Endoglin (CD105) Contributes to Platinum Resistance and Is A Target for Tumor-Specific Therapy in Epithelial Ovarian Cancer

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Abstract

Purpose: Endoglin (CD105) is a membranous protein overexpressed in tumor-associated endothelial cells, chemoresistant populations of ovarian cancer cells, and potentially stem cells. Our objective was to evaluate the effects and mechanisms of targeting endoglin in ovarian cancer.

Experimental Design: Global and membranous endoglin expression was evaluated in multiple ovarian cancer lines. In vitro, the effects of siRNA-mediated endoglin knockdown with and without chemotherapy were evaluated by MTT assay, cell-cycle analysis, alkaline comet assay, γ-H2AX foci formation, and quantitative PCR. In an orthotopic mouse model, endoglin was targeted with chitosan-encapsulated siRNA with and without carboplatin.

Results: Endoglin expression was surprisingly predominantly cytoplasmic, with a small population of surface-positive cells. Endoglin inhibition decreased cell viability, increased apoptosis, induced double-stranded DNA damage, and increased cisplatin sensitivity. Targeting endoglin downregulates expression of numerous DNA repair genes, including BARD1, H2AFX, NBN, NTHL1, and SIRT1. BARD1 was also associated with platinum resistance, and was induced by platinum exposure.

In vivo, antieンドoglin treatment decreased tumor weight in both ES2 and HeyA8MDR models when compared with control (35%–41% reduction, P < 0.05). Endoglin inhibition with carboplatin was associated with even greater inhibitory effect when compared with control (58%–62% reduction, P < 0.001).

Conclusions: Endoglin downregulation promotes apoptosis, induces significant DNA damage through modulation of numerous DNA repair genes, and improves platinum sensitivity both in vivo and in vitro. Antiendoglin therapy would allow dual treatment of both tumor angiogenesis and a subset of aggressive tumor cells expressing endoglin and is being actively pursued as therapy in ovarian cancer.

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Introduction

Epithelial ovarian carcinoma remains the most lethal gynecologic malignancy (1). While initial response to first-line therapy (consisting of surgical cytoreduction and combination platinum/taxane therapy) is usually effective, the majority of patients will ultimately recur with chemotherapy-resistant cancer and succumb to disease. This emphasizes the need for novel therapies aimed at targeting the population of cancer cells most resistant to initial therapy.

Endoglin (ENG) is a 180-kDa disulfide-linked homodimer transmembrane protein most prominently expressed on proliferating endothelial cells. It is a well-characterized angiogenic marker that is upregulated during angiogenesis, and is overexpressed in vascular endothelium in malignancies including ovarian, leukemia, gastrointestinal stromal tumors (GIST), melanoma, and laryngeal cancers, but is rarely expressed in nonendothelial cells (2, 3). It is a coreceptor of TGFBR2 that binds TGF-B and is an important mediator of fetal vascular/endothelial development (4). Recently, antiangiogenic agents have received extensive attention as new therapeutic modalities, and CD105 has become an additional target by which intratumoral angiogenesis may be targeted (5, 6). However, endoglin may serve in a capacity beyond angiogenesis alone. Studies in GIST (7) and breast cancer (8) suggest that endoglin is upregulated not only in tumor endothelial cells, but also in actual tumor
cells, and is associated with poor prognosis. Soluble endoglin has also been noted in ovarian cancer ascites (9), and increased endoglin expression in ovarian cancer endothelial cells is associated with poor prognosis (10). In addition, we have recently shown that while endoglin is rarely expressed in primary ovarian cancer cells, it is frequently expressed in recurrent platinum-resistant tumor cells, as compared with the primary untreated tumor (11). These findings suggest a broader role of endoglin in tumor cell biology beyond that of endothelial expression alone. The goal of our current study is to evaluate the effects of targeting tumor-specific endoglin in ovarian cancer both in vitro and in vivo and explore the mechanisms by which endoglin may contribute to chemoresistance.

Methods and Materials

Evaluation of endoglin expression in ovarian cancer cell lines

Multiple ovarian cancer cell lines were evaluated for the presence of endoglin, including HeyA8, HeyA8MDR, ES2, A2780ip2, A2780cp20, A2780cp55, SKOV3ip1, SKOV3Trp2, IGROV-AF1, and HIO-180. Cells were maintained in RPMI-1640 medium with 10% FBS (Hyclone). The taxane-resistant cell line HeyA8MDR was maintained in the same media with the addition of 15% ng/mL of paclitaxel. Cell lines in culture were washed with ice cold PBS twice, then fixed with 10% formalin. Endoglin downregulation by siRNA transfection

To determine the effects of endoglin downregulation in ovarian cancer cells, transient knockdown was accomplished with antiendoglin siRNA. Lipofectamine 2000 (Invitrogen) transfection was conducted on Hey8MDR and ES2 cell lines using control siRNA (target sequence: 5'-UUCUCCGAACGUGUCACGU-3', Sigma) lacking human or mouse targets, or 1 of 2 different endoglin-targeting constructs (5'-CAULcGCAGGCUGGCAAL-3' ['ENG_A'] or 5'-CAGAAA-CAGULcCAJULGUA-3' ['ENG_B'], Sigma). These anti-

