Network Analysis Identifies an HSP90-Central Hub Susceptible in Ovarian Cancer

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Abstract

**Purpose:** Epithelial ovarian cancer (EOC) is usually detected at an advanced stage and is frequently lethal. Although many patients respond to initial surgery and standard chemotherapy consisting of a platinum-based agent and a taxane, a taxane, most experience recurrence and eventually treatment-resistant disease. Although there have been numerous efforts to apply protein-targeted agents in EOC, these studies have so far documented little efficacy. Our goal was to identify broadly susceptible signaling proteins or pathways in EOC.

**Experimental Design:** As a new approach, we conducted data-mining meta-analyses integrating results from multiple siRNA screens to identify gene targets that showed significant inhibition of cell growth. On the basis of this meta-analysis, we established that many genes with such activity were clients of the protein chaperone HSP90. We therefore assessed ganetespib, a clinically promising second-generation small-molecule HSP90 inhibitor, for activity against EOC, both as a single agent and in combination with cytotoxic and targeted therapeutic agents.

**Results:** Ganetespib significantly reduced cell growth, induced cell-cycle arrest and apoptosis in vitro, inhibited growth of orthotopic xenografts and spontaneous ovarian tumors in transgenic mice in vivo, and inhibited expression and activation of numerous proteins linked to EOC progression. Importantly, paclitaxel significantly potentiated ganetespib activity in cultured cells and tumors. Moreover, combined treatment of cells with ganetespib and siRNAs or small molecules inhibiting genes identified in the meta-analysis in several cases resulted in enhanced activity.

**Conclusion:** These results strongly support investigation of ganetespib, a single-targeted agent with effects on numerous proteins and pathways, in augmenting standard EOC therapies. Clin Cancer Res; 19(18); 5053–67. ©2013 AACR.
this pathway have failed to show therapeutic efficacy in patients (1). Similarly, trials of single agents targeting HER2, RAF, c-KIT/PDGFR, mTOR, PKC, and SRC have failed to show clinical efficacy (2–9). Among the reasons for the overall lack of success, EOCs differ between individual patients in their development, histologic subtype, genetic makeup, protein expression, and pathway activation. Genomic analyses have revealed that high-grade serous carcinomas, the most common type of EOC, are commonly characterized by overexpression and/or amplification of numerous (>30) growth-stimulatory genes (10). High levels of genetic instability in these cancers may result in heterogeneity within tumors that contributes to escape from individual targeted therapeutic agents. These factors predict that monotherapy trials of agents targeting a single protein or pathway will remain unsuccessful; however, the ability to predict effective combinations of agents that will reliably inhibit EOC growth remains elusive.

Prior work from our group has shown the potential for using bioinformatics to develop target-centered signaling networks that can be used as a basis for siRNA screens designed to identify proteins regulating sensitivity to targeted therapies (11). Observations from this dataset about interactions of sensitizing proteins with catalytic partners that are the targets of existing drugs were useful in predicting therapeutic combinations that were effective in preclinical in vivo studies (11). Given the known challenges of treating EOC and the urgent need for new treatment modalities, in the present study, we have developed this initially productive strategy into a more comprehensive approach. We conducted meta-analyses of five independent siRNA screens involving different combinations of cell lines and drugs to identify the most consistently sensitizing targets. We then modeled interactions among the sensitizing dataset to identify connections to therapeutic targets.

In this extended analysis, multiple proteins directly interacting with HSP90 emerged as potent sensitizers of EOC cells to drug-induced cell death. HSP90 is an ATP-dependent molecular chaperone protein that affects the maturation, stability, and activation of a number of diverse client proteins (12). Although abundantly expressed in normal cells, its overexpression in malignant cells promotes persistent activation of many cellular kinases and transcription factors, and buffers cells from malignancy-induced cellular stresses (12). Because it mediates multiple target and pathway effects, HSP90 is an attractive therapeutic target. As an ATP-dependent chaperone, druggability of HSP90 was established in the mid-late 1990s with the natural products geldanamycin and radicicol. These agents exhibited selective toxicity for cancer cells (13), and although too toxic for clinical use, provided the chemical framework for development of additional agents. Among these, ganetespib is a particularly promising agent that does not suffer from the toxicity issues associated with earlier-generation HSP90 inhibitors and exhibits increased potency compared with first- and other second-generation agents (14–17). In our study, we show that ganetespib is a potentially valuable agent for augmenting the activity of cytotoxic therapies commonly used in EOC, both in vitro and in vivo, and that depletion of a group of proteins physically interacting with HSP90 sensitizes EOC cells to ganetespib, suggesting directions for future combination therapies.

