An Unbiased Oncology Compound Screen to Identify Novel Combination Strategies

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Abstract

Combination drug therapy is a widely used paradigm for managing numerous human malignancies. In cancer treatment, additive and/or synergistic drug combinations can convert weakly efficacious monotherapies into regimens that produce robust antitumor activity. This can be explained in part through pathway interdependencies that are critical for cancer cell proliferation and survival. However, identification of the various interdependencies is difficult due to the complex molecular circuitry that underlies tumor development and progression. Here, we present a high-throughput platform that allows for an unbiased identification of synergistic and efficacious drug combinations. In a screen of 22,737 experiments of 583 doublet combinations in 39 diverse cancer cell lines using a 4 by 4 dosing regimen, both well-known and novel synergistic and efficacious combinations were identified. Here, we present an example of one such novel combination, a Wee1 inhibitor (AZD1775) and an mTOR inhibitor (ridaforolimus), and demonstrate that the combination potently and synergistically inhibits cancer cell growth in vitro and in vivo. This approach has identified novel combinations that would be difficult to reliably predict based purely on our current understanding of cancer cell biology.

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Introduction

With few exceptions, anticancer monotherapies, whether broadly active cytotoxic or molecularly targeted drugs, have been limited in their ability to elicit robust and durable clinical responses. This is likely attributed to numerous factors including multiple dependencies evolved during tumorigenesis, feedback loops, redundant signaling pathways, and resistance mechanisms, to name a few (1, 2). Combining anticancer therapies has been in practice clinically for over 50 years as one approach to improving upon the responses achieved by weakly efficacious monotherapies into regimens that produce robust antitumor activity. This can be explained in part through pathway feedback loops, redundant signaling pathways, and resistance mechanisms, to name a few (1, 2). Combining anticancer therapies has been in practice clinically for over 50 years as one approach to improving upon the responses achieved by single therapies alone (3). Historically, this has been largely an empirical exercise based on preexisting knowledge of oncogenic pathway biologic relationships, or a clinically driven decision based on the preexisting standard of care for a particular cancer. One of the most recent promising combinations showing improved efficacy in the clinic is the combination of trametinib and dabrafenib for the treatment of BRAF-mutant melanoma. The mechanism of the improved efficacy is suggested to involve prevention of negative feedback and resistance (4).

Several large drug sensitivity screening campaigns have been reported. These include the publication of the Cancer Cell line Encyclopedia (CCLE) in which 24 anticancer drugs were screened across 479 cancer cell lines (5) and a study from The Wellcome Trust Sanger Institute in which 130 drugs were screened in 639 cell lines (6). In these studies, known biomarkers of response were validated and biomarker hypotheses were generated demonstrating the power of this approach to aid in drug development. More recently, combination screens have been undertaken to identify novel drug combinations for specific cancer indications, such as melanoma and leukemia, in which resistance to targeted agents has frequently been observed (7–9).

We performed an unbiased screen of 38 compounds in pairwise combinations in a panel of 39 cancer cell lines representing multiple cancer types to identify novel synergistic and efficacious combinations. The results of the screen identified synergy in well-known combinations as well as in novel combinations including the pairing of an mTOR inhibitor (ridaforolimus) and an inhibitor of the DNA damage checkpoint kinase Wee1 (AZD1775). This study demonstrates that unbiased high-throughput screens can be an effective way to discover active, novel synergistic drug combinations.
Materials and Methods

Drug combination screen

All cell lines were obtained from ATCC or Sigma-Aldrich and used within 6 months of receipt. All cell lines were authenticated at ATCC or Sigma-Aldrich by short tandem repeat (STR) profiling. The high-throughput screen was carried out on the fully automated GNF PolyTarget robotic platform (GNF Systems). Cells were plated in 1,536-well tissue culture-treated plates (Brooks Automation) at 400 cells/well in 10 μL growth media, followed by the addition of 50 nL of compounds in DMSO and incubation at 37°C in 5% CO₂, 95% humidity for 96 hours. The total cell viability of each well was then measured using CellTiter-Glo cell viability reagent (Promega) according to the manufacturer’s protocol. The luminescent signal was measured on a Viewlux reader (Perkin Elmer) with an integration time of 30 seconds per plate.

