Clinical and genomic crosstalk between glucocorticoid receptor and estrogen receptor α in endometrial cancer

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Abstract

Steroid hormone receptors are simultaneously active in many tissues and are capable of altering each other's molecular and biological roles. Estrogen receptor α (ER) and glucocorticoid receptor (GR) are co-expressed in the uterus and their ligands have opposing effects on uterine growth and morphology, with estrogens inducing growth and corticosteroids inhibiting growth. In endometrioid-type endometrial tumors expressing ER, we surprisingly found that the expression of GR is associated with poor prognosis and higher tumor grade. Dexamethasone reduced normal uterine growth *in vivo*; however, this growth inhibition was abolished once estrogen-induced endometrial hyperplasia was established and cancer cells increased growth when treated with dexamethasone and estradiol. To understand the underlying molecular crosstalk between ER and GR in endometrial cancer cells, we measured their genomic binding following treatment with estradiol, dexamethasone, and the combination. We found 20% overlap in bound loci when ER and GR are induced with their respective ligands individually; however, upon induction with both ligands simultaneously they co-occupy significantly more sites (47%). ER binding is only slightly affected by the presence of dexamethasone, while GR binding is significantly altered by the presence of estradiol with GR being recruited to loci bound by ER that contain estrogen response elements. The GR sites gained in the presence of estradiol consist of loci that become more accessible upon estradiol induction, supporting a model where ER assists in the chromatin loading of GR. The crosstalk in genomic binding is associated with gene expression changes upon co-treatment being more similar to estradiol than dexamethasone, but with novel regulated genes including a decrease in cell-cell adherens junction genes. Our results suggest both a phenotypic and molecular interplay between ER and GR in endometrial cancer.

Introduction

Steroid hormone receptors have similar DNA binding preferences and their genomic binding is dependent on an overlapping set of additional transcription factors (Jozwik and Carroll, 2012; Robinson et al., 2011). Therefore, it isn't surprising that the actions of one steroid hormone receptor can be altered by the induction of a different steroid hormone receptor. For example, progesterone receptor (PR) and estrogen receptor α (ER) are often co-expressed in breast cancer and the induction of PR redirects ER genomic binding and reduces estrogen-driven growth(Mohammed et al., 2015; Singhal et al., 2016). Androgens enable breast cancer growth and androgen receptor (AR) is important for ER genomic binding(D'Amato et al., 2016). Steroid hormones are also capable of compensating for one another. In prostate cancer, dexamethasone can confer resistance to anti-androgen therapy by activating glucocorticoid receptor (GR), which can substitute for AR in regulating transcription (Arora et al., 2013; Isikbay et al., 2014; Li et al., 2017). In the luminal androgen receptor subtype of breast cancer, AR compensates for ER's absence by binding to very similar genomic loci

that are also occupied by FOXA1(Robinson et al., 2011). It is clear that steroid hormone receptors do not work in isolation and that they can perform overlapping functions.

GR and ER have been shown to alter each other's regulatory and phenotypic roles. GR expression is associated with good outcomes in ER-positive breast cancer and poor outcomes in ER-negative breast cancer(Pan et al., 2011a), which is consistent with dexamethasone blocking estrogen induced growth in breast cancer cells(Zhou et al., 1989). When both steroid hormone receptors are active in breast cancer cells, GR impacts ER's genomic interactions (Miranda et al., 2013). GR activation alters chromatin accessibility enabling ER to bind to a new set of genomic regions, a mechanism known as assisted loading(Voss et al., 2011). In addition, ER and GR have been shown to both cooperate(Bolt et al., 2013) and compete(Karmakar et al., 2013; Meyer et al., 1989) for co-factors in breast cancer cells. GR has also been implicated in trans-repression of ER regulated gene expression in breast cancer (Yang et al., 2017). Estrogens and corticosteroids can elicit opposite phenotypic effects in other tissues as well(Haynes et al., 2003; Lam et al., 1996; Terakawa et al., 1985), including the uterus(Gunin et al., 2001; Markaverich et al., 1981; Rabin et al., 1990; Rhen et al., 2003).

Endometrial cancer is the most common gynecological cancer and incidence as well as mortality associated with endometrial cancer are on the rise, while survival is significantly worse now than in the 1970s. Of endometrial cancers, 80-90% are type I endometrioid tumors that express ER and are thought to be hormonally driven(Saso et al., 2011). Estrogen causes increased uterine growth and continued exposure can lead to endometrial hyperplasia(Yang et al., 2015). In contrast to ER's pro-growth role in the uterus, GR reduces uterine growth and opposes phenotypic effects of estrogens in the uterus(Bever et al., 1956; Bitman and Cecil, 1967). Despite the opposing phenotypic roles, Dexamethasone (Dex) and 17β-estradiol (E2), a GR and an ER agonist respectively, produce similar gene expression changes in the normal uterus(Rhen et al., 2003). While estrogen and corticosteroid signaling have been examined in the normal uterus, crosstalk between ER and GR has not been explored in the context of endometrial cancer on a genome-wide scale.

