Targeting the Notch Ligand Jagged1 in Both Tumor Cells and Stroma in Ovarian Cancer

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Abstract

Purpose: Jagged1, a Notch ligand, is expressed on both tumor epithelial and endothelial cells and therefore may be amenable to dual targeting of the tumor stroma and malignant cell compartments of the tumor microenvironment.

Experimental Design: We describe in vitro effects of targeting of Jagged1 on ovarian cancer cells and in vivo effects of independent targeting of stromal and malignant cell Jagged1 using species-specific human or murine siRNA constructs incorporated into chitosan nanoparticles and delivered intravenously in an orthotopic mouse model.

Results: Jagged1 expression was prominent in SKOV3ip1 and IGROV-AF1, and significantly overexpressed in SKOV3TRip2, a taxane-resistant SKOV3 subclone. Jagged1 silencing with siRNA decreased cell viability and reversed taxane chemoresistance. In two different orthotopic ovarian cancer models, treatment with anti-human Jagged1 siRNA-CH reduced growth by 54.4% to 58.3% and with anti-murine Jagged1 siRNA-CH reduced growth by 41.7% to 48.8%. The combination of both species-specific constructs reduced tumor weight by 87.5% to 93.1% and sensitized SKOV3TRip2 tumors to docetaxel in vivo. Tumors showed reduced microvessel density with anti-murine Jagged1 constructs and decreased proliferation with anti-human Jagged1 siRNAs-CH. In addition, we show that Jagged1 downregulation does not sensitize cells to taxanes through a reduction in MDRI expression, but at least in part by cross-talk with the GLI2 mediator of the Hedgehog pathway.

Conclusions: Jagged1 plays dual roles in cancer progression through an angiogenic function in tumor endothelial cells and through proliferation and chemoresistance in tumor cells. Dual inhibition represents an attractive therapeutic strategy for ovarian and potentially other malignancies. Clin Cancer Res; 17(17); 5674–85. ©2011 AACR.

Introduction

Ovarian cancer is the leading cause of death from a gynecologic malignancy. Although ovarian cancer is among the most chemosensitive malignancies at the time of initial treatment (surgery and taxane/platinum-based chemotherapy), most patients will develop tumor recurrence and succumb to chemoresistant disease (1). Evaluation of multiple chemotherapy agents in several combinations in the last 20 years has yielded modest improvements in progression-free survival, but no increases in durable cures. The clinical course suggests that a population of tumor cells has either inherent or acquired resistance to chemotherapy that allows survival with initial therapy and ultimately leads to recurrence. Targeting the cellular pathways involved in this resistance may provide new treatment modalities for ovarian cancer.

The Notch pathway plays an important role in cell growth and differentiation during embryonic development (2). Mature Notch receptors (Notch1; refs. 2–4) consist of an extracellular and transmembrane unit. Upon binding to ligands (Jagged1, 2 and delta-like ligand (DLL) 1, 3, and 4) on the surface of neighboring cells, the Notch extracellular unit is dissociated from the transmembrane unit, which is then endocytosed into ligand-expressing cells. Further cleavage of the transmembrane unit by “a disintegrin and metalloprotease” proteins (ADAM10 and/or 17) and γ-secretase produces an active intracellular fragment that translocates to the nucleus, where it forms a transcriptional complex with CSL, mastermind-like proteins (MAML1, 2, and 3), and p300. Transcriptional mediators of Notch signaling include members of the HES and HEY family. Recent reports have implicated Notch signaling in multiple
malignancies (3), including ovarian cancer (4–7), and suggest that this pathway may be especially important in maintaining the subpopulation of cancer cells with stem cell properties (8) as well as conferring resistance to chemotherapies (9, 10). The Notch ligand Jagged1 is frequently overexpressed on both ovarian cancer cells (6) and tumor-associated endothelial cells (11), suggesting that selectively targeting this protein may present a novel therapeutic strategy to target both stromal and tumor cells in ovarian cancer. The Notch pathway is highly implicated in normal and tumor-associated angiogenesis (12–14). Moreover, studies have shown that Jagged1 can activate gene expression (15) and transform kidney epithelial cells (16) without involvement of Notch signaling, indicating that Jagged1 may have its own signaling function that is important to tumorigenesis independent of the canonical Notch pathway.

As most studies have focused on the effects of inhibiting the Notch receptor and its downstream signaling, specific inhibition of Jagged1 has not been fully explored, which is especially important given potential Notch-independent effects of Jagged1. In addition, it is not known whether the greater \( m \) in vivo contribution of Notch inhibition is through its antiangiogenic mechanism or specific activity against malignant cells. In this study, we sought to determine the effects of targeting Jagged1 on the viability and taxane and platinum chemoresistance of ovarian cancer cells and tumor-associated stroma, independently and concurrently. Utilizing a novel methodology for delivering siRNA \textit{in vivo}, we independently target Jagged1 in stromal cells with anti-murine siRNA and Jagged1 in malignant cells with anti-human siRNA and show that Jagged1 plays important roles in tumor angiogenesis and chemo resistance and is an attractive target for therapy.