For single-agent studies, cells were treated with a 3-fold dilution series of eight concentrations of each drug, with six replicate treatments at each drug concentration per cell line. The starting concentrations were selected to span the IC_{50} in 96-hour proliferation assays based on our own or published data on each drug. Hierarchical clustering of single-agent response data demonstrates that drugs with similar mechanisms cluster together demonstrating the integrity of our results (Supplementary Fig. S1). For combination studies, cells were treated with a 4 by 4 matrix of drug concentrations also selected to span the IC_{50} for each drug (Supplementary Fig. S2) with four replicate treatments at each drug/drug combination concentration per cell line. In total, there were 60 assay plates per cell line screened and the typical throughput was five cell lines per day.

Reagents

Antibodies for Western blot analysis were all obtained from Cell Signaling Technology: pCdc2 cat. no. 9111, Cdc2 cat. no.9112, S6 ribosomal protein cat. no.2217, pS6 ribosomal protein cat. no. 2211, cleaved PARP cat. no. 9546.

In vitro cell viability

Cells were plated in 96-well plates at 3,500 cells/well. Cells were then treated with an eight by eight matrix of concentrations of the Wee1 inhibitor, AZD1775, and mTOR inhibitor, ridaforolimus. Ninety-six hours later, cell viability was measured using Cell Titer Glo (Promega).

In vivo efficacy

Six- to 8-week-old female athymic (CD1 nu/nu) mice from Charles River Laboratories were housed under pathogen-free conditions in microisolator cages with laboratory chow and water ad libitum. A total of 3 × 10^6 SK-OV-3 and A2780 cells in PBS: Matrigel (1:1) were injected subcutaneously into the right flank region. Tumors were allowed to reach 150 to 400 mm^3 for efficacy testing.

Table 1. Thirty-eight compounds used in the combination screen

<table>
<thead>
<tr>
<th>Compound</th>
<th>Target</th>
<th>Class</th>
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<tr>
<td>MK-2206</td>
<td>Protein kinase B (AKT)</td>
<td>Experimental</td>
</tr>
<tr>
<td>MK-4541</td>
<td>Anti-androgen</td>
<td>Experimental</td>
</tr>
<tr>
<td>MK-5018</td>
<td>Aurora kinase A</td>
<td>Experimental</td>
</tr>
<tr>
<td>Dinaciclib</td>
<td>Cyclin-dependent kinases (CDK)</td>
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</tr>
<tr>
<td>MK-8776</td>
<td>Checkpoint kinase 1 (Chk1)</td>
<td>Experimental</td>
</tr>
<tr>
<td>BEZ-235</td>
<td>Phosphatidylinositol-4,5-bisphosphate 3-kinase and mechanistic target of rapamycin (PI3K/mTOR)</td>
<td>Experimental</td>
</tr>
<tr>
<td>L-00778,123</td>
<td>Farnesyltransferase/GGPTase-I (FTI/GGTI)</td>
<td>Experimental</td>
</tr>
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<td>MRK-003</td>
<td>γ-secretase</td>
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<tr>
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<td>PARP</td>
<td>Experimental</td>
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<td>AZD1775</td>
<td>Wee1</td>
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<td>5’ AMP activated kinase (AMPK) agonist</td>
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<td>Dihydrofolate reductase</td>
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<td>Histone deacetylase (HDAC)</td>
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<tr>
<td>Etoposide</td>
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NOTE: Target corresponds to a drug target gene, protein, or organelle. Class represents approval status at time of submission.
studies (8–10 mice per group) or 350 to 600 mm$^3$ for mechanism of action studies (3 mice per group) before randomization. AZD-1775 was prepared in 0.5% methylcellullose. It was administered orally at 5 μL per gram of body weight (5 days on/2 days off). Ridaforolimus was prepared in 10% DMA (N,N-Dimethyl acetamide), 10% Tween-80, 40% PEG-400, and 40% water. It was administered intraperitoneally at 5 μL per gram of body weight (5 days on/2 days off). SK-OV-3 mice were treated for 28 days (four cycles) for the tumor growth experiment while the mice received only one treatment for the mechanism of action study. A2780 mice were treated until individual tumor reached 1,000 mm$^3$ for the tumor growth experiment while the mice received only one treatment for the mechanism of action study. After treatment, mice were sacrificed with CO$_2$. The tumors were then removed and frozen in liquid nitrogen for future protein extraction for Western blot analysis. Twice a week, xenografts were measured by a caliper. Caliper measurements were used to calculate tumor volumes using the formula $V = \text{length} \times \text{width}^2 \times 0.5$.