Here, we show that GR expression is associated with poor prognosis and higher grade in endometrioid endometrial cancers, which is unexpected considering the growth inhibitory effects of corticosteroids in the normal uterus. Consistent with this observation, we find that once E2-induced hyperplasia is established in mice, growth is no longer opposed by Dex. Analysis of GR and ER genomic binding in endometrial cancer cells uncovered an interesting relationship in which E2, in combination with Dex, enables GR to bind to an expanded repertoire of genomic loci. Based on chromatin accessibility patterns, ER appears to assist in chromatin loading of GR. Gene expression analysis indicates that double induction with E2 and Dex produces a similar response as the addition of the separate inductions; however, several genes are impacted by the double treatment in a nonlinear manner. Together our results indicate that ER impacts GR's gene regulatory and phenotypic actions in endometrial cancer cells and that GR activity may lead to more aggressive forms of the disease.

Results

Glucocorticoid Receptor expression is associated with poor prognosis in endometrial cancer

Because steroid hormone receptors can impact each other's phenotypic and gene regulatory outputs, we decided to look for association between gene expression of steroid hormone receptors and outcomes in endometrioid endometrial cancer, a hormonally driven cancer type. We focused our analysis on endometrial cancer RNA-seq and clinical data from The Cancer Genome Atlas(Cancer Genome Atlas Research et al., 2013), exclusively analyzing tumors with endometrioid histology. While ER is expressed at the mRNA level in most tumors, higher expression is associated with longer disease free survival (Figure 1A, p-value = 0.002791, Cox regression), which is consistent with previous reports for ER protein and mRNA levels(Wik et al., 2013). Higher ER expression was also associated with lower grade (Figure 1D, p-value = 1.75×10^{-7}, Wilcoxon), as previously observed with ER protein levels(Backes et al., 2016), indicating that ER expression is higher in more differentiated tumors. PR is transcriptionally regulated by ER and therefore it isn't surprising that higher expression of PR is also associated with better outcomes (Figure S1, p-value = 0.0006479, Cox regression) as previously reported(Tangen et al., 2014). Expression of AR, mineralocorticoid receptor and estrogen receptor β were not significantly associated with recurrence (Figure S1).

Figure 1

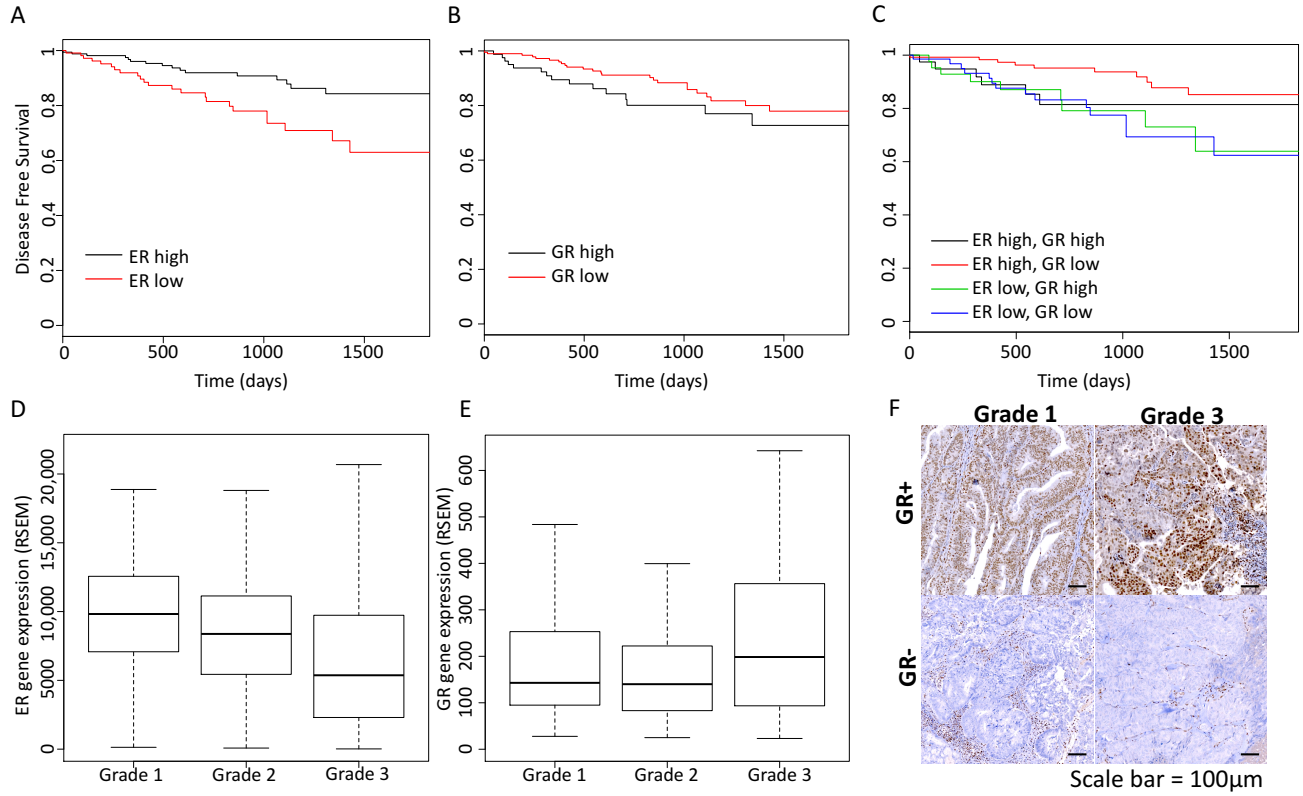

Figure 1. GR expression is associated with poor prognosis in endometrioid endometrial cancer. Kaplan-Meier curves show the association of disease free survival with ER expression (A, high is top 60% tumors), GR expression (B, high is top 30% tumors), and the combination (C). Higher ER expression is associated with better prognosis, while higher GR expression is associated with worse outcomes, but only in the context of high ER expression. ER expression is negatively correlated with tumor grade (D) and GR expression is positively correlated with tumor grade (E). F) Examples of GR immunohistochemistry staining are shown for grade 1 and grade 3 tumors.