Materials and Methods

Cell lines and culture

The ovarian cancer cell lines A2780ip2, A2780cp20, HeyA8, HeyA8MDR, IGROV-AF1, SKOV3ip1, and SKOV3-TRip2 (17, 18) were maintained in RPMI-1640 medium supplemented with 10% FBS (HyClone). A2780cp20 (platinum resistant), HeyA8MDR (taxane resistant), and SKOV3TRip2 (taxane resistant, a kind gift of Dr. Michael Seiden (19), were generated by sequential exposure to increasing concentrations of chemotherapy. HeyA8MDR and SKOV3TRip2 were maintained with the addition of 150 ng/mL of paclitaxel. The murine ovarian endothelial cell (MOEC) line was established from the immortomouse, which harbors temperature-sensitive SV40 large T antigen overexpression (20). MOEC cells allowed for the evaluation of murine-specific Jagged1 expression. All cell lines were routinely screened for \textit{Mycoplasma} species (GenProbe detection kit; Fisher) with experiments carried out at 70% to 80% confluent cultures. Purity of cell lines was confirmed with short tandem repeat repeat genomic analysis, and only cells less than 20 passages from stocks were used in experiments.

RNA extraction and reverse transcription

Total RNA was isolated from ovarian cancer cell lines by using Trizol reagent (Invitrogen) per manufacturer’s instructions. RNA was then DNase treated and purified by using the RNaseasy Mini Kit (QiAGEN). RNA was eluted in 50 \( \mu \)L of RNase-free water and stored at \(-80\)°C. The concentration of all RNA samples was quantified by spectrophotometric absorbance at 260/280 nm by using an Eppendorf BioPhotometer plus. Prior to cDNA synthesis, all RNA samples were diluted to 20 ng/\( \mu \)L using RNase-free water. cDNA was prepared by using the High Capacity cDNA Reverse Transcription Kit (Applied Biosystems). The resulting cDNA samples were analyzed using quantitative PCR.

Quantitative PCR

Primer and probe sets for GLI1 (Hs00171790_m1), GLI2 (Hs00257977_m1), HES1 (Hs00172878_m1), HEY1 (Hs00232618_m1), JAG1 (Hs01070032_m1), MDR1 (Hs00184500_m1), NOTCH1 (Hs00413187_m1), NOTCH3 (Hs01128541_m1), and RPLP0 (Hs99999902_m1; housekeeping gene) were obtained from Applied Biosystems and used according to manufacturer’s instructions. PCR amplification was carried out on an ABI Prism 7900HT sequence detection system, and gene expression was calculated by using the comparative cycling threshold \((C_{\text{t}})\) method as previously described (21). Briefly, this technique uses the formula \(2^{-\Delta\Delta C_{\text{t}}}\) to
calculate the expression of target genes normalized to a calibrator. The $C_i$ indicates the cycle number at which the amount of amplified target reaches a fixed threshold. $C_i$ values range from 0 to 40 (the latter representing the default upper limit PCR cycle number that defines failure to detect a signal).

**Western blot analysis**

Cultured cell lysates were collected in modified radioimmunoprecipitation assay lysis buffer with protease inhibitor cocktail (Roche) and subjected to immunoblot analysis by standard techniques (22) using anti-Jagged1 antibody (28H8; Cell Signaling Technology) at 1:1,000 dilution overnight at 4°C, PARP antibody (7D3-6; BD Biosciences) at 1:1,000 dilution overnight at 4°C, anti-Cleaved Notch1 antibody (Cell Signaling Technology) at 1:1,000 dilution overnight at 4°C, anti-Notch3 antibody (M-134; Santa Cruz Biotechnology) at 1:200 dilution for 1 hour at room temperature (RT), which was used to monitor equal sample loading. After washing, blots were incubated with goat anti-rabbit (for Jagged1, Notch1, and Gli2) or goat anti-mouse (for PARP and β-actin) secondary antibodies (Bio-Rad) conjugated with horseradish peroxidase. Visualization was carried out by the enhanced chemiluminescence method (Pierce Thermo Scientific).