Data analysis: calculation of normalized response and synergy

Assuming exponential growth, the number of cells at time $t$ and 0 are defined by the expression $N(t) = N(t=0) \times \exp(\mu t)$, where $\mu$ is a growth constant that depends on individual cell line growth properties. Drug effect was measured by the ratio $\mu / \mu_{\text{Max}}$, where $\mu_{\text{Max}}$ was the growth rate for cells treated with a drug and $\mu_{\text{Max}}$ for the cells treated with DMSO. For ease of use, $\mu / \mu_{\text{Max}}$ was transformed into viability units $X / X_0 = \exp(\ln(4)^\mu / \mu_{\text{Max}})$. We have used two models to estimate synergy, highest single-agent (HSA) model, and the Bliss independence ($10$). The HSA model predicts the combined effect $E_{AB}$ for two single compounds with effects $E_A$ and $E_B$ is $E_{AB} = \text{max}(E_A, E_B)$. The Bliss model predicts the combined effect $E_{AB}$ for two single compounds with effects $E_A$ and $E_B$ is $E_{AB} = E_A + E_B - E_A \times E_B$ where each effect is expressed as a fractional inhibition between 0 and 1 at the same concentration as mixture. For both models, the synergy is calculated as the difference between the observed effect of the combination and the predicted effect $E_{AB}$.

Results

The OncoPolyPharmacology screen

In an effort to identify effective combinations for inhibiting growth of cancer cells in an unbiased manner, we screened 22 experimental drugs in all possible pairwise combinations as well as in combination with 16 approved drugs (Table 1) in a panel of 39 cancer cell lines (Supplementary Table S1) for a total of 583 combinations and 22,737 experiments (Supplementary Data). The compounds included experimental inhibitors of signaling molecules such as MEK and PI3K as well as approved drugs for the treatment of cancer such as paclitaxel and doxorubicin. The cancer cell lines chosen represent the most prevalent cancer types (lung, breast, ovarian, colon, melanoma, and prostate). Eight-point dose titrations of each drug were first performed on the 39 cell lines to identify the appropriate dose ranges to be used in the combination screening. For combination screening, compounds were tested in a 4 by 4 matrix of drug concentrations representative of the cell-active concentrations of each drug (Fig. 1A).

There are many methods available to evaluate drug combination responses. In our analysis, we used both the highest single agent (HSA) and Bliss independence models. In HSA, the effect of a drug combination is compared with the maximum effect of the individual component doses, whereas the Bliss model predicts the additive effect of two drugs acting independently. For both models, to capture effects across the entire 4 by 4 matrix, we used response surface methodology to quantitate volumetric predictions and observations (Fig. 1B). The single-agent drug effects were expressed as fractional inhibition between 0 (maximal inhibition) and 1 (no inhibition) relative to DMSO-treated controls, and these values were used at each drug concentration to calculate a predicted surface area based on HSA or Bliss model predictions (Fig. 1B, blue surface). Fractional inhibition by the

Figure 1.
The OncoPolyPharmacology Screen. A, drug pairs were screened in combination over fixed 4-point titrations (4 by 4 matrix, shown above) representative of the cell-active concentrations of each drug. Cell proliferation over 96 hours in the presence of drug, relative to vehicle, was determined with CellTiter Glo. B, using either the Bliss model or the highest single agent (HSA) model, additivity predictions could be made based on single-agent effects of the compounds (light blue surface). Actual effects observed are recorded (black surface) and the volumetric difference (gray space) is calculated as a measure of synergy, or combination activity exceeding the predicted outcome. Volume differences are assigned on the basis of the Bliss model (V$_{\text{Bliss}}$) or the HSA model (V$_{\text{HSA}}$).
drug combinations was similarly used to calculate observed surface areas (Fig. 1B, black surface). From these values, volumetric effects for each combination were calculated by subtracting the actual response from the predicted response and expressed as either VHSA or VBliss (Fig. 1B, gray volume).

Both VHSA and VBliss models had a narrow distribution with VHSA centered at 0.04 and VBliss centered at 0.007. These distributions clearly suggest that synergy and antagonism are rare events. Because of the variability in drug–response data, antagonism was defined arbitrarily as VHSA ≤ −0.12 and synergy as VBliss > 0.12. Additive combinations were defined as VHSA > 0.12 and VBliss < 0.12.