Higher GR expression was associated with worse outcomes for patients with endometrioid endometrial tumors (Figure 1B, p-value = 0.012, hazard ratio = 2.1, Cox regression). Higher expression was also correlated with higher histological grade (Figure 1E, p-value = 0.04, Wilcoxon). In order to assess protein expression and GR activity in endometrioid tumors, we performed IHC and found that 27% (3/11) of grade 1 endometrioid tumors exhibited nuclear GR staining, which is indicative of active GR, and 50% (5/10) of grade 3 endometrioid tumors were positive for nuclear GR staining (examples in Figure 1F, Figure S2). The IHC confirms that GR is expressed and active in endometrial cancer cells and is more likely to be present in higher grade endometrioid endometrial tumors.

To further explore the relationship between GR expression and poor prognosis, we analyzed this association in the higher ER expressing tumors and the lower ER expressing tumors separately. Figure 1C shows that association between GR expression and disease-free survival is only seen in the tumors with higher ER expression (p-value = 0.0096, hazard ratio = 3 [1.3 - 7.3 95% confidence interval], Cox regression) and not observed in the tumors with lower ER expression (p-value = 0.94, hazard ratio = 0.97 [0.42 - 2.23 95% confidence interval], Cox regression). These results suggest that GR expression increases the aggressiveness of tumors with higher expression of ER, but has little effect on tumors with low ER expression indicating that ER and GR could be impacting the actions of one another.

Estradiol and dexamethasone in combination induce growth of endometrial cancer cells in 3D culture

Positive correlation between GR expression and the likelihood of recurrence is surprising, and appears inconsistent, in light of multiple studies connecting GR activation with reduced uterine growth (Gunin et al.,

2001; Markaverich et al., 1981; Rabin et al., 1990; Rhen et al., 2003). We hypothesized that the growth inhibitory effects of corticosteroids may be absent once hyperplasia is established. We first evaluated how ER and GR affect endometrial cancer cell growth *in vitro*. The endometrial cancer cell line Ishikawa was grown in 3D matrigel culture in the presence of hormone depleted media and then treated with E2, Dex or the combination for 14 days. We then measured ATP levels and observed an expected loss of cell growth in hormone depleted media (Figure 2A). The addition of E2 and Dex individually had subtle and insignificant effects on proliferation. However, when organoids were treated with both E2 and Dex, there was a significant increase in growth that came close to full media levels. This evidence indicates that ER and GR work together in promoting the growth of endometrial cancer cells.

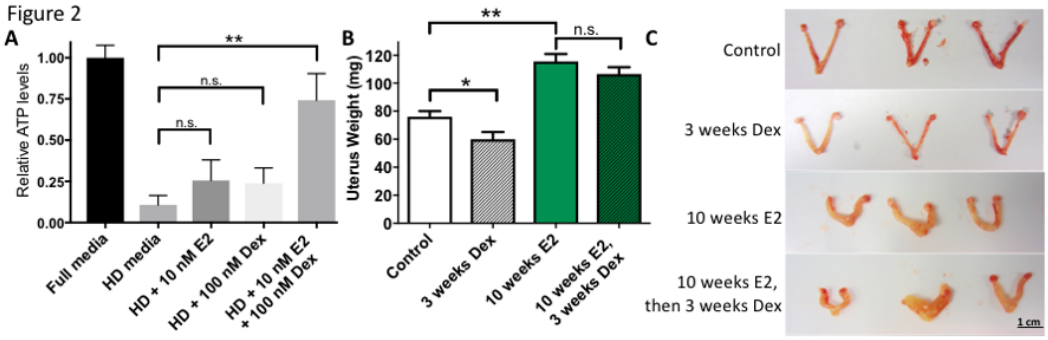

Figure 2. Growth effects of dexamethasone are impacted by estradiol. A) Hormone depleted (HD) media reduces growth of Ishikawa cells, as measured by relative ATP levels. The addition of E2 or Dex to HD media modestly increases growth and the combination of E2 and Dex restores growth to similar levels as full media. B) Uterine weight is reduced by Dex in mice. Continuous E2 exposure for 10 weeks significantly increases uterine weight and subsequent addition of Dex does not significantly reduce this effect. C) Examples of uteri from the categories in panel B. Error bars represent s.e.m. * = p-value < 0.05, ** = p-value < 0.01, and n.s. = not significant (p-value > 0.05).