### siRNA transfection

To examine downregulation of Jagged1, Gli2, Notch1, or Notch3 with siRNA, cells were exposed to control siRNA (target sequence: 5′-UUCUCCGAACGUGUCUUCU-3′; Sigma) or one of 2 tested Jagged1-targeting constructs (JAG1_A: 5′-GAUGUGAGGCCAAACCUCIU-3′ or JAG1_B: 5′-CCUUGGACAIAUAGCCCGAA-3′; Sigma) or one of 2 tested Gli2-targeting constructs (Gli2_A: 5′-GUACCAUUAACAGGCCCAU-CIU-3′ or Gli2_B: 5′-GGGUAGUAAUGCUGGAGAUU-3′; Sigma) or a Notch1-targeting construct (5′-GGUGCCAGAAGCAGCCGAA-3′; Sigma) or a Notch3-targeting construct (5′-GGUGUACACGACGUGAAU-AIU-3′; Sigma) at a 1:3 siRNA (µg) to lipofectamine 2,000 (µL) ratio. Lipofectamine and siRNA were incubated for 20 minutes at RT, added to cells in serum-free RPMI to incubate for 6 hours, followed by 10% FBS/RPMI thereafter. Transfected cells were grown at 37°C for 48 to 72 hours and then harvested for viable cell counting, quantitative PCR, or Western blot analysis.

### Assessment of cell viability with chemotherapy IC50 and cell-cycle analysis

To a 96-well plate, 2,000 cells/well were exposed to increasing concentrations of docetaxel in triplicate. Viability was assessed with 0.15% MTT (Sigma). For effects of siRNA-mediated downregulation on docetaxel IC50, cells were first transfected with siRNA (5 µg) for 24 hours in 6-well plates, then trypsinized, and re-plated at 2,000 cells per well, followed by addition of chemotherapy after attachment. IC50 was determined by finding the dose at which the drug had 50% of its effect, calculated by the equation $\left[\frac{(OD_{450\text{MAX}} - OD_{450\text{MIN}})}{2 + OD_{450\text{MIN}}}\right]$. Test of synergy was carried out by the Loewe additivity model (23), calculated by the equation $CI = \left(D_i / D_{x2}\right) + \left(D_j / D_{x2}\right)$, where a CI (combination index) of 1 suggests an additive effect, less than 1 suggests synergy, and more than 1 suggests antagonism. For cell-cycle analysis, cells were transfected with siRNA for 72 hours, trypsinized, and fixed in 75% ethanol overnight. Cells were then centrifuged, washed 2× in PBS, and reconstituted in PBS with 50 µg/mL propidium iodide (PI). PI fluorescence was assessed by flow cytometry, and the percentage of cells in sub-G0, G0–G1, S, and G2–M phases were calculated by the cell-cycle analysis module for Flow Cytometry Analysis Software (FlowJo v.7.6.1).

### Orthotopic ovarian cancer model and in vivo delivery of siRNA

For orthotopic therapy experiments using ovarian cancer cell lines, female athymic nude mice (NCr-nu) were purchased from the National Cancer Institute after Institution Animal Care and Use Committee approval of protocols, and cared for in accordance with guidelines of the American Association for Accreditation of Laboratory Animal Care. For all in vivo experiments, trypsinized cells were resuspended in 10% FBS-containing RPMI, washed with PBS, and suspended in serum-free Hanks’ balanced salt solution at a concentration of 5 × 10⁶ cells/mL, and 1 × 10⁶ cells (IGROV-AF1 or SKOV3TRip2) were injected IP in 200 µL into 40 mice per experiment. After 1 week, mice ($n = 10$ per group) were randomized to treatment with (i) 10 µg control siRNA, (ii) 5 µg murine-specific anti-Jagged1 siRNA (target sequence: 5′-CAGUAAAGCACAUCUUAAC-3′, Sigma) plus 5 µg control siRNA, (iii) 5 µg human-specific anti-Jagged1 siRNA (same as JAG1_B siRNA) plus 5 µg control siRNA, or (iv) 5 µg of both species-specific siRNA constructs. In another experiment, mice bearing SKOV3TRip2 tumors were randomized to treatment with (i) 10 µg control siRNA, (ii) 10 µg control siRNA plus docetaxel, (iii) both species-specific anti-Jagged1 siRNA constructs (5 µg each), or (iv) both species-specific constructs (5 µg each) plus docetaxel. In a separate experiment, mice bearing SKOV3TRip2 tumors were randomized to treatment with (i) 10 µg control siRNA plus docetaxel, (ii) 5 µg human-specific anti-Jagged1 siRNA plus 5 µg control siRNA plus docetaxel, (iii) 5 µg murine-specific anti-Jagged1 siRNA plus 5 µg control siRNA plus docetaxel, or (iv) both species-specific constructs (5 µg each) plus docetaxel. siRNA constructs were incorporated in chitosan nanoparticles as previously described (24, 25) and administered IV twice per week in a volume of 100 µL. Docetaxel was administered IP at a dose of 35 µg weekly. Mice were treated for 4 to 6 weeks before sacrifice and tumor collection.

### Immunohistochemical staining

Resected tumors frozen in Tissue-Tek OCT compound (Sakura) were used for immunohistochemical (IHC) analysis of microvessel density (MVD) by using anti-CD31.
were analyzed by using a 2-tailed Student’s t test and the Mann–Whitney alternative distribution were examined by using a nonparametric test. Differences between groups were considered statistically significant at P < 0.05. Error bars represent standard deviation unless otherwise stated. Number of mice per group (n = 10) was chosen as directed by a power analysis to detect a 50% decrease in tumor growth with beta error of 0.2.

