoxifen treatment when TamR cells were propagated as xenografts (Supplementary Fig. S1). As was the case in vitro KRT13, but not AGR2 expression, was inhibited by ICI treatment (Supplementary Fig. S1). Thus, while AGR2 is a robust target in ERα-dependent tamoxifen-sensitive (treatment-naive) cells, its elevated level of expression in the TamR models seems to no longer require ERα. We next addressed the impact of AGR2 on tumor biology and sought to elucidate the mechanism(s) underlying its expression in TamR cells.

AGR2 is required for proliferation and enhances migration in cellular models of tamoxifen-sensitive and -resistant breast cancer

Recently, it has been reported that AGR2 is a proto-oncogene that regulates mammary epithelial cell proliferation (33) and that elevated expression of this protein is associated with increased cell proliferation and migration in breast cancer cells (7, 8). However, a role for AGR2 in the pathology of tamoxifen-resistant breast cancer has not been defined. Therefore, we performed a comparative analysis of the impact of siRNA-mediated knockdown of AGR2 expression on the growth of MCF7 and TamR cells. The results of this study, performed using two different siRNAs, revealed that AGR2 was required for the growth and survival of both tamoxifen-sensitive MCF7 and tamoxifen-resistant TamR cell lines (Fig. 2A and Supplementary Fig. S2).
migration. As shown in Fig. 2B, E2 treatment increased the migration of TamR cells and this effect was ablated upon siRNA-mediated knockdown of AGR2 expression. To confirm the role of AGR2 in cell migration, we used a lentiviral-based approach to overexpress AGR2 in MCF7 cells. It has been established that AGR2 is a secreted protein and we were able to demonstrate that the recombinant AGR2 produced in the cell lines we developed was indeed secreted (Fig. 2C). In addition, although treatment with spent media from AGR2-overexpressing cells did not overcome the intracellular proliferative functions of AGR2 when knocked down (Supplementary Fig. S3), we demonstrated that the same spent media were sufficient to induce MCF7 cell migration and, more importantly, further potentiated the robust migratory behavior of TamR cells (Fig. 2C). Taken together, these data indicate that intracellular AGR2 promotes cellular proliferation whereas secreted AGR2 promotes migration, and that its constitutive expression in models of endocrine-resistant cancer is likely to be important in disease pathogenesis.

**AGR2 overexpression enhances E2-stimulated growth of ERx-dependent xenografts in vivo**

We next undertook a series of studies to assess the impact of AGR2 overexpression on tumor growth and tamoxifen response in MCF7 cell-derived xenografts. To this end, MCF7 Gal4 (control) or MCF7 AGR2 cells were injected subcutaneously into the mammary fat pad of ovariecotomized athymic nude mice. All mice received estrogen treatment until the tumors reached about 0.2cm³, and the mice were then randomized into four groups: (i) continued estrogen treatment, (ii) continued estrogen with co-administration of tamoxifen, (iii) estrogen withdrawal, and (iv) estrogen withdrawal with tamoxifen administration. This final group was included to determine whether overexpression of AGR2 was sufficient to permit tamoxifen-dependent growth of the tumors as observed in the TamR xenografts. One of the most important findings of this study was that the E2-treated tumors overexpressing AGR2 grew significantly faster than their Gal4-expressing counterparts (Fig. 3A). It was also observed that when compared with Gal4, AGR2 expression reduced the...
AGR2 expression in tamoxifen-resistant breast cancer cells loses its dependence on ERα

As described above, we determined that while ICI reduces basal and E2-induced AGR2 expression in the MCF7 cells, the expression of AGR2 in the TamR model in vitro and in vivo (Fig. 1 and Supplementary Fig. S1) remained consistently elevated despite treatment with ERα agonists or antagonists. These observations led us to question the extent to which ERα is required for AGR2 expression in the TamR model and how this compares to the parental tamoxifen-sensitive MCF7 cells. Using two different siRNAs, it was demonstrated that AGR2 mRNA expression in MCF7 cells was completely dependent on ERα expression (Fig. 4A), whereas a knockdown of ERα expression in TamR cells had a minimal effect on AGR2 expression (Fig. 4B). The loss of ERα dependence on AGR2 expression in the TamR line was also apparent when examined at the protein level, where it was demonstrated that robust knockdown of ERα expression did not significantly influence AGR2 expression (Fig. 4C and Supplementary Fig. S4). Therefore, while ERα regulates the expression of AGR2 in the tamoxifen-sensitive MCF7 cells, the expression of AGR2 is both elevated and loses its dependence on ERα expression in our validated model of tamoxifen resistance.