Dexamethasone inhibition of uterine growth is not observed once estrogen-driven hyperplasia is established

We next sought to determine the impact of active ER and GR on endometrial cells *in vivo*. We used an estrogen-induced endometrial hyperplasia model that utilizes a slow release E2 pellet(Yang et al., 2015). We found that 3 weeks of Dex treatment, in the absence of excess E2, reduced uterine weight by 21% (p-value = 0.042, t-test), while 10 weeks of E2 exposure increased uterine weight by 52% (p-value = 0.002, t-test) (Figure 2B,C). When we administered Dex after allowing hyperplasia to establish during 10 weeks of excess E2, we found that Dex was unable to significantly inhibit uterine growth (p-value = 0.24, t-test; 7.8% decrease) (Figure 2B,C). HIsto-pathological review of hematoxylin & eosin (H&E) stained slides from harvested and processed uteri revealed that endometrial hyperplasia persisted in 5 out of 6 mice treated with Dex after E2, as compared to 7 out of 7 mice treated with only E2. These results suggest that GR's inhibitory effect on uterine growth is significantly reduced once hyperplasia is established.

Glucocorticoid Receptor binds loci occupied by ER upon estradiol and dexamethasone treatment

The survival analysis and phenotypic observations suggest that ER and GR may be impacting the role of one another. In order to determine how this crosstalk is occurring at a molecular level, we performed ChIP-seq with antibodies targeting ER and GR in Ishikawa, a human endometrial adenocarcinoma cell line. We found that ER and GR, when induced by E2 and Dex respectively, have mostly unique binding profiles with only 19.7% of GR bound loci overlapping ER bound loci. However, when cells are treated with E2 and Dex simultaneously, GR and ER share almost half of their binding sites (46.5%). This co-occurrence in ER and GR binding upon the double induction represents a significant increase compared to ER and GR after single inductions (p-value < 2.2×10^{-16}, odds ratio = 3.96, Fisher's Exact Test, all overlaps shown in Figure S3,). These findings indicate that ER and GR are impacting one another on the level of genomic binding site selection.

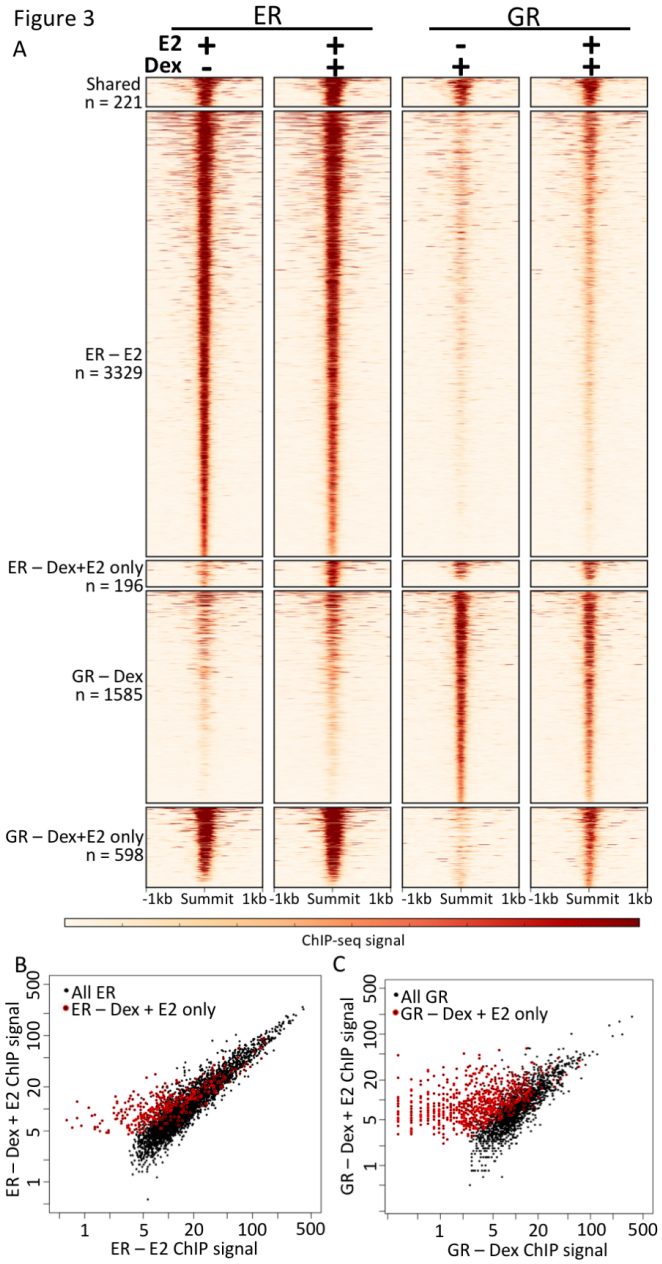

Figure 3. E2 alters GR genomic binding. A) Heatmaps of ChIP-seq signal of ER and GR after single induction and double inductions show that there are a unique set of sites where GR binds only after double induction. ChIP-seq signal is plotted for each ER (B) and GR (C) binding site comparing signal induction (x-axis) and double induction (y-axis). Sites unique to the double induction are shown in red with GR double induction sites showing markedly different signal. Signal is displayed as reads per million.