Statistical analysis
Comparisons of gene expression, PI fluorescence, mean tumor weight, and mean MVD, PCNA, and TUNEL were analyzed by using a 2-tailed Student’s t test, if assumptions of data normality were met. Those represented by alternate distributions were examined by using a nonparametric Mann–Whitney U test. Differences between groups were considered statistically significant at P < 0.05. Error bars represent standard deviation unless otherwise stated.

Results
Jagged1 expression in ovarian cancer cell lines
We first examined Jagged1 expression (both mRNA and protein) in IGROV-AF1 and 3 pairs of parental and chemoresistant ovarian cancer cell lines: A2780ip2/A2780cp20 (20-fold increased cisplatin resistance and 10-fold increased taxane resistance), HeyA8/HeyA8MDR (500-fold taxane resistant), and SKOV3ip1/SKOV3TRip2 (1,000-fold taxane resistant). mRNA expression of Jagged1, as measured by quantitative PCR, was prominent in IGROV-AF1, SKOV3ip1, and SKOV3TRip2 with little to no expression in the A2780ip2/A2780cp20 and HeyA8/HeyA8MDR lines (Fig. 1A). Western blot analysis showed similar Jagged1 expression as that obtained using qPCR (Fig. 1B). Interestingly, Jagged1 mRNA expression was 4.6-fold higher (P < 0.05) in the taxane-resistant SKOV3TRip2 line compared with its parental cell line, SKOV3ip1.

Downregulation of Jagged1 decreases viability and reverses taxane resistance in ovarian cancer cells in vitro
To determine whether Jagged1 downregulation affects ovarian cancer cell viability in vitro, IGROV-AF1 and SKOV3TRip2 cells were transiently transfected with 2 different siRNA constructs against Jagged1 (JAG1_A or JAG1_B). JAG1_B siRNA decreased Jagged1 expression to a greater extent than JAG1_A siRNA in both IGROV-AF1 and SKOV3TRip2 cells, as determined by Western blot (Fig. 2A). Concordantly, JAG1_B siRNA had the greatest effect on cell viability for both IGROV-AF1 (37.7% reduction, P < 0.05) and SKOV3TRip2 (71.5% reduction, P < 0.001) cells (Fig. 2B, data points on y-axis). Given the increased expression of Jagged1 in the taxane-resistant SKOV3TRip2 line, we asked whether downregulation of Jagged1 could sensitize resistant cells to chemotherapy. IGROV-AF1 and SKOV3TRip2 cells were transiently transfected with Jagged1-targeting siRNAs or control siRNA for 24 hours and exposed to increasing concentrations of docetaxel. Cell viability was assessed by MTT assay 4 days after the addition of docetaxel. As shown in Figure 2B, downregulation of Jagged1 did not increase the sensitivity of IGROV-AF1 cells to docetaxel (IC50 ~2 nmol/L); however, downregulation of Jagged1 reduced the docetaxel IC50 from 40 to 10.2 nmol/L in SKOV3TRip2 cells. Overcoming taxane resistance in the SKOV3TRip2 line but not in the already-sensitive IGROV-AF1 line suggests that the mechanism by which Jagged1 contributes to taxane resistance...
are the same as those responsible for acquired taxane resistance, rather than an additive effect that might be seen in any cell line. Tests for synergy indicate a CI of 0.77, suggesting moderate synergy in the SKOV3TRip2 line. To determine the mechanism by which Jagged1 downregulation may affect cell growth, cell-cycle analysis was carried out in a separate experiment. SKOV3TRip2 cells were exposed to control or anti-Jagged1 siRNA for 24 hours, followed by vehicle or docetaxel at IC50 levels for another 48 hours. Jagged1 downregulation alone and in combination with docetaxel induced a small but statistically significant increase in apoptosis (P < 0.001, compared with control siRNA; P < 0.01, compared with docetaxel alone) and an accumulation of SKOV3TRip2 cells in the G2–M phase (P < 0.001, compared with control siRNA; Fig. 2C). Induction of apoptosis was confirmed by the presence of PARP cleavage in SKOV3TRip2 cells exposed to Jagged1 siRNA (Fig. 2D). Jagged1 siRNAs had no sensitizing effect to carboplatin in SKOV3TRip2 and A2780cp20 cells (data not shown) and had no significant effect on the viability of Jagged1-negative A2780ip2 cells (Fig. 2E).