Materials and Methods

Network analysis

Data for drug sensitization profiles for 638 genes encompassed in the siRNA library, corresponding to a receptor tyrosine kinase/cancer signaling network (detailed in ref. 11), were pooled from five independent screens of cancer cell lines. These data included sensitization of HCT116 to irinotecan or erlotinib (see Supplementary Methods), A431 cells to irinotecan or erlotinib (11), and H1155 cells to paclitaxel (18). Validated sensitizing siRNAs were sorted by rank for each screen, and assigned a value from 638 (most sensitizing) to 1 (least sensitizing). Comparison of the rank across screens nominated 171 siRNAs that were among the 20% strongest sensitizers in two or more screens. The proteins depleted by these siRNAs were imported into Cytoscape (19) and a protein–protein interaction network constructed. The network was expanded using the MiMi plugin (20) to include nearest neighbors by at least two proteins in the initial gene set. Analysis in Ingenuity (http://www.ingenuity.com/index.html) and DrugBank (21) was used to identify drugs targeting genes in the expanded protein set. The cumulative group of 130 drug targets was queried against the original group of 171 sensitivity-regulating proteins, and topological parameters of the network were calculated in Cytoscape. The degrees (the total interactions of each protein in this subnetwork) of each node were used to calculate the number of connections of each of the 130 drug targets to the initial set.
of 171 most sensitizing genes. After HSP90 was identified as of particular interest, combined application of Ingenuity and STRING (Search Tool for the Retrieval of Interacting Genes/Proteins, ref. 22), together with manual inspection of data included in ref. (23), and the database of the HSP90 machine interactome [ref. (24) and http://www.picard.ch/Hsp90Int/index.php] to capture all known interactions. The prevalence of proteins from this extended dataset among the subsets of genes with varying sensitization levels was used to calculate the enrichment of HSP90 targets in each subset compared with the whole library, using hyper-geometric distribution.

**Antibodies and drugs used**

Antibodies used and commercial sources are as follows: JAK2, pJAK2\(^{Y1007/Y1008}\), STAT3, pSTAT3\(^{Y705}\), STAT5, pSTAT5\(^{Y694}\), pSRC\(^{Y416}\), S6, pS6\(^{S235/236}\), pCDK1\(^{Y15}\), AKT, JAK2, pJAK2\(^{Y1007/Y1008}\), STAT3, pSTAT3\(^{Y705}\), STAT5, pSTAT5\(^{Y694}\), pSRC\(^{Y416}\), S6, pS6\(^{S235/236}\), pCDK1\(^{Y15}\), AKT, pAKT\(^{S473}\), c-MYC, BCL-X\(_L\), EGFR, MCL-1, NF-κB, p50, PKC\(_\alpha\), PKC\(_\varepsilon\), PKC\(_\beta\), MEK1, PI3K, FYN, CK2\(_\alpha\), RIP1, PDK1, N-WASP, and caspase-3 (Cell Signaling Technology); cyclin D1, CDK1, HSC70, and β-actin (Santa Cruz Biotechnology); SRC and p53 (EMD Millipore); β-actin (Sigma-Aldrich); HIP1 and Ki-67 (Abcam); EGFR (BD Biosciences); HSP70 (Enzo Life Sciences), and PARP (RayBiotech). Drugs used and their commercial sources are as follows: ganetespib (Synta Pharmaceuticals Corp.), paclitaxel and cisplatin (FCCC), and alisertib, and ruxolitinib (Selleck Chemicals); erlotinib (LC laboratories); and GSK23344470 (Sigma-Aldrich).

**Cell culture**

Human OVCAR-5, OVCAR-8, and A1847 EOC cell lines were grown in RPMI (Life Technologies), with 10% FBS (Atlanta Biologicals), 2 mmol/L L-glutamine, penicillin/streptomycin [100 U/mL and 100 μg/mL, respectively; Life Technologies (Invitrogen)], and 0.25 units/mL insulin (Novo Nordisk). SKOV-3 cells were grown in McCoy's 5A (Life Technologies) supplemented with 10% FBS, 2 mmol/L L-glutamine, penicillin/streptomycin, and 0.25 U/mL insulin. OVCAR-5 and A1847 cells were transduced with a retroviral firefly luciferase construct (pWZL-Luc; a gift from Dr. Maureen Murphy, The Wistar Institute, Philadelphia, PA) using standard methods (25) and selected in the presence of 75 μg/mL hygromycin B (Life Technologies).