Flow cytometry

After trypsinisation and centrifugation, the cell pellet was washed and resuspended in washing buffer (PBS containing 2% FBS and 0.1% sodium azide). 1 x 10^7 cells were resuspended in 50 μL of 10% goat buffer for 1 hour on ice. Cells were incubated in antibody against endoglin (Sigma HPA011862) in 10% goat serum for 1 hour on ice. Alexa-488-conjugated anti-rabbit antibody was applied on cells for 30 minutes and incubated on ice. The cells were washed twice in PBS and analyzed by fluorescence-activated cell sorting (FACS).
human sequences have no more than 8 consecutive bp homology with murine CD105 (by BLASTN) and therefore should not affect murine endoglin expression. Lipofectamine was added to 5 μg siRNA at a 3:1 v/v ratio (or as otherwise specified, as in Fig. 1E) were incubated for 20 minutes at RT, added to cells in serum-free RPMI to incubate for 12 hours in 6-well plates, then maintained in 10% FBS/RPMI for an additional 12 hours, trypsinized and replated on a 96-well plate at a concentration of 2,000 cells per well. Cells were treated with vehicle or increasing doses of carboplatin or paclitaxel to generate an IC50 curve. After 5 days, cells were washed and incubated with MTT reagent (Sigma) for 2 hours at 37°C. Media was then removed, cells dissolved in dimethyl sulfoxide, and optical density measurements at 570 nm read with a spectrophotometer. The IC50 was the chemotherapy concentration giving the OD IC50 reading, calculated by the formula

\[
\text{OD}_{50/2} = \frac{(\text{OD}_{\text{MAX}} - \text{OD}_{\text{MIN}})}{2 + \text{OD}_{\text{MIN}}}.
\]

Assays were repeated in triplicate.

Figure 1. A, endoglin expression in multiple ovarian cancer cell lines, as measured by Western blot analysis. B, as assessed by IHC, endoglin expression is predominantly cytoplasmic, although some cells with strong membranous staining are noted (arrows). C, a small but distinct endoglin-positive population is seen by flow cytometry. D, endoglin was effectively downregulated with siRNA. By TUNEL assay, Annexin V/PI colocalization shows a decrease in viable cells, and an increase in both early and late apoptosis, both alone and in combination with cisplatin. E, cells treated with increasing doses of cisplatin after endoglin downregulation were also assessed by MTT, with the OD570 reflecting the absorbance produced by viable cells. Endoglin downregulation resulted in a significant reduction in cell viability, and increased cisplatin chemosensitivity about 4-fold in ES2 model and 2-fold in HeyA8MDR. Lines denoting the calculated IC50 for control and endoglin-siRNA treatment are shown (gray lines).
Apoptosis analysis

Analysis of apoptosis was conducted with the Annexin V assay combined with propidium iodide (PI, eBiosciences #88-8005-74). ES2 and HeyA8MDR cells were transfected with either control siRNA or antiendoglin siRNA in serum-free RPMI growth media for 12 hours, followed by maintenance in 10% FBS/RPMI. Cells were trypsinized 96 hours following transfection, washed twice in PBS, and then resuspended in 200 μL 1 × binding buffer containing 5 μL of Annexin V. 10 μL of PI was added, cells were incubated for 10 minutes at RT in the dark. Fluorescent signal (FITC and PI) in cells were analyzed by FACS and data were analyzed with FlowJo v.7.6.1.

Alkaline comet assay

ES2 cells (n = 400,000 in 6-well plate) were transfected with endoglin and control siRNA. Twenty-four hours following transfection, cells were exposed to cisplatin at a concentration of 1 μmol/L (the approximate IC80 level for this line) for either 1 or 4 hours, carefully rinsed to remove the drug, and cultured in regular media. Vehicle or control siRNA were included in all experiments. At the indicated time points, cells were collected and subjected to alkaline comet assay according to the manufacturer’s instructions (catalog # 4250-050-K; Trevigen). Briefly, cells were combined with low melting agarose onto CometSlides (Trevigen). After lysis, cells were subjected to electrophoresis and stained with SYBR green. Subsequently, cells were visualized using fluorescent microscopy (Carl Zeiss). At least 200 comet images were analyzed for each time point using Comet Score software (version 1.5; TriTek Corp.). The number of tail-positive cells with small and large nuclei was manually counted by an examiner blinded to treatment group, and expressed as a percentage of all cells evaluated. Experiments were repeated in triplicate.