**Human versus murine in vivo downregulation of Jagged1**

We have previously shown that Jagged1 and other Notch family members are overexpressed in tumor-associated endothelial cells, and that Jagged1 downregulation prevented tube formation of HUVEC cells in vitro (11). Given the effects of Jagged1 downregulation on tumor cells as well, we sought to determine the relative effects of targeting Jagged1 in the stromal and malignant cell compartments individually. In addition, inhibition of both compartments would simulate effects that would be expected in patients. There are no known inhibitors of Jagged1 for in vivo studies. Therefore, we utilized a method for delivery of siRNA in vivo by using chitosan nanoparticles. siRNA holds the
additional advantage of inhibiting both Notch-dependent and Notch-independent effects mediated by Jagged1 through bidirectional signaling. We have previously shown that twice weekly administration of siRNA incorporated into biodegradable chitosan nanoparticles results in siRNA delivery to the tumor parenchyma with subsequent target downregulation in both stromal and malignant tumor cells (24, 25, 28, 29). In this study, nude mice were injected intraperitoneally with either SKOV3TRip2 or IGROV-AF1 cells and randomized to four treatment groups: (i) control siRNA, (ii) murine-specific anti-Jagged1 siRNA, (iii) human-specific anti-Jagged1 siRNA, or (iv) both species-specific constructs. The specificity of each Jagged1 siRNA construct against the human or murine species was first showed in vitro by using human SKOV3TRip2 and murine MOEC cell lines by Western blot analysis (Fig. 3A). For in vivo studies, siRNAs were incorporated into chitosan nanoparticles and administered IV twice per week. After 4 weeks of treatment, all mice were sacrificed and total tumor weight recorded. In SKOV3TRip2 xenografts (Fig. 3B), there was a reduction in tumor growth with anti-murine Jagged1 siRNA-CH (41.7%, \( P = 0.089 \)) compared with control siRNA, and human-specific anti-Jagged1 siRNA-CH significantly reduced tumor weight by 58.3% (\( P = 0.042 \)). The combination of both species-specific constructs resulted in significantly reduced tumor weight by 87.5% compared

![Figure 3. Human versus murine in vivo downregulation of Jagged1. A, species-specific downregulation of Jagged1 in human SKOV3TRip2 and mouse MOEC cell lines was determined by Western blot analysis. B, mice injected intraperitoneally with SKOV3TRip2 cells were treated with siRNAs incorporated in chitosan (CH) nanoparticles. Mice treated with the combination showed a significant reduction in tumor weight compared with treatment with control siRNA or either single species-specific Jagged1 siRNA. C, similarly, mice injected with IGROV-AF1 cells had significantly decreased tumor weight after treatment with combination murine- and human-Jagged1 siRNAs compared with control siRNA or either single species-specific siRNA. Mean tumor weights with SD are presented. D, SKOV3TRip2 tumors were subjected to IHC analysis of CD31 to evaluate MVD. Xenografts treated with anti-murine Jagged1 siRNA had significantly decreased MVD compared with those treated with control siRNA. Representative histologic sections are shown for the various treatment groups (black bar, 100 \( \mu \)m) with mean and SD values across each treatment group shown in the adjoining graph (E). Cntrl, control; Hs, human; Mm, murine; siRNA-CH, siRNA in chitosan nanoparticles. *, \( P < 0.05 \).]
with control siRNA (P = 0.019). This represented an 82.1% reduction compared with murine siRNA-CH alone (P = 0.13) and a 70% reduction compared with human siRNA-CH alone (P = 0.03). Similarly, in IGROV-AF1 xenografts (Fig. 3C), there was a moderate reduction in tumor weight with just murine-specific anti-Jagged1 siRNA-CH (48.8%, P = 0.24) or human-specific anti-Jagged1 siRNA-CH (54.4%, P = 0.27) compared with control siRNA. However, treatment with combined species-specific anti-Jagged1 siRNAs-CH again resulted in a significant decrease in tumor weight by 93.1% compared with control siRNA-CH (P = 0.008), by 84.9% compared with anti-human Jagged1 siRNA-CH alone (P = 0.0046), and by 86.5% compared with anti-murine Jagged1 alone (P = 0.012). There was not a statistically significant reduction in the number of nodules in each group, suggesting that the primary mechanism of reduced tumor size is reduced growth, rather than implantation and uptake of the tumor implants.

Given the Notch pathway’s implication in angiogenesis, IHC analysis of CD31 was carried out to evaluate MVD to determine whether species-specific targeting of Jagged1 has antiangiogenic effects. As shown in representative sections in Figure 3D, MVD was significantly reduced in SKOV3-TRip2 tumors treated with anti-murine Jagged1 siRNA-CH (alone or in combination with anti-human Jagged1 siRNA-CH) compared with those treated with control siRNA (from 21.2 to 8.7 vessels per hpf, Figure 3E, P < 0.01). Anti-human Jagged1 siRNA-CH alone had no significant effect on MVD.