FOX1 is required for AGR2 expression in both tamoxifen-sensitive and -resistant cells

The observation that AGR2 expression did not require ERα in tamoxifen-resistant TamR cells, but that ERα expression requires AGR2 in both tamoxifen-sensitive MCF7 and tamoxifen-resistant TamR cells (Supplementary Fig. S5) raised the question as to the identity of the transcription factor(s) required for the expression of AGR2 in TamR cells. To resolve this issue, we performed a comparative analysis of the Cancer Cell Encyclopedia (CCLE) and The Cancer Genome Atlas (TCGA) breast cancer datasets to identify genes that are highly co-expressed with AGR2 in ERα-positive breast tumors. In this manner, we determined (at the mRNA level) that the expression of tetraspanin-13 (TSPAN13) and forkhead box transcription factor 1 (FOX1) was most closely correlated with AGR2 mRNA expression (Fig. 5A). Interestingly, the genes for AGR2 and TSPAN13 map to the same locus on chromosome 7. We therefore elected to focus our studies on FOX1 as (i) it has been shown to function as a pioneer factor for ERα on many genes, (ii) its expression has been associated with tamoxifen resistance in published studies (34, 35), (iii) we and others (36, 37) have demonstrated that the expression of an AGR2 promoter luciferase reporter could be induced in heterologous cells by expressing FOX1 (data not shown), and (iv) the interaction of FOX1 with this promoter could be demonstrated by chromatin immunoprecipitation (Supplementary Fig. S6). For these studies, two independent siRNAs were used to knockdown FOX1 expression in TamR cells. Using this approach, quantitative ablation of FOX1 mRNA expression could be accomplished and

efficacy of tamoxifen, although the differences between these groups did not reach statistical significance (Fig. 3A). The effect of AGR2 on tamoxifen pharmacology was more apparent when the data were presented as time to event (tumors > 400 mm³; Fig. 3B). Upon E2 withdrawal alone, no changes were observed between the Gal4- and AGR2-expressing tumors (Fig. 3C). However, it was observed that upon E2 withdrawal, the efficacy of tamoxifen was reduced in AGR2-expressing tumors (Fig. 3C). Taken together, these data indicate that AGR2 affects the pathobiology and pharmacology of tumors in mice, although its expression alone is not sufficient to confer tamoxifen resistance in the selected models.
MCF7 cells were treated with siER to a state of tamoxifen resistance. Extracts were immunoblotted for ER to siLuc-vehicle. AGR2 expression was analyzed by qRT-PCR, normalized to the expression of the 36B4 housekeeping gene, and presented as fold change relative to Mock + Vehicle controls.

Figure 4. AGR2 expression in tamoxifen-resistant breast cancer cells loses its dependence on ERα. A, AGR2 expression is regulated by ERα in MCF7 cells. MCF7 cells were treated with siERα and plated for 48 hours in phenol red–free media supplemented with CFS and then treated with 1 nmol/L E2 for 24 hours. AGR2 expression was analyzed by qRT-PCR. B, ERα regulation of AGR2 is diminished in TamR cells. TamR cells were treated with siERα and plated for 48 hours in phenol red–free media supplemented with CFS and then treated with 1 nmol/L E2 for 24 hours. AGR2 expression was analyzed by qRT-PCR. C, ERα regulation of AGR2 is diminished in TamR cells. TamR cells were treated with siERα for 48 hours and then treated with E2 for 24 hours. The resulting whole-cell extracts were immunoblotted for ERα, AGR2, and cytokeratin 18 (KRT18) expression.

Discussion

Recently, there has been renewed interest in identifying specific genes that are causally linked to the development of resistance to endocrine therapy in breast cancer and the identification of pathways downstream of ERα that may be amenable to targeted therapeutic intervention in this disease. It is within this context that we undertook a study to probe the role of the proto-oncogene AGR2 in tamoxifen pharmacology in breast cancer. In general, ERα+ breast tumors are associated with a more favorable prognosis, considered to be less aggressive, and are likely to respond to SERMs such as tamoxifen. However, ERα+ AGR2-overexpressing breast tumors treated with tamoxifen are significantly more aggressive and exhibit a poor prognosis (8, 12, 15). Consequently, ERα+ AGR2-overexpressing tumors are considered to be intrinsically resistant to tamoxifen and/or are poised to develop resistance to endocrine therapy. It was of significance, therefore, that we observed that heterologous expression of AGR2 increased the growth of MCF7 cell-derived xenografts and altered their response to tamoxifen. These findings suggest a causal role for AGR2 in the processes of pathologic importance in breast cancer and highlight its likely role in the development of tamoxifen resistance.