γ-H2AX foci formation

ES2 cell lines were cultured and seeded on sterile cover slips. Twenty-four hours following transfection with control or antiendoglin siRNA, cells were exposed to 1 μmol/L cisplatin for either 1 or 4 hours, carefully rinsed to remove the drug, and cultured in regular media. Following the treatment period, immunohistochemistry (IHC) was conducted as previously described (12, 13) with slight modification for foci staining. Briefly, cells were rinsed in PBS and incubated for 5 minutes at 4°C in ice-cold cytoskeleton buffer (10 mmol/L Hepes/KOH, pH 7.4, 300 mmol/L sucrose, 100 mmol/L NaCl, and 3 mmol/L MgCl2) supplemented with 1 mmol/L phenylmethylsulfonylfluoride, 0.5 mmol/L sodium vanadate and proteasome inhibitor (Sigma, 1:100 dilution) followed by fixation in 70% ethanol for 15 minutes. The cells were blocked and incubated with primary antibody (1:500 dilution, antiphosphoH2AX Ser139, Millipore, catalog # MI-07-164). The secondary antibody was anti-rabbit Alexa Fluor 488–conjugated antibody (1:2,000 dilution; Invitrogen). γ-H2AX (DPAT; Invitrogen, catalog # D21490) was used for nuclear staining. The cover slips were subsequently mounted onto slides with mounting media (Aqua poly mount, Polysciences, Inc. catalog # 18606) and analyzed via fluorescence microscopy (Carl Zeiss). Positive and negative controls were included on all experiments. A total of 500 cells were assessed. For foci quantification, cells with greater than 10 foci were counted as positive according to the standard procedure. Experiments were repeated in triplicate.

RNA extraction from cell lines

Total RNA was isolated from ovarian cancer cell lines using Trizol reagent (Invitrogen) per manufacturer's instructions. RNA was then DNase treated and purified using the RNaseasy Mini Kit (QiAGEN). RNA was eluted in 50 μL of RNase-free water and stored at −80°C. The concentration of all RNA samples was quantified by spectrophotometric absorbance at 260 of 280 nm using an Epoch Microplate Spectrophotometer (BioTek Instruments, Winooski, VT).

DNA repair qPCR array

ES2 and HeyA8 cells in culture were exposed to siRNA against endoglin in Lipofectamine 2000 as described above. After 48 hours, cells were collected and miRNA extracted. Two replicates per cell line were conducted. These 4 samples were then subjected to a quantitative PCR (qPCR) array consisting of 84 genes from DNA damage/repair pathways (plus additional housekeeping genes; the RT2 Profiler PCR Array Human DNA Damage Signaling Pathway, SA Biosciences Cat# PAHS-209Z, conducted per manufacturer’s instructions). Briefly, extracted RNA was converted to cDNA and amplified using the RT² qPCR PreAMP cDNA Synthesis Kit (SA Biosciences). Quality of cDNA was confirmed with the Human RT² RNA QC PCR Array (SA Biosciences). Gene expression was analyzed using the Human DNA Damage Signaling Pathway RT² Profiler PCR Array (SA Biosciences), which profiles the expression of 84 genes involved in pluripotent cell maintenance and differentiation (14). Functional gene groupings consist of the ataxia telangiectasia mutated (ATM) and ATM and Rad3-related (ATR) signaling, nucleotide excision repair, base-excision repair, mismatch repair, double strand break repair, apoptosis, and cell cycle checkpoint regulators. PCR amplification was conducted on an ABI Prism 7900HT sequence detection system and gene expression was calculated using the comparative Ct method (15).

Reverse transcription and quantitative PCR

Extracted RNA samples were diluted to 20 ng/μL using RNase-free water. cDNA was prepared using the High Capacity cDNA Reverse Transcription Kit (Applied Biosystems). The resulting cDNA samples were analyzed using qPCR. Primer and probe sets for ENC (PPH01140F) ATM (PPH00325C), BARD1 (PPH09451A), DDIT3 (PPH00310A), H2AFX (PPH12636B), BN (PPH00946C), NTHL1 (PPH02720A), PPR1R1SA (PPH02081E), SIRT1 (PPH02188A), ATPB (PPH06148A), and RPLP0 (Hs09999990_m1, housekeeping gene) were obtained.
from SA Biosciences and used according to manufacturer’s instructions. PCR amplification was conducted on an ABI Prism 7900HT sequence detection system and gene expression was calculated using the comparative Ct method.

**Orthotopic mouse model**

Female athymic nude mice (nu-nu) were obtained from the National Cancer Institute Frederick Cancer Research and Development Center (Frederick, MD). Mice were cared for in accordance with American Association for Accreditation of Laboratory Animal Care guidelines, the United States Health Services Commissioned Corps “Policy on Human Care and Use of Laboratory Animals,” and University of Alabama at Birmingham Institutional Animal Care and Use Committee policies. ES2 tumors were established by intraperitoneal (IP) injection of 1 x 10^6 cells suspended in 200 μL of serum-free RPMI media. Hey8MDR tumors were established in a similar way, using 5 x 10^5 cells. To evaluate the effectiveness of endoglin-targeted therapy in vivo, siRNA was incorporated into chitosan (CH) nanoparticles as previously described (16, 17). Therapy was initiated 1 week after tumor cell injection. Mice were randomized to 1 of 4 treatments (n = 10 per group): (i) control siRNA alone (150 ug/kg twice weekly injected IV), (ii) control siRNA with IP carboplatin (160 mg), (iii) antiendoglin siRNA (150 μg/kg twice weekly) alone, or (iv) antiendoglin siRNA with carboplatin. All treatments were suspended in 100 μL 0.9% normal saline. Mice were monitored for adverse effects, and all treatment groups sacrificed when control mice became uncomfortable with tumor burden. ES2 tumors behaved aggressively, and were harvested following 2 weeks of treatment. Hey8MDR tumors were harvested after 3 weeks of therapy. Mouse weight, ascites volume, tumor weight, and distribution of tumor were recorded. Representative tumor samples were obtained from 5 mice in each treatment group, formalin fixed, paraffin embedded, and cut into 5 micron sections for evaluation of proliferating cell nuclear antigen (PCNA), terminal deoxynucleotidyl transferase–mediated dUTP nick end labeling assay (TUNEL), γH2AX (phosphorylation of Histone 2A protein), and 53BP1 (a mediator of the DNA damage checkpoint).