**Cell viability, apoptosis, and cell-cycle assays**

Cell viability was determined in ganetespib-treated cells (0.1–1,000 nmol/L) using the CellTiter-Blue Cell Viability Assay (Promega) according to the manufacturer's instructions. Apoptosis was evaluated by Annexin V staining (Guava Nexin Reagent; Millipore) in cells treated with 0–100 nmol/L. ganetespib for 24, 48 or 72 hours. Briefly, 1 × 10\(^5\) cells were harvested and centrifuged at 300 × g for 5 minutes at room temperature. Cells were washed in PBS and suspended in 100 μL of serum-containing medium and 100 μL of Guava Nexin Reagent was added to each sample. The samples were stained for 20 minutes at room temperature in the dark and analyzed on the Guava EasyCyte PCA-96 system and the accompanying CytoSoft 3.6.1 software (EMD Millipore). Annexin V–PE (+)/(-) cells were identified in the early stages of apoptosis and Annexin V–PE (+)/7-AAD (+) cells were identified in the late stages. For cell-cycle analysis, cells seeded at 2.5 × 10\(^5\) cells per well in a 6-well plate were exposed to 0, 5, 25, and 50 nmol/L ganetespib or 100 μmol/L etoposide as a positive control. After 24 and 48 hours, cells were harvested and stained with propidium iodide (Sigma-Aldrich), analyzed on the Guava EasyCyte System (EMD Millipore) according to the manufacturer’s instructions.

**Drug synergy testing**

Ganetespib, paclitaxel, cisplatin, dasatinib, erlotinib, GSK2334470, alisertib, and ruxolitinib were tested individually or in combination. A1847 and OVCAR5 cells were plated at 3,000 cells per well in 96-well plates. After 24 hours of incubation, cells were treated with serial dilutions of individual drugs or combinations of two drugs at a constant molar ratio. After 72 hours of incubation, cell viability was measured with CellTiter-Blue (Promega) using an EnVision Plate Reader (PerkinElmer). Combination index (CI) values were established by the Chou–Talalay method (26, 27) calculated using the CompuSyn software package (CompuSyn).

**Immunoblot assays and analysis**

Cells and tumor tissue were lysed in Mammalian Protein Extraction Reagent (MPER) and Tissue Protein Extraction Reagent (TPER), respectively (Thermo Scientific). Lysis buffer was supplemented with Halt Phosphatase Inhibitor Cocktail (Thermo Scientific) and Complete Mini Protease Inhibitor Cocktail (Roche Diagnostics), and protein concentrations were determined using the BCA assay (Thermo Scientific). Proteins were resolved on 4% to 12% gradient gels (Life Technologies) and transferred to polyvinylidene difluoride (PVDF) membrane (EMD Millipore). Membranes were blocked in nonfat dry milk, incubated overnight at 4°C in primary antibody, followed by horse-radish peroxidase–conjugated secondary antibody (GE Healthcare) and signal was detected with SuperSignal West Pico Chemiluminescent Substrate (Thermo Scientific). Immunoblots were quantified using ImageJ as described previously (28). Briefly, a rectangle region of interest (ROI) was drawn to outline each lane. The Analyze Gels function was used to create a plot of the average pixel intensity over the length of the ROI. A straight line was then used to close each peak and the area under the curve was measured and the density relative to β-actin was calculated for each band.

**Mouse models and in vivo imaging**

All procedures involving mice were approved by the FCCC Institutional Animal Care and Use Committee (IACUC). Female C.B-17 severe combined immunodeficient (SCID) mice (FCCC Laboratory Animal Facility) were used for intrabursal injections as described previously (29, 30). Mice were given unilateral intrabursal (left side)
injections of OVCAR-5-Luc or A1487-Luc cells (8 × 10⁵) suspended in 5 μg/μl final concentration of BD Matrigel Matrix High Concentration (BD Biosciences). Baseline bioluminescent imaging (BLI) scans were acquired using the IVIS Spectrum (PerkinElmer, Caliper Life Sciences) as described previously (29, 30) to confirm the presence of tumors. Transgenic IgMISIIR-TAg mice and in vivo MRI and volumetrics analysis have been described previously (31–33). Ganetespib, 125 mg/kg formulated in 10/18 DRD (10% DMSO, 18% Cremophor RH 40, 3.6% dextrose, and 68.4% water), or 10/18 DRD (vehicle), was administered once weekly by intraperitoneal injection. Mice with OVCAR-5-Luc and A1487-Luc xenografts were treated for 3 and 6 weeks, respectively, and tumor growth was monitored by weekly BLI. Briefly, ROI of identical size encompassing the luminescent signal were assigned, and the total flux was calculated for each mouse using Living Image software (PerkinElmer; Caliper Life Sciences). Statistical analyses were conducted by selecting pairs of datasets to the Wilcoxon two-sample test; P < 0.05 was considered significant.