### Taxane sensitization with dual-compartment Jagged1 downregulation in vivo

To determine the effect of Jagged1 downregulation on taxane sensitivity in vivo, nude mice were injected intraperitoneally with SKOV3TRip2 cells and randomized to four treatment groups (to begin 1 week after cell injection): (i) control siRNA-CH, (ii) control siRNA-CH + docetaxel, (iii) combined human and mouse-specific anti-Jagged1 siRNAs-CH, or (iv) combined human and murine-specific anti-Jagged1 siRNAs-CH + docetaxel. After 5 weeks of treatment, mice were sacrificed and total tumor weight recorded. As shown in Figure 4A, control siRNA-CH + docetaxel treatment had no effect on SKOV3TRip2 tumor weight. In contrast, treatment with combined human and mouse-specific anti-Jagged1 siRNAs-CH significantly reduced tumor weight (by 78.4%) compared with control siRNA-CH + docetaxel (P = 0.038). In addition, the combination of species-specific anti-Jagged1 siRNAs-CH and docetaxel further decreased tumor weight by 94.8% compared with control siRNA-CH + docetaxel (P = 0.017) and by 76.0% compared with dual-compartment Jagged1 downregulation alone (P = 0.04).

To determine whether decreases in SKOV3TRip2 tumor weights following Jagged1 downregulation (alone and in combination with docetaxel) were because of decreased cell proliferation, apoptosis, or both, IHC analysis of PCNA and TUNEL staining was carried out. Proliferation rates were significantly decreased in tumors treated with anti-human Jagged1 siRNA-CH, whether anti-human siRNA was used alone, in combination with anti-murine Jagged1 siRNA-CH, or in combination with anti-murine Jagged1 siRNA-CH plus docetaxel (23.3%, 11.4%, and 5.8%, respectively) compared with both control siRNA-CH (72.5%) or control siRNA-CH plus docetaxel (69.4%, P < 0.001; Fig. 4B and C). Rates of apoptosis were not significantly different for the treatment groups ranging from 3.9% to 6.6% (data not shown). The small percentage of cells undergoing apoptosis following Jagged1 downregulation (both in vitro and in vivo) suggest that decreased cell proliferation, rather than apoptosis, largely contributes to Jagged1 knockdown effects.

To determine whether increased taxane sensitivity observed with combined species-specific anti-Jagged1 siRNAs is because of effects on tumor cells, murine stromal cells, or both, SKOV3TRip2 xenografts were treated with docetaxel plus control siRNA-CH, anti-human Jagged1 siRNA-CH, anti-murine Jagged1 siRNA-CH, or combined anti-human/anti-murine Jagged1 siRNA-CH. As shown in Figure 4D, anti-murine Jagged1 siRNA-CH plus docetaxel had no effect on SKOV3TRip2 tumor weight compared with control siRNA-CH plus docetaxel. In contrast, treatment with either anti-human Jagged1 siRNA-CH plus docetaxel or anti-human/anti-murine Jagged1 siRNA-CH plus docetaxel significantly decreased tumor weight (by 79.8%, P = 0.001 and 74.6%, P = 0.003, respectively). These data would suggest that unlike its role in angiogenesis, Jagged1’s role in taxane resistance is a characteristic of tumor cells, rather than transmitted through signals from the tumor stroma.

### Jagged1 downregulation contributes to decreased ovarian cancer cell viability in part through downregulation of GLI2

To confirm that Jagged1 targeting was working through the Notch pathway, we evaluated mRNA levels of the Hes1 and Hey1 transcription factors, known downstream mediators of Notch signaling, by quantitative PCR. Surprisingly, downregulation of Jagged1 resulted in a modest increase in both HES1 (1.7-fold, P = 0.27) and HEY1 (1.8-fold, P = 0.22), rather than a decrease that would be expected from targeting Notch signaling (Fig. 5A). Therefore, alternate pathways of effect were sought. The primary mediator of taxane resistance in general, and in the SKOV3TRip2 cell line specifically, is expression of MDR1, with 110-fold increased expression compared with parental SKOV3ip1 (30). Therefore, we first examined whether Jagged1 downregulation reduced MDR1 expression. Paradoxically, decreasing Jagged1 with transient siRNA actually led to a nearly significant 1.75-fold increase (P = 0.06) in MDR1 expression (Fig. 5B). To explore other potential mechanisms, we examined the Hedgehog signaling pathway (in particular, the downstream effectors GLI1 and GLI2) because of its involvement in stem cell maintenance, similar to the Notch pathway. Previous investigators have noted links between stem cell signaling pathways, such as the Notch and Wnt pathways (31) and the Notch and...
Hedgehog pathways (32). Expression of GLI1 was not significantly affected by Jagged1 siRNA compared with control siRNA; however, GLI2 expression was significantly reduced (by 2.20-fold, \( P = 0.0016 \)) following Jagged1 downregulation (Fig. 5B). In addition, it was found that JAG1 and GLI2 (but not GLI1) gene expression levels significantly correlated among the ovarian cancer cell lines examined in this study (\( r = 0.81, P = 0.0273 \)).