**Tumor PCNA immunohistochemistry and TUNEL**

Sections were deparaffinized and rehydrated, and antigen retrieval was conducted with citrate buffer (pH 6.0) in pressure cooker for 5 minutes. Endogenous peroxidase activity was quenched with 3% hydrogen peroxide solution in methanol for 15 minutes. Sections were blocked with CytolQ immune diluent and block and probed with PCNA primary antibody (PCNA-PC10, Cell signaling Technology, 1:5,000 dilution) at 4°C overnight. Sections were washed and incubated with the Mach 3 mouse HRP polymer system. After rinsing, the sections were incubated with DAB chromophoric solution (Scytek Labs) for 5 minutes at room temperature, then counterstained with Gill’s hematoxylin (Rica chemicals). Four x40 microscopic fields were counted from each section, averaged over 5 mice in each treatment group, and expressed as a percentage of the total number of tumor cells. Apoptosis was determined by TUNEL assay with a colorimetric apoptotic cell detection kit (Promega), per manufacturer’s instruction. As with PCNA IHC, 4 microscopic fields at x40 magnification were evaluated from each section. Stained cells were recorded as a percentage of the total number of tumor cells.

**Tumor γH2AX and 53BP1 IHC**

Formalin fixed tissues were heated at 60°C for 1hr and rehydrated according to standard protocol. Subsequently, the tissues were permeabilized in 0.5% Triton X-PBS for 10 minutes, blocked in 2% BSA-0.1% Triton-X-PBS for 1 hour, and incubated with primary antibodies (1:500 dilution, anti phospho H2AX Ser139, Millipore, catalog #MI-07-164; 1:500 dilution, anti-53BP1, Novus Biologicals, and catalog # NB100-304). The secondary antibody was anti-rabbit Alexa Fluor 488–conjugated antibody (1:2,000 dilution; Invitrogen). DAPI (Invitrogen, catalog # D21490) was used for nuclear staining. The slides were subsequently mounted using mounting media (Aqua poly mount, Polysciences, Inc. catalog # 18606) and analyzed via fluorescence microscopy (Carl Zeiss). Positive and negative controls were included on all experiments. A total of 500 cells were assessed. For foci quantification, cells with greater than 10 foci were counted as positive according to the standard procedure. Experiments were repeated in triplicate. Data show the mean and SEM.

**Statistics**

Analysis of normally distributed continuous variable was conducted using a 2-tailed Student’s t test. Those data with alternate distribution were examined using a nonparametric Mann–Whitney U test. A P < 0.05 was considered statistically significant.

**Results**

**Effects of endoglin downregulation on cell viability and platinum sensitivity**

Endoglin is expressed by multiple ovarian cancer cell lines (Fig. 1A), most prominently in HeyA8, HeyA8MDR, and ES2 cells. Weak expression was detected in the HO180, A2780ip2, A2780cp20, SKOV3ip1, SKOV3TRp2, and IGROV-AF1 cell lines. This was previously showed at the mRNA level by qPCR (11). To confirm that expression was predominantly at the cell surface, consistent with its function as a coreceptor for TGFβ, we conducted immunohistochemistry on the ES2 and HeyA8MDR cell lines. Surprisingly, the predominant staining was noted in the perinuclear cytoplasm (Fig. 1B). This was confirmed by flow cytometry, where interestingly not only was membranous staining rare, but there was a very distinct separate population with 100-fold fluorescent intensity (rather than a global shift among all cells), consistent with a separate small population of cells with strong endoglin surface expression (Fig. 1C). This population represented 6.0% of HeyA8MDR and 5.4% of ES2 cells. On close examination of IHC on cultured cells, a minority of the cells could be seen to have
strong membranous expression of CD105 (arrows, Fig. 1B). A separate endoglin-positive population has previously been noted in renal cell carcinoma cells, which did exhibit stem-cell properties (18). However, these data are conclusive that the majority of endoglin expression in ovarian cancer is cytoplasmic, suggesting a role other than just as a coreceptor for TGF-beta.