ELISA assay

Levels of HSP70 and pSTAT3 Y705 (activated STAT3) present in tumor protein lysates isolated 6 or 24 hours after vehicle- or ganetespib-treatment were assayed using an enhanced chemiluminescent ELISA assay (MesoScale Discovery) according to the manufacturer’s instructions.

Reverse phase protein array

Triplicate samples of OVCAR-5 cells were treated with vehicle, 30 nmol/L ganetespib, 1 nmol/L paclitaxel, or 30 nmol/L ganetespib + 1 nmol/L paclitaxel for 24 hours. Following standard protocols of the RPPA (reverse phase protein array) Core Facility at MD Anderson Cancer Center (Houston, TX), cells were lysed on ice, and lysates cleared by centrifugation and denatured in SDS sample buffer, then submitted for analysis as described previously (34, 35). Data were visualized using the MultiExperiment Viewer (MeV) program (http://www.tm4.org/mev/) and analyzed by one-way ANOVA and Tukey multiple comparison test using GraphPad Prism version 5.04.

Tissue preparation and immunohistochemistry

Mice were euthanized, necropsied, and examined for the presence and location of primary tumors and tumor nodules. Reproductive tracts were removed and primary tumors were weighed and caliper measurements of length (l) and width (w) were made to determine tumor volume (l × w² × 0.5). Tumor nodules present in the abdomen were counted. Individual portions of tumors were snap-frozen in liquid nitrogen for preparation of protein lysates, and fixed in 10% (v/v) neutral buffered formalin and paraffin embedded for staining with hematoxylin and eosin. Custom tumor tissue microarrays (TMA) were constructed by arraying duplicate cores from primary OVCAR-5 and A1847 tumors isolated from mice at 6 and 24 hours after treatment with vehicle or ganetespib. Immunohistochemical staining was conducted as described previously (30, 31) with the following antibodies at the indicated dilutions: Ki-67 (1:100), caspase-3 (1:300), PARP (1:100), STAT3 (1:400), and pSTAT3 (1:25). Stained TMAs were scanned and analyzed using the Vectra imaging system (PerkinElmer; Caliper Life Sciences.). Images of immunohistochemical staining were acquired on a CCD camera and Nikon Eclipse E600 microscope with NIS-Elements D3.0 software (Nikon) at identical exposure times.

Sensitization testing for siRNAs

For the set of siRNAs defined in Results, sensitization to ganetespib was conducted essentially as described in detail for library screening (Supplementary Methods). Two independent siRNA duplexes independently prevalidated for each target were used in A1847 and OVCAR5 cells, using optimized reverse transfection conditions to introduce siRNAs into 3,000 cells arrayed in 96-well microtiter plates, in duplicate. Plates were treated with ganetespib at a previously established IC₅₀ concentration, or DMSO, after 24 hours, and viability assessed with CellTiter-Blue 96 hours after transfection, using an EnVision Plate Reader.

Results

Network analysis identifies HSP90 as a candidate for evaluation in EOC

To identify genes that consistently sensitized tumor cells to drug treatment, we conducted meta-analysis of results from five independent siRNA drug sensitization screens that queried 638 genes in a signaling network enriched for many targets relevant to EOC pathology, including the previously assessed HER2, RAF, SRC, and mTOR; their physically interacting partners and downstream effectors; the TGF-β effector cascades, which have been associated with drug resistance and aggressive tumor phenotypes; and others [(11, 18); details of cell line selection and analysis are described in Supplementary Fig. S1 and Supplementary Table S1]. To identify siRNAs with the most consistent sensitizing activity, we sought those active in more than one cell line, and/or active against at least two of three drugs with different modes of activity: the topoisomerase inhibitor irinotecan, the microtubule-targeting agent paclitaxel, and the EGFR inhibitor erlotinib. By these criteria, 171 genes were identified as among the 20% scoring highest for mediating resistance to drug treatment, including 15 encoding proteins that are targets of drugs in preclinical development or clinical use (Fig. 1A).