**Landscape of combination synergy and response**

In our dataset, the majority of the drug combinations showed no synergy (Fig. 2A and B) in one or more cell lines. Synergistic (VBliss > 0.12) or antagonistic (VHSA < −0.12) combinations were observed much less frequently at 0.05% and 0.01%, respectively. To visualize combinations with synergy across multiple cell lines, a heatmap illustrating the number of cell lines with synergy for each pairwise combination is shown (Fig. 2C). A similar heatmap was also generated for antagonism (Fig. 2D). As mentioned above, antagonism and synergy are rare events. However, many combinations can be found that have synergy or antagonism in at least one cell line. Of the 538 combinations tested, 287 (~50%) were synergistic in at least one cell line and 176 (~30%) were antagonistic in at least one cell line. We identified few broadly synergistic combinations including the Wee1 inhibitor combined with the Chk1 inhibitor (11) and PARP inhibitor combined with temozolomide (12, 13). Context-dependent synergistic drug combinations were also identified, including the mTOR inhibitor/AKT inhibitor combination and mTOR inhibitor/ERK inhibitor combination.

The aforementioned synergistic combinations have biologic rationale supporting them and therefore might have been predicted. However, the unbiased nature of the screen allowed us to identify novel combinations that one would not have necessarily predicted on the basis of our current understanding of the mechanisms of action of each agent. Examples of such novel synergistic combinations include the HSP inhibitor with the farnesy transferase inhibitor, the MEK inhibitor with vinblastine, and the Wee1 inhibitor with the mTOR inhibitor (Fig. 2D). Because of the novelty at the time of the screen as well as the advanced stage of each compound in clinical development, we chose to further validate and characterize the Wee1 inhibitor (14)/mTOR inhibitor (15) combination.

**Figure 2.**
Global view of synergy and antagonism. A, VHSA score distribution across 22,737 experiments. B, VBliss score distribution across 22,737 combination experiments. C, heatmap indicating the number of cell lines where synergy was observed for each combination (scale to the right). The cutoff for synergy was VBliss > 0.12. D, heatmap indicating the number of cell lines where antagonism was observed for each combination. The cutoff for antagonism was VHSA < −0.12. Gray indicates untested combinations.
Characterization of the novel Wee1 inhibitor/mTOR inhibitor combination

The combination of the Wee1 inhibitor and mTOR inhibitor was identified in the primary screen as synergistic in multiple cell lines and indications (Fig. 3A). To validate these primary screen results, we treated two cell lines in which the combination was synergistic, A2780 and SKOV3, with an 8 by 8 dose titration matrix of these compounds. Viability was then assessed 96 hours posttreatment. As shown in Fig. 3B, the expected versus observed surface plot of the 8 by 8 matrix viability data demonstrates synergy at multiple doses.

To further explore the Wee1 inhibitor and mTOR inhibitor combination, the tolerability of combining these two agents in vivo was determined. When mice were dosed with the MTDs of the monotherapies, the combination produced some body weight loss but was tolerated (Fig. 4A). To investigate the in vivo activity of this combination, efficacy was tested for the monotherapies and combination in two xenograft models of ovarian cancer. These models were selected on the basis of their robust in vitro synergy and response. For the A2780 xenograft model, mice were dosed for 3 weeks. The Wee1 inhibitor and mTOR inhibitor combination significantly inhibited tumor growth compared with either monotherapy ($P = 0.0066$ and $0.0063$ compared with mTOR inhibitor alone and Wee1 inhibitor alone, respectively; Fig. 4B). The combination resulted in 71% tumor growth inhibition at the end of the dosing period compared with 14% and 12% for monotherapy arms of the study. After the 3-week dosing period, mice were monitored until their tumors reached 1,500 mm$^3$. The time for the tumors in combination-treated mice to reach 1,500 mm$^3$ was significantly longer (61 days) than the tumors in mice treated with either Wee1 inhibitor or mTOR inhibitor monotherapies (36, 50 days, respectively; $P = 0.005$ and <0.0001 compared with mTOR inhibitor alone and Wee1 alone, respectively; Fig. 4C). To further test the efficacy of the combination in an additional ovarian cancer model, we treated mice bearing SKOV3 ovarian xenograft tumors. We again found that the combination was significantly better in inhibiting tumor growth than either monotherapy in this model. The combination inhibited tumor growth by 95% at the end of the 4-week dosing period compared with 71% and 62% for the Wee1 inhibitor and mTOR inhibitor, respectively ($P = 0.0282$ and 0.0508...
compared with mTOR inhibitor alone and Wee1 inhibitor alone respectively; Fig. 4D).