Further analysis of the ER and GR bound sites following double induction revealed that GR is moving to sites that are bound by ER. The vast majority (91.8%) of ER bound sites in the double induction were bound by ER in cells treated with E2 alone (Figure 3A) and the sites unique to the double induction appear to be accompanied by small changes in ChIP-seq signal (Figure 3B). In contrast, 63.1% of GR bound sites in the double induction were bound by GR in cells treated only with Dex and the sites unique to the double induction exhibit large changes in ChIP-seq signal (Figure 3C). Of the 598 sites that were bound by GR only in the double induction, 67.5% overlapped with ER suggesting that most of the new GR binding sites in the double induction are loci that are bound by ER after both E2 and E2 + Dex treatments. The presence of estrogen response elements (EREs) and glucocorticoid receptor binding elements (GRBEs) are consistent with this

idea; we found that loci bound by GR only after the double induction are enriched for both full and half site EREs compared to GRBEs (Table 1). Overall, these results indicate that ER is enabling GR to bind new genomic loci when both steroid hormone receptors are active.

Table 1. Motif occurrences at ER and GR bound loci

Motif	ER – E2	ER – Dex + E2 only	GR – Dex	GR – Dex + E2 only
ERE full site	27%	8%	3%	21%
ERE half site	91%	76%	55%	82%
GRBE full site	6%	14%	45%	11%
GRBE half site	53%	64%	81%	60%

Chromatin accessibility patterns are consistent with ER assisting GR in chromatin loading

One potential explanation for ER enabling GR genomic binding is assisted loading, where one transcription factor makes it easier for another factor to bind by increasing accessibility to the genomic site(Voss et al., 2011). This phenomenon has been observed in breast cancer cells, although in the opposite direction with GR enabling ER binding (Miranda et al., 2013). To test this model, we performed ATAC-seq on Ishikawa cells treated with Dex, E2 or vehicle controls for 1 hour. We focused our analysis first on loci that were bound by GR either after induction with Dex or only after induction with both E2 and Dex. The loci bound only after the double induction exhibited significantly higher E2-induced chromatin accessibility as measured by ATAC-seq (Figure 4A; p-value < 2.2×10^{-16}, Wilcoxon). This result is consistent with ER creating a more permissive binding environment for GR, enabling GR to bind only after the double induction. Figure 4C and 4D show example loci bound by GR only after double induction that also become more accessible upon E2 induction. In total, 65% of loci bound by GR only after the double induction exhibit increased accessibility after E2 treatment, compared to 43% of all GR bound loci. We performed a similar analysis for loci bound by ER only after double induction and found that chromatin accessibility significantly increases upon Dex induction (Figure 4B; p-value = 0.0001223, Wilcoxon), but the effect is more subtle with 55% of these loci showing increased accessibility after Dex treatment. The ATAC-seq findings are consistent with a model where ER increases chromatin accessibility, allowing GR to bind new loci.

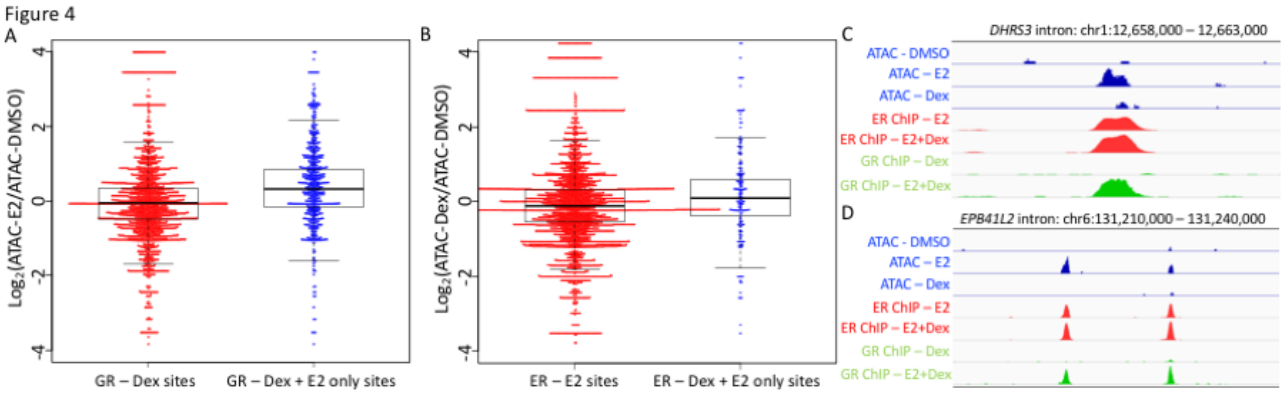

Figure 4. Chromatin accessibility is increased at double induction-specific GR bound sites. The log ratio of ATAC-seq signal after E2 treatment vs. vehicle control (A) and Dex treatment vs. vehicle controls (B) is shown for all (red) and double induction-specific (blue) GR (A) and ER (B) sites. ATAC-seq signal is increased upon E2 induction at GR sites only observed after E2 + Dex treatment. Signal tracks of ATAC-seq signal (blue), ER ChIP-seq signal (red) and GR ChIP-seq signal (green) are shown for loci nearby *DHRS3* (C) and *EPB4IL2* (D). Signal tracks of the same type are shown on the same scale.