We next used this dataset to identify commonalities in signaling among the set of most sensitizing genes. Numerous studies of synthetic lethality have established that close physical interactions between proteins predict common functionalities that can be exploited for cell killing (36, 37). From the starting gene set, we constructed an interaction network in Cytoscape among their encoded proteins,
which we augmented to include additional "nearest neighbor" interactors shared by at least two proteins in the initial group of 171 proteins. In the resulting expanded network of 1,391 proteins, 130 are drug targets (Supplementary Table S2). We then conducted a topological analysis of the network, and extracted the number of direct connections between each of the 130 drug targets and the 171 proteins regulating sensitization. From this analysis, we identified a subset of drug targets as particularly densely connected to proteins in the sensitizing set (Fig. 1B). Within the subset of targets of the top 10 drugs, we observed that two subunits of HSP90 (HSP90AA1 and HSP90AB1) were among the most densely connected to proteins in the sensitizing set (Fig. 1B; Supplementary Fig. S2; Supplementary Table S2). We also identified a statistically significant enrichment of HSP90-interacting proteins among the 20% most sensitizing siRNAs in two or more screens \((P = 0.03)\), and under-representation among the group of siRNAs that were never among the most sensitizing 20% \((P = 0.04)\). Moreover, many of the drug targets densely connected to the sensitizing set were themselves clients or interactors of HSP90. These included STAT3, EGFR, ERBB2 (HER2), ESR1 (estrogen receptor-α), and multiple SRC family kinases, each of which is already implicated in EOC pathogenesis (Fig. 1B; refs. 38–48).

Ganetespib inhibits EOC cell viability and HSP90 clients in vitro and in vivo

HSP90 has been reported as the tumor-associated antigen targeted by antibodies in the ascites of patients with late-stage EOC (49), whereas separate studies have shown that elevated HSP90 levels are common in peritoneal and pleural effusions of patients with advanced-stage EOC (50). On the basis of these reports, and the strong connections of EOC to many HSP90 client proteins, we directly assessed ganetespib, a small-molecule inhibitor of HSP90 (17), in commonly studied EOC cell lines, including OVCAR-5, OVCAR-8, A1847, and SKOV-3 cells. Ganetespib treatment resulted in dose-dependent inhibition of cell viability with IC\(_{50}\) values at 72 hours ranging from 9 to 48 nmol/L (Fig. 2A). Treatment of cells within the IC\(_{50}\) range (e.g., 5–50 nmol/L) for 48 hours resulted in a significant increase in the percentage of apoptotic cells, whereas increasing the dose (10–100 nmol/L) and duration (72 hours) of exposure increased the percentage of apoptotic cells further (Fig. 2B). Exposure to ganetespib (25–50 nmol/L) also resulted in the accumulation of cells in the G\(_2\)-M phase of the cell cycle (Fig. 2C). In addition, comparable concentrations of ganetespib (i.e., 25–50 nmol/L) reduced the expression of canonical HSP90 clients including total and
phosphorylated (p) proteins, including JAK2, pJAK2, pSTAT3, and pSRC (Fig. 2D and E).

We next used orthotopic xenograft and transgenic mouse models of EOC to assess the in vivo efficacy of ganetespib monotherapy. Drug treatment was well tolerated in both models, with no apparent toxicities. For the xenograft model, OVCAR-5-Luc cells were implanted by injection into the intrabursal space surrounding the ovary. Mice were monitored in vivo by longitudinal BLI from the stably integrated luciferase (Luc; Fig. 3A and B). The BLI data indicated statistically significant inhibition (P < 0.01) of xenograft growth rate, and endpoint assessments confirmed this observation, showing significantly decreased final tumor volume, weight, and...
dissemination of tumor nodules following 3 weeks of treatment with 125 mg/kg ganetespib (Fig. 3B). In ovarian tumor-bearing transgenic mice, tumor growth was monitored and quantified by MRI (29), and it similarly showed decreased tumor growth rate in ganetespib-treated mice (Fig. 3C).

