Genotype-Selective Combination Therapies for Melanoma Identified by High-Throughput Drug Screening

Matthew A. Held, Casey G. Langdon, James T. Platt, Tisheeka Graham-Steed, Zongzhi Liu, Ashok Chakraborty, Antonella Bacchiocchi, Andrew Koo, Jonathan W. Haskins, Marcus W. Bosenberg, and David F. Stern

ABSTRACT

Resistance and partial responses to targeted monotherapy are major obstacles in cancer treatment. Systematic approaches to identify efficacious drug combinations for cancer are not well established, especially in the context of genotype. To address this, we have tested pairwise combinations of an array of small-molecule inhibitors on early-passage melanoma cultures using combinatorial drug screening. Results reveal several inhibitor combinations effective for melanomas with activating \( \text{RAS} \) or \( \text{BRAF} \) mutations, including mutant \( \text{BRAF} \) melanomas with intrinsic or acquired resistance to vemurafenib. Inhibition of both EGF receptor and AKT sensitized treatment-resistant \( \text{BRAF} \) mutant melanoma cultures to vemurafenib. Melanomas with \( \text{RAS} \) mutations were more resistant to combination therapies relative to \( \text{BRAF} \) mutants, but were sensitive to combinations of statins and cyclin-dependent kinase inhibitors \( \text{in vitro} \) and \( \text{in vivo} \). These results show the use of combinatorial drug screening for discovering unique treatment regimens that overcome resistance phenotypes of mutant \( \text{BRAF} \)- and \( \text{RAS} \)-driven melanomas.

SIGNIFICANCE: We have used drug combinatorial screening to identify effective combinations for mutant \( \text{BRAF} \) melanomas, including those resistant to vemurafenib, and mutant \( \text{RAS} \) melanomas that are resistant to many therapies. Mechanisms governing the interactions of the drug combinations are proposed, and in \( \text{in vivo} \) xenografts show the enhanced benefit and tolerability of a mutant \( \text{RAS} \)-selective combination, which is currently lacking in the clinic. Cancer Discov; 3(1); 1–16. ©2012 AACR.

INTRODUCTION

Inhibition of oncogenic drivers by targeted agents improves patient response rates (1–3), but primary and secondary resistance to these drugs is common (4–6). In melanoma, about half of patients harbor activating mutations in the BRAF oncogene (7). Most of these patients respond to the mutant BRAF inhibitor vemurafenib (PLX4032); however, some patients have primary resistance to therapy (8, 9). Acquired resistance occurs over a period of months in nearly all patients who do respond (8, 9). A large number of resistance mechanisms have been identified (10–18), and combinatorial therapies with vemurafenib will be needed to prevent disease progression and improve survival of patients.

Another roadblock to progress in melanoma therapeutics is the lack of effective therapies for mutant RAS-driven melanomas, which are found in up to one fifth of patients with melanoma (7, 19). RAS mutations in general (NRAS, KRAS, and HRAS) occur in up to a third of all human cancers (20) and are associated with relatively poorer prognoses in many cancer types, including lung and melanoma (21, 22). Furthermore, activating mutations in NRAS are one mechanism for secondary (acquired) vemurafenib resistance in a subset of mutant BRAF melanomas (14). Thus, an urgent need has arisen to identify effective drug combinations that attack mutant RAS-driven tumors and prevent treatment resistance. To date, no reports have described any systematic method for identifying the most effective drug combinations for either mutant RAS or BRAF melanomas. Therefore, we have used a combinatorial high-throughput drug screening (cHTS) approach to evaluate the selectivity of drugs, alone and in pairs, in the context of BRAF- or RAS-activating mutations, using early-passage melanoma cultures.

We identify several unique cytotoxic combinations with agents commonly used in the clinic that have pronounced genotype selectivity for RAS mutant or BRAF mutant melanomas, including those with primary and acquired resistance to vemurafenib. Furthermore, we confirm the effectiveness of select combinations in vitro and in vivo and provide mechanistic reasoning for their cooperation. The results show that combinatorial drug screening illuminates positive drug interactions in melanoma otherwise obscured with single-agent screening alone, and that these findings may guide the implementation of new combinatorial drug trials.