Figure 4. Taxane sensitization with dual-compartment Jagged1 downregulation in vivo. A, mice injected intraperitoneally with SKOV3TRip2 cells were treated with either control siRNA, control siRNA + docetaxel, combined human- and murine-Jagged1 siRNAs, or combined Jagged1 siRNAs + docetaxel. All siRNA constructs were incorporated in chitosan (CH) nanoparticles. Mice treated with the combination species-specific Jagged1 siRNAs + docetaxel showed a significant reduction in tumor weight compared with treatment with either Jagged1 siRNAs or docetaxel alone. Mean tumor weights with SD are presented. *, \( P < 0.05 \). B, SKOV3TRip2 tumors were subjected to IHC analysis of PCNA to evaluate cell proliferation. Xenografts treated with anti-human Jagged1 siRNA or combined species-specific Jagged1 siRNAs (alone and in combination with docetaxel) had significantly decreased proliferation rates compared with those treated with control siRNA or control siRNA plus docetaxel. Representative histologic sections are shown (B) for the various treatment groups (black bar, 100 \( \mu m \)) with mean and SD values across each treatment group shown in the adjoining graph (C). *, \( P < 0.05 \), **, \( P < 0.001 \). D, mice injected intraperitoneally with SKOV3TRip2 cells were treated with docetaxel plus either control siRNA, anti-human Jagged1 siRNA, anti-murine Jagged1 siRNA, or combined human- and murine-Jagged1 siRNAs. All siRNA constructs were incorporated in chitosan nanoparticles. Mice treated with anti-human and not anti-mouse Jagged1 siRNA showed a significant reduction in tumor weight in combination with docetaxel. Mean tumor weights with SD are presented. *, \( P < 0.01 \).
To further explore this potentially unique relationship between Jagged1 and the hedgehog transcription factor Gli2, we first examined whether this mechanism was Notch dependent because downregulation of Jagged1 appeared to have no effect on Notch downstream targets. To this end, we knocked down expression of Notch1 and Notch3, key Notch receptors implicated in stem cell maintenance and ovarian cancer (5, 33), and examined JAG1 and GLI2 gene expression. As shown in Figure 5C and D, downregulation of either Notch1 or Notch3 had no effect on JAG1 or GLI2 expression, suggesting that Jagged1 influences Gli2 in a Notch-independent fashion. To examine the downstream effects of reduced Gli2 expression, we selectively targeted Gli2 using two different siRNA constructs (Fig. 5E). First, we examined effects of apoptosis with Gli2 knockdown and noted significant induction of PARP cleavage compared with control siRNA (Fig. 5E). Interestingly, we found that Gli2 downregulation in turn significantly decreased JAG1 expression (1.64-fold, \( P = 0.0028 \), Fig. 5F), further suggesting a link between these signaling peptides. To determine if Gli2 plays a role in Jagged1-mediated taxane sensitization, SKOV3TRip2 cells were transiently transfected with Gli2 siRNAs for 24 hours before the addition of increasing concentrations of docetaxel. Gli2 siRNAs alone reduced cell viability by up to 68% (Fig. 5G, \( P < 0.001 \)), but reduced the docetaxel IC50 only slightly from 40 to 29 nmol/L. Because the taxane sensitizing effects of Gli2 targeting are not as pronounced as Jagged1 targeting alone, it seems that both Gli2 and...
additional Notch-independent pathways are at work in taxane resistance.

Discussion

In this study, we found that targeting Jagged1 in tumor cells induces apoptosis, reduces cell viability, and reverses taxane resistance in ovarian cancer cells both in vitro and in vivo, at least in part through downregulation of the Hedgehog mediator GLI2. In addition, knockdown of Jagged1 in tumor stromal cells reduces tumor growth through an antiangiogenic mechanism. The participation of Jagged1 in both stromal and malignant cell compartments makes it an attractive target for therapy and shows the utility of a model whereby these compartments can be targeted independently to delineate the various contributions of different cells in the tumor microenvironment.