In separate pharmacodynamic studies, mice with established orthotopic OVCAR-5 tumors were treated...
acutely with ganetespib and tumors collected 6 or 24 hours later for evaluation of protein expression levels by immunoblot analyses of total and phosphorylated forms of more than 25 proteins (antibodies listed in Materials and Methods). Among the proteins affected by ganetespib-treatment, there were many established HSP90 clients, with some more predominantly inhibited at 6 hours posttreatment (pJAK2, pSTAT3, total and pS6, and pAKT), some at 24 hours (pSTAT5, total and pCDK1, and AKT), and some inhibited at both time points (total JAK2 and c-MYC; Fig. 4A and B). Consistent with the previously described HSF1-mediated induction of heat shock response elicited by HSP90 inhibitors, that is, tansipemin and radicicol derivatives (51), levels of HSP70 protein were increased in tumors 6 and 24 hours after ganetespib treatment (Fig. 4A and B). Independent ELISA analyses confirmed the significant induction of HSP70 (2-fold at 6 hours and 2.4-fold at 24 hours) and inhibition of pSTAT3 (2.6-fold decreased at 6 hours) in tumors from ganetespib-treated mice (Fig. 4C and D). Immunohistochemical staining revealed no significant differences in Ki-67, caspase-3, PARP, or total STAT3 levels at 6 or 24 hours postdosing (not shown), but further confirmed significantly reduced levels of pSTAT3 present in tumor tissues 6 hours after ganetespib treatment (Fig. 4E). These results suggested that there are differences in the timing and duration of client inhibition in vivo, and that the mechanisms of tumor inhibition likely involve multiple signaling pathways with variable kinetics. The observed single-agent activity of ganetespib in EOC cells, an orthotopic xenograft model, and transgenic mice predicted that this agent may be promising for the treatment of patients, but also suggested that maximum clinical advantage might be gained by combining ganetespib with other therapeutic agents in standard use or development for EOC.

**In vitro assessment of ganetespib combination potential in EOC cells**

Few targeted agents are effective as monotherapy in EOC. For example, erlotinib (inhibiting EGFR) and dasatinib (inhibiting SRC family kinases) have each been evaluated in patients with EOC, but neither drug showed single-agent activity (7, 52). However, given the close connection of the HSP90 clients EGFR and SRC to the sensitization network (Fig. 1), we assessed erlotinib and dasatinib for combination with ganetespib. For this purpose, we conducted Chou–Talalay analysis (53), combining each compound with ganetespib at different ratios in cultured cells. Ganetespib combined with either of these agents inhibited the growth of both A1847 and OVCAR-5 cells much more significantly than either drug administered independently (Supplementary Table S3). We next investigated the effect of combining ganetespib with paclitaxel and cisplatin, standard first-line cytotoxic agents used to treat patients with EOC (54–56). Notably, the combination of ganetespib was synergistic with both cisplatin and paclitaxel at all ratios tested in A1847 cells, and at some ratios in OVCAR-5 cells (Supplementary Table S3 and Supplementary Fig. S3).

**Combination of ganetespib with paclitaxel potently inhibits orthotopic ovarian xenograft growth in vivo**

To confirm the in vitro findings showing ganetespib-mediated sensitization to paclitaxel, the effects of single agent and combination therapy with ganetespib and paclitaxel were evaluated in two human ovarian carcinoma xenograft models (Fig. 3D–G and Supplementary Fig. S4). Treatment of mice bearing orthotopic OVCAR-5-Luc cell xenografts with ganetespib or paclitaxel alone resulted in significantly (P < 0.001) reduced in vivo tumor growth and final tumor volume and weight determined at necropsy (Fig. 3D–F). The overall tumor growth inhibition (TGI) observed was 57% and 61% for ganetespib- and paclitaxel-treated mice, respectively. Importantly, 85% TGI and 77% fewer tumor nodules were observed in mice treated with the combination therapy compared with vehicle-treated mice. The observed TGI and reduction in tumor nodules was significantly greater (P < 0.01) in mice treated with the combination therapy than with either drug used as a single agent (Fig. 3D–G). Similarly, treatment of mice harboring orthotopic A1847-Luc xenografts with either ganetespib or paclitaxel significantly inhibited tumor growth rate and primary tumor volume and weight (Supplementary Fig. S4A–S4C). As with OVCAR-5-Luc tumors, inhibition of several HSP90 client proteins (e.g., JAK2, pSTAT3, total and pS6, pAKT, c-MYC, cyclin D1, and survivin) was confirmed in mice bearing A1847-Luc tumors treated with ganetespib (Supplementary Fig. S4D–S4F). Combination of ganetespib + paclitaxel was significantly better than ganetespib alone (77% TGI compared with 43% TGI, respectively). Mice with A1847 xenografts exhibited greater sensitivity to paclitaxel alone than mice with OVCAR-5 xenografts (72% vs. 61% TGI); therefore, while combination therapy in A1847 resulted in 77% TGI, the difference between single-agent paclitaxel and combination therapy was not significant (P = 0.12) due to the potent effect of paclitaxel. Taken together, these data suggest that the combination of ganetespib with paclitaxel may be a promising clinical therapeutic strategy.