The combination of estradiol and dexamethasone cooperate to regulate gene expression

We sought to determine how crosstalk between ER and GR at the genomic binding level impacts gene expression. In order to analyze gene expression responses to E2, Dex and the combination, we performed RNA-seq and analyzed differential gene expression. We identified 286 genes that were regulated by E2 alone (188 up-regulated and 98 down-regulated) and 128 genes significantly regulated by Dex alone (120 up-regulated and 8 down-regulated). There was little overlap in the genes that were regulated by both E2 and

Dex individual treatments with 24 overlapping genes that go in the same direction (19% of all Dex regulated genes) and 6 overlapping genes that are regulated in opposite directions (5% of all Dex regulated genes) (Figure S4A). Upon treatment with both E2 and Dex, 371 genes were significantly affected (240 up-regulated and 131 down-regulated) and the combination treatment samples appeared more similar to the E2 treated samples. Most E2 induced gene expression changes were observed with the combination (69%, Figure S4B), while less than half of the Dex induced expression changes were also seen with the combination treatment (43%, Figure S4C). This relationship is also clear when analyzing principal components (Figure 5A). The overall pattern of gene expression upon E2 and Dex treatment suggests that E2 dominates the combination treatment, explaining the pro-growth phenotype, but Dex contributes by expanding the genes affected. The genes unique to the double induction are enriched in down-regulation of cell-cell adherens junctions (adjusted p-value = 0.001, DAVID(Jiao et al., 2012)), including alpha catenin(Knudsen, 1995), vinculin(Carisey and Ballestrem, 2011) and cingulin(Citi et al., 1988) (Figure S4D-F). The down regulation of cell adhesion proteins could partially explain the aggressiveness of ER and GR expressing tumors (Figure 1C).

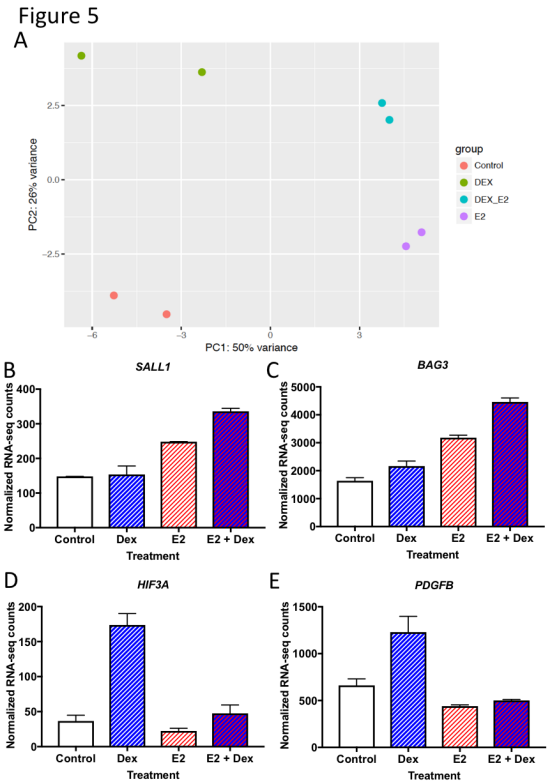

Figure 5. Gene expression consequences of double induction. A) Principal component analysis of RNA-seq from E2, Dex and the combination treatments, shows that E2+Dex (cyan) treated samples are more similar to E2 (purple) treated samples than Dex treated (green) or vehicle treated (red) samples. Examples of genes that exhibit unexpected gene expression levels upon double treatment are *SALL1* (B), *BAG3* (C), *HIF3A* (D), and *PDGFB* (E). Error bars represent s.e.m.

For the 525 genes that exhibited differential gene expression in any treatment compared to controls, we performed regression analysis to look for genes that have a significant E2:Dex interaction term. We identified 112 genes with significant interactions terms; 21 genes had higher expression in the double induction than expected based on the single inductions and 91 genes had lower than expected expression in the double induction. Of the genes with lower than expected double induction expression, 61 (67%) were affected more by Dex alone than E2 alone, indicating a loss of Dex responsiveness that is consistent with altered GR binding. Figure 5B shows the expression of *HIF3A* and *PDGFB* as examples. Both *HIF3A* and *PDGFB* have regulatory loci nearby that exhibit less ATAC-seq signal upon E2 treatment as well as less GR binding after the

double induction (Figure S5A, B). Of the genes with higher than expected double induction expression, 62% were affected more by E2 alone than Dex alone, suggesting that GR may be assisting ER in regulating some genes. The examples of *SALL1* and *BAG3* are shown in Figure 5B. The intron of BAG3 exhibits increased ER binding with the double induction and a SALL1 downstream site is only bound by GR upon treatment with both E2 and Dex (Figure S5C, D). Our results indicate that ER and GR can influence one another's ability to regulate gene expression through both increasing and decreasing genomic binding.

Discussion

ER and GR play opposite phenotypic roles in the normal endometrium with ER promoting growth and GR inhibiting growth. Here we show that in endometrial cancer, GR expression is associated with worse outcomes, as well as higher grade tumors, and this association is only observed in the context of high ER expression. These findings seem to contradict the anti-growth effects of corticosteroids; however, our results show that growth inhibition is no longer observed after estrogen-induced hyperplasia has formed *in vivo* and that Dex, in combination with E2, promotes endometrial cancer cell growth in culture.