Our interest in AGR2 originated from the observation that it was an estrogen-responsive gene that was overexpressed in breast cancer. However, it has since been found to be expressed in many cancer types, including pancreatic, ovarian, and esophageal carcinomas (10, 13). This dramatically reduced AGR2 expression in both MCF7 and TamR cells at the level of mRNA (Fig. 5B) and protein (Fig. 5C). Interestingly, confounding the interpretation of these data was the observation, somewhat unexpectedly, that ERα expression was completely dependent on FOXA1 expression in both cell lines. Thus, it was unclear whether FOXA1 was having a direct role on AGR2 expression or if it participated in an indirect manner by regulating ERα expression, an issue of particular importance in understanding AGR2 regulation in TamR cells. This mechanistic question was addressed by expressing GFP-tagged ERα under the control of a heterologous CMV promoter (GPS ER) in MCF7 cells. Knockdown of FOXA1 expression decreased the expression of endogenous ERα mRNA and protein in the MCF7 cell line, whereas the expression of the exogenous GFP-ERα cells was not drastically affected (Fig. 5D and E and Supplementary Fig. S7). Of note, however, was the observation that even in the background of stable ERα overexpression, siRNA-mediated knockdown of FOXA1 abrogated AGR2 expression. It is important to note that FOXA1 expression is equivalent in both MCF7 and TamR cells suggesting that in the latter cells, the increased activity of a factor (or process) diminishes the need for ERα. Taken together, these data suggest that the expression of the AGR2 proto-oncogene in both MCF7 and TamR cells requires FOXA1 but that the requirement for ERα in the regulation of this gene is lost as cells progress to a state of tamoxifen resistance.
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11, 38), where it plays critical roles in cell migration, growth factor secretion, and proliferation. Likewise, in breast cancer, we and others have shown that AGR2 expression promotes cell survival, proliferation, and metastasis (7, 8). Of particular importance was the finding that elevated expression of AGR2 in the index biopsy of primary tumors is associated with early progression in patients treated with tamoxifen (8), a result that has led to the suggestion that this protein may contribute to tamoxifen resistance. These findings heightened interest in using AGR2 as a potential biomarker of resistance to endocrine therapy in ERα+ breast cancers. However, until this current study, the mechanisms by which AGR2 influences the development of tamoxifen resistance had yet to be explored. In this study, it was shown that AGR2 was absolutely required for the growth of both tamoxifen-sensitive and -resistant breast cancer cells in vitro. Furthermore, it was demonstrated that heterologous overexpression of AGR2 enhanced the estrogen-dependent growth of MCF7-derived tumor xenografts and that the resultant tumors were less sensitive to the anti-estrogenic actions of tamoxifen. These findings also highlight the importance of the observation that AGR2 expression was elevated in a validated model of tamoxifen-resistant breast cancer and that its expression loses its dependence on ERα.

We determined that the induction of AGR2 expression by tamoxifen in MCF7 cells is a direct, ERα-dependent, transcriptional response. However, we are as yet unable to reconcile these findings with those of others in the same cell line, which indicates that the induction of AGR2 gene expression in response to tamoxifen occurs as a result of the nongenomic activity of ERα on signaling molecules in an AKT-dependent manner (39). This encouraged us to undertake a comparative bioinformatics analysis to define proteins and/or processes that may be involved in AGR2 expression in this context. The results of this analysis informed a series of genetic studies that indicated that FOXA1 was required for AGR2 expression in the assayed breast cancer cell types. However, the observation that FOXA1 expression levels did not change as cells progressed from a tamoxifen-sensitive to a tamoxifen-resistant phenotype was a key contributor to the resistance phenotype. Identification of the proteins and/or processes that affect FOXA1 activity is thus a major focus of our efforts in this area.