RESULTS

Evaluation of Melanoma Responses to Single Agents

To address the impact of genotype on response to a range of anticancer agents, we curated a panel of 150 small-molecule compounds, including traditional chemotherapies and targeted agents (Supplementary Table S1), and tested the concentration–response behaviors in early-passage patient-derived melanomas characterized for activating mutations in
growth inhibition was observed for all mutant related pharmacologic classes (Supplementary Fig. S1C). Responses (Supplementary Fig. S1B), as did compounds in different plates yielded similar concentration-dependent (Supplementary Table S3). Compounds arrayed in duplicate cell lines (Cluster 3). Reclustering of drugs showing variable efficacy (Cluster 2), and agents with variable efficacies across cell lines (Cluster 3). Concentrations required to inhibit 50% of cell growth (GI\textsubscript{50}) were variable among cell lines (Supplementary Table S3). Compounds arrayed in duplicate on different plates yielded similar concentration-dependence responses (Supplementary Fig. S1B), as did compounds in related pharmacologic classes (Supplementary Fig. S1C).

Unsupervised clustering of single-agent efficacies (maximal growth inhibition achieved) was conducted to identify agents that selectively inhibit growth of genotypic subsets. Drugs were partitioned into 3 clusters, including agents lacking effect (Fig. 1A, Cluster 1), agents with uniform high efficacy (Cluster 2), and agents with variable efficacies across cell lines (Cluster 3). Reclustering of drugs showing variable efficacies confirmed mutant BRAF selectivity of vemurafenib, PLX4720, and GDC-0879 as well as clustering of other agents belonging to the same specific classes, including ErbB, SRC/ABL, and mitogen-activated protein kinase (MEK) inhibitors (Fig. 1B). In agreement with previous studies, growth-stimulatory effects of vemurafenib were seen in some mutant RAS and WT melanomas, and incomplete growth inhibition was observed for all mutant RAS lines at concentrations up to 10 μM vemurafenib (Fig. 1C; refs. 23, 24). Approximately 25% of mutant RAS cultures were intrinsically resistant to vemurafenib, showing a GI\textsubscript{50} beyond 3 μM (Fig. 1D), as observed elsewhere (25). It has been suggested that PTEN deficiency may hinder vemurafenib-induced apoptosis (16), whereas co-occurring PTEN and RB1 deficiency may attenuate growth inhibition in vemurafenib (18). Although we did not evaluate the contribution of apoptosis to growth inhibition in the limited number of lines deficient in PTEN (YUGEN8, YUMUT, and YUKADI) or RB1 (YUSAC2), we observed growth inhibition resistance to vemurafenib in the setting of normal PTEN and RB1 expression (Fig. 1E; Supplementary Table S2), suggesting that loss of either or both is not essential for primary vemurafenib resistance. Indeed, others have observed that primary resistance to vemurafenib can occur by alternative mechanisms, including increased MET/hepatocyte growth factor receptor (HGFR) signaling (26, 27).

We found that other drugs eliciting selectively higher growth inhibition in mutant BRAF melanomas included the SRC/ABL inhibitor bosutinib, the fibroblast growth factor receptor (FGFR) inhibitor dovitinib and the EGF receptor (EGFR) inhibitor gefitinib (Supplementary Fig. S1D). No drugs were selective exclusively for the WT melanomas, likely owing to the greater genetic heterogeneity of this group. MEK inhibitors U0126 and CIP-1374 were selective as single agents for both the mutant BRAF and RAS groups (Supplementary Fig. S1D), but were more effective for mutant BRAF lines. Lines with primary resistance to vemurafenib were also less sensitive to MEK blockade (Fig. 1B), in agreement with other reports (28). Interestingly, the 3-hydroxy-3-methylglutaryl CoA reductase (HMG-CoA reductase) inhibitor simvastatin, which indirectly interferes with posttranslational processing of RAS proteins (29), was the only drug to show a trend toward a higher degree of growth inhibition in the mutant RAS group (Fig. 1F). Collectively, these data reveal a limited number of single agents with genotype-selective efficacy (Supplementary Table S4). Moreover, unless used at high concentrations (10 μM or greater), these single agents inhibited cell growth incompletely, which likely reflects that these agents are incompletely cytotoxic at lower concentrations.

**Combinatorial Drug Screening**

The limited responses to single agents prompted us to determine whether more defined genotype-selective patterns and higher efficacies could be observed using cHTS. Forty representative agents with high or variable efficacies (Fig. 1A, Clusters 2 and 3) were chosen for cHTS (Supplementary Table S5). As a group, these agents inhibit many of the signaling pathways important in cancer (Supplementary Fig. S2A). As melanoma lines varied in their sensitivities to each agent, we chose 3 consensus concentrations based on corrected median values for the GI\textsubscript{50}, GI\textsubscript{50}, and GI\textsubscript{50} effect levels across all melanoma lines (Supplementary Fig. S2B), together giving 9 pairwise combinations per drug pair. Nineteen melanoma lines, including 8 mutant BRAF, 6 mutant RAS (5 NRAS mutants and 1 HRAS mutant), and 5 WT lines, were screened against more than 7,000 pairwise combinations in parallel with single-agent controls.