One possible explanation for the difference in GR induced growth effects is that ER and GR are expressed in different compartments of the endometrium with GR expressed in stromal cells and ER is expressed in endometrial glands(Bamberger et al., 2001). GR signaling in stromal cells, through either autocrine or paracrine changes, causes growth inhibition of the normal uterus. However, GR activity in hyperplastic or cancerous endometrial cells, when co-expressed in the same cells as ER, no longer inhibits growth and may lead to more aggressive tumors. In fact, gene expression profiling of cells induced with both Dex and E2 uncovered a down regulation of cell adherence genes, which has the potential to cause a more metastatic phenotype. These findings are consistent with work in breast cancer showing that GR expressing tumors differentially regulate cell adhesion genes(Pan et al., 2011b). Our findings indicate that the administration of dexamethasone during treatment of endometrioid histology endometrial cancer should be re-evaluated.

Molecular characterization of ER and GR crosstalk in endometrial cancer cells revealed that ER is the dominant steroid hormone receptor in this setting. ER genomic binding is mostly unaffected by the activation of GR. On the other hand, more than one third of GR binding is altered by the activation of ER. This is the opposite pattern than is observed in breast cancer cells, where GR is dominant in dictating ER binding (Miranda et al., 2013). Interestingly, the difference in dominance between GR and ER is associated with differences in prognosis. GR is dominant over ER in breast cancer cells resulting in a better prognosis when both are expressed (Pan et al., 2011a), while ER is dominant over GR in endometrial cancer cells resulting in a worse prognosis when both are expressed (Figure 1C). This leads to a model in which GR is generally growth inhibitory, ER is generally growth promoting, and the dominant factor dictates the aggressiveness of the tumor. It is unclear why ER is dominant in one setting and GR is dominant in another, but differences in co-factor abundance is an interesting possibility.

To explore how ER was altering GR genomic binding, we used ATAC-seq to identify changes in chromatin accessibility. We found that the majority of GR binding sites that are gained upon treatment with both Dex and E2 exhibit increased chromatin accessibility after E2 induction. These results are consistent with ER assisting in loading GR onto genomic loci, which is similar to breast cancer cells where GR assists in loading ER onto genomic loci (Miranda et al., 2013). We attempted co-immunoprecipitation of ER and GR and were unable to pull down one factor with an antibody that recognizes the other factor (data not shown), suggesting that ER and GR are not forming heterodimers while further supporting the model that crosstalk between ER and GR is occurring through alteration of each other's chromatin interactions.

The genomic binding crosstalk between ER and GR has gene expression consequences. When endometrial cancer cells were induced with either Dex or E2 in isolation, there was very little overlap in the genes affected. When cells were treated with both Dex and E2, the transcriptional response was more similar to an E2 response, but with additional genes changing expression, including a down regulation of cell-cell adherens junction genes. Unlike a recent report in breast cancer(Yang et al., 2017), GR does not appear to repress an E2 transcriptional response in endometrial cancer cells. Overall, about one-fifth of genes affected by any treatment exhibited an unexpected gene expression level after double induction as determined by significant

interaction terms in a linear model. Taken together, our findings are consistent with ER altering GR's genomic actions, where GR switches from regulating a distinct set of genes to promoting and enhancing an E2-driven transcriptional program in endometrial cells.

Methods

TCGA data analysis

RNA-seq and clinical data was downloaded from the TCGA data portal in December 2015. Gene expression measurements were taken from the level 3 RNAseqV2 normalized RSEM data. Only samples with Endometrioid histology were analyzed for survival analysis. Cox regression to evaluate the association between gene expression and progression-free survival was performed in R using binary classification of high and low expression for each steroid hormone receptor. For each steroid hormone receptor, we tried each decade percentile increment between 20th percentile and 80th percentile in order to identify the cutoff between high and low expression that gave the most significant association with progression free survival. The following cutoffs were used for each gene: GR - top 30th percentile was labelled high, ER - top 60th percentile, PR - top 80th percentile, AR - top 20th percentile, mineralocorticoid receptor - top 60th percentile, and estrogen receptor β - top 60th percentile.

Immunohistochemistry

Immunohistochemical staining of formalin-fixed paraffin slides of murine uteri was performed by ARUP laboratories. In brief, 4-5 um thick tissue sections were prepared. The slides were placed on the automated immunostainer and de-paraffinized with the EZ Prep solution. The slides were then treated with CC1 (Cell Conditioning 1, pH 8.5) for 68 minutes at 95°C. The primary antibody against GR (Cell Signaling, clone D6H2L, #12041) was applied for 1 hour at a dilution of 1:100 at 35°C. Following removal of the primary antibody, the secondary antibody (Goat anti-rabbit IgG Sigma-aldrich, # B8895) was applied for 1 hour at a dilution of 1:100 at 37°C. These slices were then exposed to the IView DAB Map detection kit and counterstained with hematoxylin for 8 minutes. Slides were removed from the autostainer and placed in a dH2O/DAWN mixture, and then dehydrated in graded alcohol. After dipping each slide 10 times in 4 changes of xylene, cover slips were put on and slides were read by board certified pathologists.