In both MCF7 and TamR cellular models, we found that knockdown of AGR2 expression resulted in a quantitative downregulation of ERα gene transcription and a loss of the receptor protein. A similar conclusion was arrived at by others studying ERα expression in T47D and ZR751 breast cancer cell models (7). However, the mechanisms by which this occurs is elusive and resolution of this issue awaits a more comprehensive analysis of the biochemical activities and potential targets of AGR2. Regardless, it appears that ERα can regulate AGR2 expression and that this in turn upregulates ERα expression. Interestingly, although AGR2 expression in tamoxifen-resistant cells no longer requires ERα, the sustained expression of ERα still requires AGR2. Thus, the ERα/AGR2 step of the normal ERα/AGR2/ERα regulatory loop is dysregulated in tamoxifen-resistant cancer as a consequence, we believe, of an alteration in FOXA1 activity.

This study highlights the importance of the FOXA1/ERα/AGR2 signaling axis in luminal breast cancers and its likely utility as a therapeutic target for the treatment of breast cancer. The importance of FOXA1 in breast cancer physiology has been established, although in and of itself is not likely to be a druggable target. On the other hand, as it is a secreted protein, AGR2 may be a viable target using a neutralizing antibody approach. Such an intervention may have utility as an alternative to, or in conjunction with SERMs or SERDs, as a treatment for ERα− cancers. It also remains to be determined how, with no change in expression, FOXA1 is able to sustain the expression of AGR2 in a manner that no longer requires ERα. Indeed, it is inferred from our work that the pathways that impinge on FOXA1 to facilitate its ERα independent activity are also likely to be useful targets for the treatment of breast cancer. Taken together, this study shows that the FOXA1/ERα/AGR2 signaling axis is a viable option for therapeutic intervention and that the specific targeting of the proto-oncogene AGR2 is likely to provide an option for the future therapeutic treatment of breast cancer.

Figure 5. FOXA1 drives AGR2 expression in both tamoxifen-sensitive and -resistant ERα+ breast cancer. A, Definition of the AGR2 expression network identifies FOXA1 as a regulator of AGR2 expression. A comparative analysis of CCLE and TCGA was performed to predict genes whose expression is highly associated with AGR2. From the genes identified, FOXA1 was one of the top represented genes of the list. CCLE correlation is represented by size with larger circles predicting higher co-expression and TCGA correlation is colored from blue to red to represent degree of positive correlation. B, FOXA1 regulates AGR2 mRNA expression. MCF7 and TamR cells were treated with siFOXA1 and plated for 4 days in phenol red-free media supplemented with CFS. FOXA1 and AGR2 expression was analyzed by qRT-PCR, normalized to the expression of the 36B4 housekeeping gene, and presented as fold change relative to siCtrl-treated cells. C, FOXA1 regulates AGR2 expression in MCF7 and TamR cells. MCF7 and TamR cells were treated with siFOXA1 for 4 days in phenol red-free media with CFS. The resulting whole-cell extracts were immunoblotted for FOXA1, AGR2, ERα, and β-actin (ACTB) expression. D, FOXA1 regulates AGR2 expression when ERα expression is induced. MCF7 and MCF7 GPS ER cells were treated with siFOXA1 for 4 days in phenol red-free media with CFS. The resulting whole-cell extracts were immunoblotted for FOXA1, AGR2, ERα, and β-actin (ACTB) expression. E, FOXA1 regulates AGR2 mRNA expression with induced ER expression. MCF7 and MCF7 GPS ER cells were treated with siFOXA1 and plated for 4 days in phenol red-free media supplemented with CFS. FOXA1, ERα 3'UTR (untranslated region), ERα, and AGR2 expression was analyzed by qRT-PCR, normalized to the expression of the 36B4 housekeeping gene, and presented as fold change relative to siCtrl-treated cells.
Disclosure of Potential Conflicts of Interest
S.E. Wardell and D.P. McDonnell are consultants/advisory board members for Pfizer. D.P. McDonnell reports receiving a commercial research grant from Novartis and other commercial research support from Pfizer. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions
Conception and design: T.M. Wright, S.E. Wardell, R. Safi, E.R. Nelson, D.P. McDonnell
Development of methodology: T.M. Wright, S.E. Wardell
Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): T.M. Wright, S.E. Wardell, J.P. Stice, E.R. Nelson
Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): T.M. Wright, S.E. Wardell, J.S. Jasper, R. Safi, E.R. Nelson, D.P. McDonnell
Writing, review, and/or revision of the manuscript: T.M. Wright, S.E. Wardell, J.P. Stice, R. Safi, E.R. Nelson, D.P. McDonnell
Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): T.M. Wright, D.P. McDonnell
Study supervision: T.M. Wright, D.P. McDonnell

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Tricia M. Wright, Suzanne E. Wardell, Jeff S. Jasper, et al.


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