To determine whether siRNA-mediated downregulation of endoglin had significant effects on viability and chemosensitivity, 2 different siRNA constructs (ENG_A siRNA and ENG_B siRNA) were examined. Both effectively reduced endoglin expression at 48 hours at the mRNA (Fig. 1D) and protein level (11). Both were previously shown to reduce cell viability (11). To determine the mechanism by which endoglin knockdown reduced viability, evaluation of apoptosis was conducted by the TUNEL assay. Annexin V/PI cofluorescent staining conducted 48 hours following transfection indicated significantly fewer viable cells in those treated with antiendoglin siRNA than those treated with control siRNA (47.2% vs. 65.1%, *P < 0.05*). A sample flow cytometry plot and a graph of average over 3 experiments are shown in Fig. 1D. Those treated with antiendoglin siRNA had increased percentages of cells in both early apoptosis (21.5% vs. 17.9%, *P < 0.05*) and late apoptosis (18.9% vs. 12.0%, *P < 0.05*). Effects were more pronounced when combined with cisplatin. To determine whether Endoglin knockdown had an effect on viability in combination with chemotherapy, cells were exposed to siRNA, then replated after 24 hours, and incubated with increasing concentrations of cisplatin or paclitaxel. Because endoglin downregulation alone was associated with substantial cell death in the HeyA8MDR model, knockdown was conducted with several dilutions of siRNA in an effort to more clearly delineate effects on platinum sensitivity. In both ES2 (normal IC50 for cisplatin = 0.7 μmol/L) and HeyA8MDR (normal IC50 for cisplatin = 0.65 μmol/L) models, increased cisplatin chemosensitivity was noted (up to 4-fold and 2-fold reduction in IC50, respectively, Fig. 1E). Similar experiments were conducted with paclitaxel, which did not show an increased sensitization with endoglin downregulation (data not shown).

**Downregulation of endoglin induces DNA damage in vitro**

Because platinum toxicity is mediated primarily through induction of DNA damage, we evaluated whether the enhanced cisplatin sensitivity from endoglin knockdown was a result of increased DNA damage. DNA damaging agents can induce both single-stranded breaks (SSB) and double stranded breaks (DSB) which can lead to initiation of apoptotic pathways. DNA damage in the ES2 line was first assessed via an alkaline comet assay, which detects both SSB and DSB. As quantified in Fig. 2A, increased DNA damage over 24 hours was observed with cisplatin, endoglin downregulation with siRNA, and the combination (although combination therapy was not significantly increased compared with either single-agent treatment). A representative section showing common effects on nearly all cells is shown (Fig. 2B). Because a long comet tail can be the result of either DNA damage without death or apoptosis-associated DNA release, the nucleus size was also quantified. A small nucleus would be associated with apoptosis, whereas a long comet tail associated with a normal (larger) nucleus would indicate just DNA damage. As shown in Fig. 2C for cells treated for 24 hours, those cells with a long tail present predominately still had a large nucleus. Because most toxic effects on viability noted previously were assessed at 48 hours or longer, this DNA damage may be a precursor to apoptosis induction. But it does show that DNA damage is the inciting event, rather than a result of apoptosis triggered by other mechanisms.

To further characterize the specific nature of DNA damage, development of foci of activated γ-H2AX was conducted (Fig. 2D). ES2 cells were used, because of the rapid toxicity and cell death noted with endoglin downregulation with HeyA8. Phosphorylation of the histone protein H2AX on serine 139 (γ-H2AX) occurs at sites flanking DNA DSBs. The phosphorylation of thousands of H2AX molecules forms a focus in the chromatin flanking the DSB site that can be detected in situ. A higher proportion of cells with persistent γ-H2AX foci were noted with endoglin downregulation, to an even greater extent than cisplatin alone. The combination of cisplatin and endoglin downregulation induced more DSB repair than either agent alone. Collectively, these data suggest that a primary mechanism of DNA damage after endoglin downregulation is through induction of double-strand breaks in DNA.

**Endoglin-targeting DNA damage is through effects on multiple mediators of DNA repair**

To determine the mechanism by which downregulation of endoglin induces DNA damage, we first subjected both ES2 and HeyA8MDR cells treated with control siRNA or endoglin-siRNA for 48 hours to a qPCR-based array of 84 genes participating in DNA damage and repair pathways. This exploratory analysis found multiple genes that were either downregulated or upregulated in response to decreased endoglin, some of which were only associated with changes in 1 cell line (Supplemental Table S1). Select genes were then chosen for confirmatory assessment with qPCR (Fig. 3A). Genes for these analyses were selected based on the degree to which they were altered, the associated *P* value, and whether the change was noted in both cell lines. With endoglin downregulation, significant concurrent downregulation was noted by qPCR in H2AFX (36%–43%), BARD1 (47%–71%), NBN (38%–41%), NTHL1 (39%–53%), and SIRT1 (34%–49%). A significant induction of mRNA was noted in DDR1 (1.9–2.6-fold) and PPP1R15A (1.27–1.74-fold). There was no single DNA repair pathway subclass that comprised all affected genes, but consistent with data from the γ-H2AX assay, most were participants in either the double stranded break repair (BARD1, H2AFX, NBN) or nucleotide excision repair (SIRT1, NTHL1).