To identify potential mechanisms underlying the ganetespib-mediated sensitization to paclitaxel, we compared the effects of treatment of OVCAR-5 cells with ganetespib and paclitaxel as single agents or in combination by RPPA analysis. Results of this experiment supported the immunoblot analyses (Figs. 2D and 4A and B), and identified additional proteins that were significantly affected in cells treated with ganetespib alone or combined with paclitaxel (Fig. 4F and Supplementary Table S4). This analysis showed significant depletion of AKT/mTOR and mitogen-activated protein kinase (MAPK) signaling pathway proteins, kinases, and transcription factors, as well as increased levels of apoptotic proteins and E-cadherin (Fig. 4F and Supplementary Table S4). However, the analysis did not reveal proteins that were significantly more
Figure 4. Ganetespib (gan)-treatment inhibits HSP90 client protein expression and activation in tumors. A, pharmacodynamic analysis was conducted on tumors isolated from mice treated with vehicle (veh) or ganetespib at 6 and 24 hours posttreatment (n = 4 mice/group/time point). Protein lysates were prepared and subjected to immunoblot analysis with the indicated antibodies. B, immunoblots were subjected to densitometric analysis using ImageJ 1.44 (NIH) to quantify each target protein levels relative to β-actin. Statistically significant differences were determined by two-way ANOVA, followed by Bonferroni posttests (\(P < 0.05\), \(P < 0.01\), \(P < 0.001\), \(P < 0.0001\)). Detection of HSP70 (C) and pSTAT3 (D) levels present protein lysates by enhanced chemiluminescent ELISA assay (\(P < 0.001\)). E, immunohistochemical detection of pSTAT3 in tumors. Data are presented as the H score (\(P < 0.01\)), considering both staining intensity and the percentage of positively staining cells with representative micrographs of pSTAT3 staining in tumor tissue isolated 6 and 24 hours after vehicle or ganetespib treatment (scale bar, 50 μm). F, heatmap of RPPA analysis showing proteins with significantly decreased (blue) and increased (yellow) protein expression following treatment with ganetespib, paclitaxel, or ganetespib þ paclitaxel.
affected by the combination of ganetespib and paclitaxel compared with either drug alone.

**HSP90-interacting proteins sensitize EOC cells to ganetespib**

In sum, the preceding data suggested considerable potential for supplementing standard paclitaxel regimens for EOC with ganetespib. As noted earlier, a number of members of the original group of HSP90-interacting proteins that led us to nominate HSP90 as a target have previously been linked to EOC pathogenesis, and in some cases been explored as drug inhibition targets in EOC. Among this group, some (including the genes *PDPK1* (encoding PDK1), *PRKCE* (PKCe), *RIPK* (encoding RIP1), *HIP1*, and *PRKCD* (PKCδ)) were rapidly degraded following treatment of EOC cell lines or tumors with ganetespib (Fig. 5A and B).

To gain additional insights into the functional relationship of these proteins in HSP90 activity, we assessed whether their depletion affected sensitization to ganetespib in OVCAR-5 and A1847 cells. This identified a group of 20 siRNAs, targeting *RAF1*, *PDPK1*, *RIPK1*, *FGR*, *STAT3*, *AURKA*, and others, that increased the sensitivity of cells to ganetespib in both cell lines (Fig. 5C; Supplementary Fig. S5; and Supplementary Table S5). We therefore directly tested whether drug inhibition of *AURKA* (with alisertib), *JAK2* (an upstream activator of *STAT3*, with ruxolitinib), or *PDK1* (with GSK2334470) enhanced ganetespib activity. Chou–Talalay analysis indicated...
Table 1. Combination index (Cl) values of ganetespib and targeted therapeutic agents alisertib, ruxolitinib, and GSK2334470 in OVCAR-5 and A1847 cells

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<sup>Values indicate: CI > 1, antagonism; CI = 1, additive effects; CI < 0.9, synergy; and CI < 0.5 strong synergy.</sup>
significant synergy between each of these agents (alisertib, ruxolitinib, and GSK2334470) and ganetespib at several different combination ratios in OVCAR-5 and A1847 cells (Table 1 and Fig. 6). Collectively, these findings suggest the capacity of ganetespib to sensitize ovarian carcinoma cells to a broad range of cytotoxic and targeted therapeutic agents.