Relationships between genotype and drug combination efficacy were first assessed by unsupervised clustering of the most effective combination of the 9 tested for each drug pair per cell line (Fig. 2A). Two clusters are apparent, with one dominated by mutant BRAF melanomas that are sensitive to a substantial number of combinations, and the other dominated by mutant RAS and WT melanomas, which were generally less sensitive to the combinations. To ascertain genotype-selective combinations, we filtered data for drug pairings that yielded an average 15% or greater growth inhibition exclusively in a genotypic group. Mutant BRAF-selective drug pairs greatly outnumbered drug pairs selective for mutant RAS or WT groups (1,021; 75; and 22 combinations, respectively). Agents most frequently paired in combinations selective for the mutant BRAF group (“sensitizers”) included the FGFR inhibitor PD173074, the pan-BCL2 family inhibitor obatoclax, vemurafenib, bosutinib, the c-MET inhibitor Pha665752, the ErbB inhibitor lapatinib, and the AKT inhibitor MK-2206 (Fig. 2B). All of these agents were selective for BRAF mutant cultures at multiple concentration combinations (Supplementary Table S6), reinforcing their cooperative effect. Vemurafenib was not the most frequent sensitizer, possibly because of the lower concentrations used in combination screening (Supplementary Table S5) as well as the presence of 2 intrinsically vemurafenib-resistant lines used in the screens (YUKSI and 501Mel, Fig. 1D). At the concentrations tested in cHTS, none of these sensitizers were exclusively selective for mutant BRAF melanomas in single-agent screening.

Strikingly, 52% of mutant RAS-selective drug combinations involved simvastatin (Fig. 2C), the only agent with a lower median GI\textsubscript{50} in the mutant RAS group in single-agent screening (Fig. 1F). Despite the low number of mutant RAS-selective combinations, 25 other drugs paired with simvastatin showed greater effectiveness in the mutant RAS group, whereas only 4 drugs in combination with simvastatin were more effective in mutant BRAF lines, and were all general
Genotype-Selective Drug Combinations for Melanoma

Figure 1. Single-agent HTS. A, unsupervised clustering heatmap of efficacy, or maximum growth inhibition, for each single agent (columns) per melanoma cell line (rows) relative to dimethyl sulfoxide (DMSO) controls. Cell lines named in red have BRAF mutations; green, RAS mutations; blue, wild-type (WT) RAS and BRAF (WT). B, second round of unsupervised clustering on drugs from Cluster 3 in A to survey for genotype-associated bias. Varying levels of efficacy are seen across melanomas. BRAF V600E–targeting drugs vemurafenib, PLX4720, and GDC0879, marked in red, were effective in many mutant BRAF melanomas, yet less effective in others (yellow box). Black boxes surrounding compound names are those with shared targets that grouped together when clustered. C, Concentration–effect curves fitted to median growth inhibition values for vemurafenib in the mutant BRAF, mutant RAS, and WT genotypic groups. Bracket indicates the concentration range of significant differences in drug potency; ***, $p < 0.0001$. Kruskal–Wallis test. D, comparison of vemurafenib concentrations required to induce 50% GI50 in mutant BRAF melanoma lines. Red datapoints indicate cell lines with primary resistance to vemurafenib and extant PTEN. Green datapoints mark sensitive lines with PTEN homozygous deletion. E, PTEN and RB1 protein status confirming no association with vemurafenib resistance in these lines. F, concentration–effect curves of median growth inhibition values for simvastatin in the 3 genotypic groups. A trend in higher potency of the drug in mutant RAS lines was observed (2–10 μmol/L).

Sensitizers of this group (Supplementary Table S7). Sixty-two of 64 combinations that elicited more than 50% inhibition in the mutant RAS group included simvastatin (Supplementary Table S8). Agents that combined with simvastatin at different concentrations selective for the mutant RAS group included vopiridol (Supplementary Table S6). None of these agents and the pan–cyclin-dependent kinase (CDK) inhibitor flavopiridol (Supplementary Table S6). None of these agents showed greater potency exclusively in the mutant RAS group with single-agent screening (Fig. 1B; Supplementary Table S4).

Finally, no drug combination partners were selective for the WT group of melanomas. Some combinations were effective (≥GI50) for all genotypic groups, although many included compounds that have not been used in the clinic, or were tested at higher concentrations of clinically tested agents shown to be genotype selective in combinations. Supplementary Table S8 collectively lists the genotype-selective and -nonselective combinations.