To explore potential mechanisms of action of the Wee1 inhibitor and mTOR inhibitor combination, we performed an acute pharmacodynamic study in mice bearing A2780 xenograft tumors. Mice were given 1 dose of either the Wee1 inhibitor (60 mg/kg), the mTOR inhibitor (1 mg/kg), or the combination. Mice were sacrificed 4 or 24 hours after treatment. As expected, we found that the levels of pS6 ribosomal protein were reduced in tumors from mice treated with the mTOR inhibitor (Fig. 5).

Likewise, we observed decreased levels of pCdc2 in tumors from mice treated with the Wee1 inhibitor for 4 hours. Surprisingly, we found that in mice treated with the combination, the phosphorylated S6 ribosomal protein levels were lower than in mice treated with the mTOR inhibitor alone. In addition, phosphorylated Cdc2 levels were lower in mice treated with the combination than in mice treated with the Wee1 inhibitor at the 4-hour time-point. These results suggest a previously unknown interaction between the mTOR and DNA damage pathways. We also observed increased levels of cleaved PARP indicating increased levels of apoptosis in tumors from mice 24 hours after treatment with the combination compared with tumors from mice treated with vehicle or either monotherapy.

Discussion
We have shown here through an unbiased large-scale combinational screening campaign that synergistic and efficacious
combination pairs can be identified. Our primary objective was to identify novel combinations that would not have been appreciated simply by using pathway knowledge to guide combination testing. We have discovered several novel combinations using this methodology and have presented here in detail the characterization of the Wee1i + mTORi combination.

Several important findings can be concluded from the data presented here. First, combination synergy and antagonism are a relatively infrequent phenomenon. Second, compounds that have multiple targets (i.e., sunitinib, sorafenib) frequently combine synergistically with multiple compounds with unrelated mechanisms of action. While this observation is intuitive, it has not been demonstrated systematically in a large combination screen, as reported here. Third, in addition to intra-pathway synergistic combinations (PI3K + PI3K pathway inhibitors, MAPKi + MAPKi pathway inhibitors, and DNA damage/cell-cycle checkpoint pathway combinations), which is consistent with a wealth of publications demonstrating intrapathway synergy (16), we also discovered novel interpathway combinations. Although broadly synergistic combinations may seem the most attractive, we suspect that many of these combinations may not be well tolerated in mice and human patients. Notably, the mTORi inhibitor/Wee1 inhibitor combination was well tolerated at the respective MTDs while the Chk1 inhibitor/Wee1 inhibitor was not (11, 17). Context-dependent combinations, especially those that combine drugs targeting two different pathways, are less likely to have overlapping toxicities.

The Wee1i + mTORi combination was identified in the primary screen and would not have been obvious from known mechanisms of action of both compounds. Wee1 is a central regulator of CDK1/2 and prevents premature CDK activation in unperturbed drug treatments. In the context of the combination remains to be determined. However, data presented here indicate that there may be effects on the PI3K pathway after treatment with the Wee1 inhibitor. In the context of the combination, we found more robust inhibition of phospho-S6. Conversely, we also found that the combination more robustly inhibited phospho-Cdc2. Therefore, previously unknown interactions between the mTOR and Wee1 pathways may account for the synergy and increased efficacy.

While we were preparing this manuscript, another group identified the Wee1i + mTORi combination in a screen to identify compounds that enhance the activity of the mTOR inhibitor, Torin, in RAS-mutant leukemia (24). In our work, we show that although the combination is efficacious in a context-dependent manner, combination benefit is not exclusively observed in RAS-mutant cancer cell lines or in cell lines with high RAS signature (Supplementary Table S1), which we believe is a better predictor of RAS pathway activation (23). Because the cell line panel used here consisted of only 39 cell lines in six different indications, it was not powered to determine responder populations/predictive biomarkers. We are in the process of using a large cell line panel to determine biomarkers predictive of combination response for the Wee1i + mTORi combination as well as other combinations of interest.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

Authors’ Contributions


Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): J. O'Neil, M. Chenard, B. Roberts, Y. Liu, J. Li, W. Arthur, B.B. Haines


Writing, review, and/or revision of the manuscript: J. O'Neil, Y. Benita, I. Feldman, M. Chenard, B. Roberts, Y. Liu, J. Li, S. Lejnine, R. Cristescu, B.B. Haines, C. Winter, A. Bloecher, S.D. Shumway

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): J. O'Neil, Y. Benita

Study supervision: A. Kral, S.D. Shumway

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References


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