Discussion

Early efforts to target HSP90 with natural product antibiotics with antitumor activity such as geldanamycin and its analogs, including tanespimycin (17-AAG) and alvespimycin (17-DMAG), showed promising activity in clinical trials, particularly in cancers that are highly dependent on key HSP90 clients (e.g., HER2+ breast cancer) or that are sensitive to proteotoxic stress (e.g., multiple myeloma; refs. 57, 58). Some assessments with these first-generation agents were conducted in EOC cells or tumors (59, 60) and showed antiproliferative and proapoptotic effects suggesting possible clinical benefit (60–63). Despite these encouraging data, these first-generation agents suffered from limitations related to hepatic toxicity, issues related to solubility and formulation, and consequently the inability to achieve sufficient doses required for sustained client depletion (12, 64), and clinical development of these agents was ceased.

The results of our meta-analysis emphasizing the importance of HSP90 in EOC were well-timed to benefit from intensive efforts focused on the development of second-generation small-molecule synthetic inhibitors of HSP90 with favorable biologic and clinical properties. Ganetespib (formerly STA-9090) is a highly promising anticancer agent (17). In preclinical studies, ganetespib exhibited potent in vitro cytotoxicity, degradation of client proteins, superior activity to tanespimycin, and in vivo antitumor activity in several solid tumor models including non–small cell lung carcinoma (NSCLC), melanoma, prostate, and gastric cancers (17, 65–68). In the clinic, ganetespib has been given to more than 700 patients and is well tolerated, with the most common side effects including fatigue, diarrhea, constipation, nausea, vomiting, anorexia, and abdominal pain. Single-agent clinical activity has been seen in patients with advanced breast cancer, NSCLC, gastrointestinal stromal tumor, colorectal cancers, and melanoma (http://www.syntapharma.com). Comparisons between ganetespib and other HSP90 inhibitors including 17-
DMAG and AT13387 also emphasized the greater potency of ganetespib (14–17). In our study, we show that ganetespib significantly reduced EOC cell viability and cell-cycle progression, increased apoptosis, and decreased client protein expression and stability in vitro. Ganetespib also significantly reduced tumor growth and dissemination in vivo, in the absence of any observed drug-related toxicities. Mechanistically, using both a candidate approach and RPPA-mediated screens, we found that ganetespib limited expression and/or activation of client proteins, with many linked to EOC pathogenesis, including AK2, pSTAT3, EGFR, SRC, S6, AKT, mTOR, NF-kB, and c-MYC. Pharmacodynamic analysis conducted both in vitro and in vivo showed that ganetespib treatment resulted in depression of many targets for 24 hours; enough to interrupt the cycle of continuous utilization of proliferative pathways required for the viability of transformed cells, and to trigger an apoptotic response. The stronger responses to ganetespib observed in pure populations of cultured tumor cells than in tumors likely reflects the more heterogeneous cell population in the primary tumor, as well as the presence of drug-metabolizing enzymes; nevertheless, there was clear evidence for a significant depression of known HSP90 clients in tumor tissue.

As with most targeted therapeutics, there is concern over intrinsic or acquired resistance. Therefore, continued preclinical work directed at identification, analysis, and validation of additional targets that sensitize EOC to ganetespib is warranted to understand mechanisms of resistance and potential ways to circumvent it. Our return to network analysis led us to investigate whether siRNAs and small-molecule inhibitors of proteins from the original dataset are particularly promising, as patients with recurrent and platinum-refractory disease are frequently treated with paclitaxel (83). These encouraging results established evaluation of the combination of ganetespib and paclitaxel in the clinical setting as an obvious next step.

Disclosure of Potential Conflicts of Interest

D. A. Prota is employed as Director, Cancer Biology in Synta Pharmaceuticals Corp. No potential conflicts of interest were disclosed by the other authors.

Authors’ Contributions

Conception and design: I.G. Serebriiskii, E.A. Golemis, D.C. Connolly

Development of methodology: H. Liu, F. Xiao, I. Attasaturov, E.A. Golemis, D.C. Connolly

Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): H. Liu, F. Xiao, S.W. O’Brien, M.A. Magnatly, D.A. Prota, D.C. Connolly

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): H. Liu, F. Xiao, I.G. Serebriiskii, S. Litwin, L.P. Martin, D.A. Prota, E.A. Golemis, D.C. Connolly

Writing, review, and/or revision of the manuscript: H. Liu, F. Xiao, I.G. Serebriiskii, L.P. Martin, D.A. Prota, E.A. Golemis, D.C. Connolly

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): D.C. Connolly

Study supervision: E.A. Golemis, D.C. Connolly

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Targeting HSP90 Inhibits Ovarian Cancer Growth and Progression


Network Analysis Identifies an HSP90-Central Hub Susceptible in Ovarian Cancer

Hanqing Liu, Fang Xiao, Ilya G. Serebriiskii, et al.