Previous studies have shown aberrant expression of the Notch pathway in ovarian cancer (4–7). In particular, Jagged1 was found to be the primary Notch ligand expressed in ovarian cancer cells compared with Jagged2 and DLL1, 3, and 4 (6). Jagged1 was also found to be overexpressed in endothelial cells purified from ovarian cancers compared with normal ovaries (11). Taken together, these studies indicate that Jagged1 would be a desirable therapeutic target in ovarian cancer, both from an antitumor and antiangiogenic standpoint. In our study, we found that downregulation of Jagged1 resulted in decreased ovarian cancer cell viability in vitro, most likely mediated through reduced cell proliferation and, to a lesser extent, induction of apoptosis. Our study is the first to show that targeting Jagged1 diminishes tumor burden in vivo. Because there are no known inhibitors of Jagged1, we used chitosan nanoparticles to deliver Jagged1 siRNAs in tumor-bearing mice. These positively charged nanoparticles allow for the transport of siRNA across cellular membranes and are biodegradable, biocompatible, and have low immunogenicity (34, 35). Targeting Jagged1 using this delivery system may also avoid the dose-limiting toxicities inherent to systemic Notch inhibitors such as gamma-secretase inhibitors (36). Selective targeting of Jagged1 by using chitosan greatly decreased tumor burden and increased taxane sensitivity in orthotopic ovarian cancer mouse models. These results, combined with our observations in vitro, indicate that Jagged1 plays an important role in ovarian cancer cell survival. Whether these effects occur entirely through Notch signaling remains an open question. It has been suggested by Choi and colleagues (6) and others (15, 16) that Jagged1 may have its own signaling function that is independent of the canonical Notch pathway. Indeed, the lack of a decrease in the expression of Notch downstream targets, HES1 and HEY1, following Jagged1 downregulation in our study supports this mechanism. This potentially unique Notch-independent function of Jagged1 in human cancers, however, has yet to be fully explored.

The interaction between cancer cells and the surrounding stroma is increasingly becoming a focus of study in cancer research due to its role in tumor progression. This tumor-associated stroma is composed primarily of endothelial cells, which are necessary for tumor angiogenesis, and fibroblasts, which can secrete growth factors to the adjacent cancer cells. Recent reports suggest that Notch signaling can occur between tumor and stromal cells in some malignancies (37, 38), indicating that targeting the Notch-ligand interaction in endothelial cells can have therapeutic applications. In addition, studies have shown that Jagged1 expression is crucial for normal vascular development during embryogenesis and that mutations of the JAGGED1 gene can cause Alagille syndrome, a disease characterized by, among other deformities, congenital heart defects (39, 40). In our study, we found that selectively targeting Jagged1 in the tumor stroma significantly reduced MVD (as measured by CD31) and, when combined with Jagged1 antagonism in cancer cells, the overall antitumor effect was greater than either anti-Jagged1 method alone. These data suggest that, unlike most cancer-associated targets which are expressed in only one compartment of the tumor, inhibiting Jagged1 activity could be used to target both the tumor and its developing vasculature, thereby having a potentially greater therapeutic benefit.

Chemoresistance remains a persistent obstacle in the treatment of ovarian cancer. Although the clinical behavior of ovarian cancer suggests that most cancer cells are initially sensitive to chemotherapy, they subsequently either develop resistance or contain a population of cells that are inherently resistant. The latter hypothesis is consistent with what has become known as cancer stem cells or cancer initiating cells (CIC). These CICs are commonly believed to have enhanced tumorigenicity, differentiation capacity, and resistance to chemotherapy in comparison with non-CICs. It is because of these features that CICs have been examined for molecular pathways and markers that could be targeted for therapeutic purposes. Recent studies have shown that the ancient developmental pathways Hedgehog, Wnt, and Notch play important roles in the maintenance of CICs and that inhibiting these pathways may provide enhanced chemosensitivity when combined with traditional chemotherapies (8, 41–43). In our study, we sought to determine the mechanism whereby Jagged1, a known target of Wnt/β-catenin signaling (44, 45) and a Notch ligand, might sensitize ovarian cancer cells to docetaxel. We chose to focus on the hedgehog pathway because of its involvement in CIC maintenance and multidrug resistance (46–49). Interestingly, expression of GLI2, a hedgehog transcriptional effector, was significantly decreased following Jagged1 knockdown whereas expression of GLI1 and MDR1 was not. This relationship, one that seems to be Notch independent, between Jagged1 and GLI2 was also found to work both ways as knockdown of GLI2 diminished Jagged1 expression. Moreover, selective targeting of GLI2 using siRNA constructs decreased viability and increased sensitivity of ovarian cancer cells to docetaxel, although to a lesser degree than Jagged1 knockdown. These results suggest that inhibition of GLI2 contributes to the cell death and chemosensitization resulting from Jagged1
knockdown with other, as yet undefined, mechanisms likely playing a role as well. This connection between Jagged1 and Gli2 has not been previously identified and may have important therapeutic implications because targeting both Notch and Hedgehog, especially in combination with chemotherapy, is increasingly being advocated for the treatment of a variety of malignancies (3, 8, 50).

Collectively, the data presented in this study show that the Notch ligand Jagged1 contributes to taxane resistance, and targeting Jagged1 in ovarian cancer cells as well as in surrounding stroma significantly reduces growth through antiproliferative, apoptotic, antiangiogenic, and taxane-sensitizing effects. With the ability to identify subsets of cancer patients with Jagged1 overexpression, antagonism of this signaling molecule could ultimately provide a useful therapeutic strategy for ovarian cancer.

References


Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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