The downregulation of BARD1 was particularly interesting. BARD1 is an oncogenic regulator of BRCA1, and
downregulation would be expected to result in export of BRCA1 from the nucleus and impairment of DNA repair. Furthermore, BARD1 was noted to be significantly upregulated in chemoresistant tumor samples from patients, compared with their primary tumors (11). BARD1 expression is prominent in ES2 and HeyA8MDR, which follows if it is under transcriptional regulation by endoglin.

Therefore, we examined BARD1 induction in response to platinum treatment in a progressively platinum-resistant triad of cell lines derived from A2780: A2780ip2 (which generates IP tumors more consistently than the parental line but is chemosensitive), A2780cp20 (having a platinum IC50 of 20 μmol/L), and A2780cp55 (with an IC50 of 55 μmol/L). The A2780cp20 and cp55 lines are stably platinum resistant, and not chronically maintained in platinum. BARD1 expression is minimal in the parental A2780ip2 line, but increases at baseline (“Untreated”) with each degree of platinum resistance (Fig. 3B). In addition, when exposed to an IC50 concentration of carboplatin, BARD1 mRNA production is significant increased in both A2780ip2 and A2780cp20. Levels were unchanged with carboplatin exposure in A2780cp55, likely because of its high baseline expression. A significant reduction in BARD1 with endoglin downregulation and an induction of BARD1 in response to platinum exposure strongly implicate this gene and its control on BRCA1 as a major mechanism through which endoglin downregulation may lead to DNA damage, apoptosis, and sensitivity to platinum.

In addition to enhanced DNA repair mechanisms, a major mechanism of platinum resistance is through increased export of platinum agents through copper transporters such as ATP7B (19). Therefore, we also examined the effects of endoglin downregulation on ATP7B by qPCR. SiRNA-mediated targeting of endoglin resulted in a significant downregulation of ATP7B (by 20%–24%, \( P < 0.05 \), Fig. 3C). While significant, this was not to the same extent many DNA repair genes were induced or activated.

**Evaluation of tumor growth with antiendoglin treatment in an orthotopic murine model**

To determine if endoglin downregulation was an effective therapy in vivo, an orthotopic murine model was used using human specific antiendoglin siRNA delivered within a CH nanoparticle. CH is a natural nanoparticle that has been previously shown to result in efficient delivery of siRNA to tumor after IV administration, with subsequent protein

![Figure 2](https://example.com/figure2.png)
downregulation and gene-specific modulation (16, 20–22). Because the siRNA delivered is specific to the human endoglin mRNA, any observed effect would be expected to be because of targeting the tumor cells, rather than the vasculature, which would require murine-specific siRNA. ES2 and HeyA8MDR cells were injected IP, and treatment was started 1 week later with (i) control siRNA-CH alone, (ii) control siRNA-CH plus carboplatin, (iii) antiendoglin siRNA-CH alone, or (iv) antiendoglin siRNA-CH plus carboplatin. Carboplatin was used instead of cisplatin because of its preferable side-effect profile in vivo, which has led to its choice as standard of care in ovarian cancer patients. Tumors showed reduced growth both with endoglin downregulation alone and in combination with platinum. In the ES2 model (Fig. 4A), mice treated with carboplatin had similar tumor burden to control ($P = 0.555$), an expected result because of the highly platinum-resistant nature of the ES2 cell line, which is derived from a patient with clear cell carcinoma. Mice treated with antiendoglin siRNA alone had a significantly reduced tumor weight, by 35.6% ($P = 0.014$). Combined END-siRNA-CH with carboplatin was more effective than either agent alone, with a 57.7% reduction in tumor weight compared with control ($P < 0.001$). Furthermore, combination therapy was more effective than
siRNA-endoglin-CH alone, with an additional 34.3% reduction ($P = 0.033$). In the HeyA8MDR model (Fig. 4B), mice treated with carboplatin, endoglin-siRNA-CH, or combination therapy had significantly less tumor weight when compared with control (34% reduction $P = 0.027$, 41.2% reduction $P = 0.002$, and 61.2% reduction $P < 0.01$, respectively). Those treated with carboplatin and control siRNA-CH had similar tumor burden reduction as those treated with endoglin-siRNA-CH ($P = 0.628$). Combination therapy was again more effective than either single-agent carboplatin (additional 40.6% reduction, $P = 0.069$), or endoglin-siRNA alone (34%, $P = 0.048$). In the resected tumors, reduced expression of endoglin was confirmed with immunohistochemistry, in both groups of tumors treated with endoglin-siRNA-CH. Representative sections are pictured (Fig. 4C). With both models, there was not a significant difference in mouse weight in any group. The distribution of tumor was also similar in all groups, suggesting there was not a significant effect on particular site of growth, adhesion, or migration.