Animal studies

A total of thirty-five 8-week-old female Balb/c mice were used in this study. To induce estrogen-driven endometrial hyperplasia, E2 pellets were prepared and surgically implanted into mice (n=21) as previously described (Yang et al., 2015). Following 10 weeks of E2 exposure, mice were divided into three treatment arms to receive Dex, PBS, and 5% ethanol (n=7 per arm). Fourteen mice did not receive E2 pellet implants and were divided into two groups for administration of Dex and PBS (n=7 per group). Dex was dissolved in 5% ethanol and administered through intraperitoneal injection at a dose of 1mg/kg and a frequency of 5 days on 2 days off for a total of 21 days. Animals were sacrificed upon reaching the primary study endpoint on day 22 and necropsy including tissue harvesting ensued. Uteri were grossly examined and uterine weights were measured. Tissues were processed into FFPE blocks and stained with hematoxylin and eosin for histo-pathological analysis. Animals were housed in the Animal Facility of the Comparative Medicine Center at the University of Utah under standard conditions. All procedures conducted were approved by the Institutional Animal Care and Use Committee (IACUC).

Cell culture

Ishikawa cells (Sigma-Aldrich) were grown in RPMI-1640 with 10% fetal bovine serum and 50 units/mL penicillin and 50 μg/mL streptomycin. At least four days before induction, cells were moved to phenol-red free RPMI-1640 with 10% charcoal-dextran stripped fetal bovine serum to remove hormones. Cells were treated with DMSO, 10 nM E2, 100 nM Dex or the combination for either 1 hour for ChIP-seq and ATAC-seq or 8 hours for RNA-seq.

3D Culture

Ishikawa cells were grown and transferred to hormone-depleted RPMI-1640 as described above. Cells were suspended in Matrigel (Corning, growth factor reduced, phenol-red free) and 500 cells were plated with 9 µL Matrigel and 500 µL media per well in a 48-well glass bottomed plate (MalTek, 48mm glass bottom). Cells were treated with DMSO, 10nM E2, 100nM Dex or combination of both 10nM E2 and 100nM Dex. Relative ATP levels were measured using CellTiter Glo 3D (Promega).

ChIP-seq

After inductions, cells were crosslinked with 1% formaldehyde for 10 minutes at room temperature and then treated with 125 mM Glycine for 5 minutes to stop crosslinking. Crosslinked cells were then washed with cold PBS and scraped to harvest. Chromatin immunoprecipitation was performed as previously described (Reddy et al., 2009). Sonication was performed on an Active Motif EpiShear probe-in sonicator with 8 cycles of 30 seconds, with 30 seconds of rest, at 40% amplitude. The antibodies used were ER (Santa Cruz HC-20) and GR (Santa Cruz E-20). ChIP-seq reads for each treatment were compared to ChIP-seq libraries from control (DMSO) treated cells for the same factor (e.g. GR in Dex was compared to GR in DMSO). Reads were aligned to the hg19 build of the human genome using Bowtie with the following parameters: -m 1 -t --best -q -S -l 32 -e 80 -n 2. Peaks were called using MACS2(Zhang et al., 2008a) with a p-value cutoff of 1e-10 and the mfold parameter constrained between 15 and 100. Counts between sets were calculated using bedtools coverage(Quinlan and Hall, 2010) to find read depth at all sites covered by peaks called by MACS2. These data were combined using gawk and examined and graphed using R. Motif finding was performed on 100bp surrounding the top 500 peaks based on their integer score (column 5 of narrowPeak file). Motifs were discovered using the meme suite(Bailey et al., 2009) searching for motifs between 6 and 50 bases in length with zero or one occurrence per sequence. We used Patser(Hertz and Stormo, 1999) to count the number of sites with significant full and half site EREs and GRBEs within 50bp of each peak's summit.

RNA-seq

After inductions, cell lysates were harvested with buffer RLT Plus (Qiagen) supplemented with 1% beta-mercaptoethanol and passed through a 21-gauge needle to shear genomic DNA. RNA was purified using RNA clean and concentrator with the optional DNase treatment (Zymo Research). Poly(A)-selected RNA-seq libraries were constructed with KAPA Stranded mRNA-seq kit (Kapa Biosystems) using 1 ug total RNA. Sequencing reads were aligned to the hg19 build of the human genome using HISAT2 (Kim et al., 2015). Sam files were converted to bam format and sorted using samtools (Li et al., 2009). Reads mapping to genes were counted using featuresCounts from the SubRead package(Liao et al., 2014). Reads were normalized and differential analysis was done in a pairwise manner using DESeq2 (Love et al., 2014). Genes were considered significant if they had an adjusted p-value of <= 0.1. In order to find significant E2:Dex interaction terms, we constructed linear models in R using the 'lm' function and looked for E2:Dex coefficients that are significantly different than 0 with a p-value<0.05.

ATAC-seq

ATAC-seq was performed on 250,000 cells for each library as described by Buenorostro et al (Buenrostro et al., 2013). Tn5 transposase, with Illumina adapters, was constructed as outlined by Picelli et al (Picelli et al., 2014). Sequencing reads were aligned to hg19 using bowtie(Langmead et al., 2009) with the following parameters: : -m 1 -t --best -q -S -l 32 -e 80 -n 2. Sam files were converted to bam files sorted using samtools (Li et al., 2009). Macs2 (Zhang et al., 2008b) was used to call peaks without a control input. We used a cutoff p-value of 1e-10 when calling peaks. FeatureCounts (Liao et al., 2014) was used to quantify reads that aligned in regions +/- 250 bp from an ER or GR binding site summits from the ChIP-seq experiments. These reads were then normalized and differential expression was determined by comparing samples in a pairwise manner using the DESeq2 package for R (Love et al., 2014).

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