**Figure 4.** An orthotopic murine model using ES2 and HeyA8MDR cell lines was used to evaluate treatment with control siRNA-CH alone, control siRNA-CH with carboplatin, antiendoglin siRNA-CH alone, or antiendoglin siRNA-CH plus carboplatin. A, in the ES2 model, carboplatin was ineffective, as expected given the platinum-resistant nature of the ES2 cell line. Mice treated with anti-endoglin siRNA-CH alone and combined with carboplatin showed less tumor burden when compared with control or carboplatin alone. Those treated with both antiendoglin siRNA-CH and carboplatin also showed reduced tumor burden when compared with those endoglin-siRNA-CH alone ($P = 0.03$). B) In the HeyA8MDR model, tumors were smaller in mice treated with carboplatin or antiendoglin siRNA-CH alone, and again combination therapy was more effective than either agent alone ($P < 0.05$). C, by qualitative assessment with IHC, endoglin expression was reduced in the tumors treated with endoglin-siRNA-CH therapy.
Endoglin downregulation induces DNA damage and apoptosis in vivo

Our in vitro findings suggest a role of DNA damage and apoptosis following endoglin downregulation. To validate these findings in vivo, tumors from each treatment group described above were examined for proliferation, apoptosis, and induction of DNA damage. PCNA IHC was conducted and revealed no significant differences in percentage of PCNA positive cells, with approximately half of cells being positive in each treatment group (Fig. 5A). A lack of effect on progression through the cell cycle and proliferation may explain why combination with taxanes was not synergistic with endoglin downregulation in vitro. TUNEL assay was conducted to evaluate differences in apoptosis between treatment groups. Control, carboplatin and anti-endoglin siRNA groups were not significantly different. However, the cohort receiving combination therapy had a significantly higher percent of apoptotic cells when compared with control ($P < .001$, Fig. 5B). This increase, although statistically significant, is relatively small, which may be because of clearance of dead cells over the course of the 4-week experiment. To determine if DNA damage was still noted in the tumors collected at completion of therapy, fluorescent IHC was conducted to evaluate for γ-H2AX as an indicator of DNA damage. There was a significantly higher amount of DNA damage in both treatment groups receiving anti-endoglin treatment when compared with control or single-agent carboplatin (Fig. 5C). Finally, 53BP1 is a key protein in the DNA damage checkpoint that was evaluated by IHC. A significantly higher amount of 53BP1 was noted in both cohorts that received anti-endoglin treatment when compared with either control or single-agent carboplatin (Fig. 5D).

Figure 5. Tumors from each treatment group in our orthotopic mouse model were collected and analyzed by PCNA immunohistochemistry, TUNEL assay, γ-H2AX IHC, and 53BP1 IHC. A, there were no significant differences in PCNA IHC, with approximately half of cells being positive. B, there was a significant increase in apoptosis in the cohort receiving combination therapy when compared with control as shown by TUNEL assay. C, fluorescent IHC was conducted to evaluate for γ-H2AX as an indicator of DNA damage. There was a significantly higher amount of DNA damage in both treatment groups receiving anti-endoglin treatment when compared with control or single-agent carboplatin. D, finally, 53BP1 is a key protein in the DNA damage checkpoint that was evaluated by IHC. A significantly higher amount of 53BP1 was noted in both cohorts that received anti-endoglin treatment when compared with either control or single-agent carboplatin.
Discussion

Endoglin is overexpressed in solid tumor vasculature and is a reliable marker of angiogenesis (5). Multiple antiangiogenic therapies have been studied in ovarian cancer, and antiendoglin therapy has been proposed for several cancers in which increased endothelial endoglin expression has been noted (23). However, to date, few studies address the expression of endoglin on tumor cells and its potential role in cancer progression. Building on our previous findings that Endoglin is increase in recurrent samples when compared with matched primary tumors (11), we have shown that endoglin expression is highly expressed in many ovarian cancer cell lines, and that downregulation results in induction of cell death through induction of DNA damage and a synergistic killing effect with platinum agents both in vitro and in vivo. These novel findings show that therapeutic targeting endoglin may affect both the vasculature and malignant cells within the tumor microenvironment.

The primary canonical role of endoglin is as a coreceptor for TGF-β (24–26). As such, its expression on endothelial cells is primarily on the cell membrane (27). However, we interestingly found endoglin expression in ovarian cancer cells was predominantly cytoplasmic, and clustered together in the perinuclear region of the cell. This would suggest that endoglin either has a separate TGF-β–independent function dependent on nuclear proximity, or trafficking to the cell membrane is an important component of its regulation. Only a small (5%–6%), but well-defined population had surface expression. This distinct population would be consistent with a cancer stem cell-like population, as has been previously described in endoglin-positive renal cell carcinoma (18). Endoglin-positive meningioma cells have been previously described in endoglin-positive renal cell carcinoma (18). Endoglin-positive meningioma cells have similar increased tumorigenicity and capacity to differentiate into adipocytes and osteocytes (28).

Henriksen and colleagues evaluated endoglin expression in primary ovarian cancer cells and found that high tumor cell endoglin staining correlated with short overall survival (29). Another group has shown that cells from cultured ascites that progressed toward a mesenchymal phenotype were high in endoglin (30). We identified endoglin as a potential target for therapeutics through a screen of stem cell pathways overexpressed in recurrent ovarian cancer samples. Among members of the TGF-β, Notch, Wnt, and Hedgehog pathways, endoglin was most significantly and consistently overexpressed in recurrent ovarian cancer samples when compared with their matched primaries, suggesting a role in chemoresistance (11). We specifically examined stem cell pathways to address the question of whether the cancer stem cell population may be responsible for surviving initial chemotherapy. Endoglin has previously been implicated in stem cell biology, having originally been described on hematopoietic progenitor cells (31), and later showed to identify precursor cells capable of tissue-specific differentiation (32, 33).

It makes sense that cells with prolonged survival, such as stem/progenitor cells, would reply on pathways to mediate DNA damage. Because of the association noted with increased endoglin expression in platinum (and taxane)-resistant recurrent ovarian cancers (11), and the contribution of enhanced DNA repair for platinum resistance (19), we further examined the contribution of endoglin to DNA repair. We have found a previously unknown contribution of endoglin to expression of numerous DNA repair genes. These encompass several subtypes of DNA repair, predominantly double stranded break repair (BARD1, H2AFX, and NBN), but also nucleotide excision repair (SIRT1, NTHL1), and cell-cycle arrest (DDIT3, PPP1R15A), which may be a reactionary process to accomplish DNA repair. Recently BARD1 has been implicated in ovarian cancer pathogenesis for its interaction with BRCA1 and 2. BARD1 and BRCA1 interact with each other through their amino terminal RING finger domains. This interaction is required for BRCA1 stability, as well as for nuclear localization. The BRCA1-BARD1 complex serves as an E3 ubiquitin ligase, which has been noted to have critical activity in both the cell-cycle check point through H2AX, NPM, and γ-tubulin and in DNA fragmentation (34, 35). In addition, patients with mutations of both BARD1 and BRCA2 have a substantially increased risk for development of both breast and ovarian cancer. While BARD 1 has been found to interact and colocalize with BRCA1 at the spindle poles in early mitosis, it also interacts with BRCA2 at late mitosis in the midbody. Therefore BARD1 has been found to sequentially link the function of these (36) 2 proteins. In our analysis, BARD1 expression was reduced by 50% to 75% and H2AX expression was reduced 35% to 50% following endoglin knockdown. endoglin-mediated downregulation of BARD1 and its subsequent effects on BRCA1 and 2 and H2AX may therefore explain why we found substantial decreased cell viability, DNA damage and increased apoptosis (34).

Silent Information Regulator Type 1 (SIRT1) is a nicotinamide adenine dinucleotide-dependent class III histone deacetylase. SIRT1 has is associated with longevity and has been found to act primarily by inhibiting cellular senescence. SIRT1 is upregulated in tumor cell lines and human tumors, and may be involved in tumorigenesis (36). It has also been found to be overexpressed in chemoresistant tumors of cancer patients. SIRT1 inhibition leads to decrease in MDR1 expression and increase in drug sensitivity in ovarian cancer cell lines (37). Our research suggests that endoglin knockdown was associated with a 30% to 50% reduction in SIRT1. This inhibition may help account for the increased platinum sensitivity we found with endoglin downregulation.

In regards to therapeutic development in cancer patients, delivery of siRNA constructs has the potential to offer long duration of target inhibition as well as reduced toxicity compared other approaches (16, 20, 38–44). However, development of a delivery modality for siRNA constructs remains the rate-limiting step in translational research. Early delivery modalities included delivery of "naked" siRNA. Later attempts included high-pressure siRNA injections and intratumoral injections, neither of which has shown substantial success. The development of CH encapsulation and nanoliposomes to deliver siRNA has become widely accepted in translational studies and is and...
promising as a therapeutic modality as modifications to enhance in vivo delivery progress (22). SiRNA-mediated therapeutics are being used in ongoing trials with patients with macular degeneration, acquired immunodeficiency syndrome, malignant melanoma, acute renal failure, hepatitis B, and now in cancer patients, where phase I trials are in development. One particular advantage of siRNA-based therapeutics over conventional treatment modalities would apply to endoglin-based targeting. If indeed, the cytoplasmic portion of endoglin is important to chemoresistance, downregulation of production at the mRNA level may be more effective than antibody-based targeting currently aimed at inhibiting angiogenesis (45, 46).

Because of the rarity of endoglin expression in normal tissues, antendoglin therapy has the potential to offer tumor-directed therapy in addition to antiangiogenic therapy. Antiendoglin therapy is being explored as a therapeutic in several cancers as an antiangiogenic agent. In ovarian cancer, endoglin-targeted therapies may offer the additional advantage of targeting tumor cells overexpressing endoglin, including platinum-resistant tumors. Its effects on BRCA1 and 2 and H2AX through BARD1 downregulation, and its association with SIRT1 downregulation contribute to DNA damage repair and enhancement of platinum sensitivity. Our data strongly suggest that endoglin-targeted therapy has the potential to improve platinum sensitivity through induction of DNA damage and should be actively pursued as a potential therapy in the treatment of ovarian cancer.

**References**
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Endoglin (CD105) Contributes to Platinum Resistance and Is A Target for Tumor-Specific Therapy in Epithelial Ovarian Cancer

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