Synergistic and Cytotoxic Drug Interactions in Mutant BRAF and RAS Melanomas

Drug combinations were analyzed for additive, synergistic, or antagonistic interactions. Single-agent effects assessed in cHTS were plotted in relation to theoretical combinatorial effects using the Bliss independence model (30) and to their measured effects for each of the 9 concentration combinations per drug pair, depicted globally as drug “interaction signatures” (Fig. 3A). The majority of mutant BRAF melanomas shared a pattern of extensive synergies, whereas combinations in mutant RAS lines were more often antagonistic (i.e., less effective than predicted additivity; Fig. 3B). To identify genotype-selective synergistic drug pairs, we conducted unsupervised
clustering of average synergy values obtained from the 9 concentration combinations for each drug pair. Drugs that frequently appeared in combinations showing significantly higher synergies included lapatinib, vemurafenib, bosutinib, nilotinib, and PD173074 (Fig. 3C), and were usually observed in BRAF mutant melanomas. In contrast, these combinations were often antagonistic in mutant RAS melanomas (Fig. 3D). Lapatinib was the most frequent synergizing partner showing specificity for mutant BRAF lines (Fig. 3E).

A significant number of patients with BRAF-mutated melanoma do not respond to vemurafenib (9). YUKSI and 501Mel cell lines harbor activating BRAF mutations but show primary resistance to vemurafenib (Fig. 1D). These lines also showed higher relative resistance against many drugs paired with vemurafenib, even at the highest concentrations tested (Fig. 3F). Nevertheless, both resistant lines were more sensitive to the same set of combinations that were effective for vemurafenib-sensitive melanomas, including vemurafenib paired with bosutinib, lapatinib, obatoclax, PD173074, or Pha665752 (Fig. 3F, highlighted area). Combinations that overlapped in our queries for highest average synergy and average efficacy specific to mutant BRAF lines often included lapatinib and MK-2206 (summarized in Table 1). This finding suggests a shared mechanistic susceptibility in BRAF mutants to inhibition of the targets of these agents, regardless of vemurafenib sensitivity. MK-2206 and lapatinib were not found to be selective for mutant BRAF melanomas in single-agent screens, indicating that the genotype selectivity of these agents in combination, as based on BRAF or RAS mutation status, was not predictable by single-drug screening alone. Combinations most selective for RAS-mutated melanomas were mainly additive and included simvastatin with the pan-CDK inhibitor flavopiridol or the HSP90 inhibitor 17-DMAG.

We next confirmed cytotoxic and synergistic properties of select drug pairs that overlapped in our analyses for highest average synergy and efficacy (Table 1). For mutant BRAF-specific combinations, we chose the AKT inhibitor MK-2206 paired with lapatinib or bosutinib (Fig. 3G; Supplementary Fig. S3A and S3D). For mutant RAS-specific combinations, we chose simvastatin with flavopiridol or with 17-DMAG (Fig. 3H; Supplementary Fig. S3B and S3E). Finally, vorinostat with flavopiridol was selected as a genotype-independent combination (Supplementary Fig. S3C). Isobologram analyses (31)
Figure 3. Efficacious drug combinations for RAS mutant and vemurafenib-resistant BRAF mutant melanomas. A, drug interaction signatures for each cell line representing all combinatorial data compiled in a 40 by 40 drug matrix. Inset at bottom: magnified view of the 9 concentration combinations for each drug pair (rows) for each melanoma line (columns), and average antagonisms. Only drug pairs showing significant differences are shown. B, compilation of the total number of drug pair synergies, additivities, and antagonisms. P values calculated by χ² test. P < 0.05 for BRAF versus RAS for number of synergies and RAS versus BRAF or WT for number of antagonisms. C, unsupervised hierarchical clustering of average synergy values obtained from the 9 concentration combinations tested for each drug pair (rows) for each melanoma line (columns), and average antagonisms of the 9 combinations. Only drug pairs showing significant differences are shown. F, percent growth inhibition of mutant BRAF lines treated with vemurafenib combined with other agents at maximal concentrations tested (see Supplementary Table S5). YUKSI [red], the line most intrinsically resistant to vemurafenib, was also less sensitive to these combinations. The second-most vemurafenib-resistant line SO1Mel (black) used in cHTS was also less sensitive to many combinations. The most vemurafenib-sensitive line YULAC (green) was most sensitive to combinations with vemurafenib in almost all cases. Yellow highlight marks vemurafenib combinations that showed increased growth inhibition in the vemurafenib-resistant lines. G, drug combinations excluding vemurafenib, which showed highest selectivity toward mutant BRAF melanomas, were with lapatinib and the AKT inhibitor MK-2206. YUKSI and SO1Mel were also sensitive to these combinations. Bars indicate means. Indicated P values calculated by Kruskal–Wallis ANOVA. Post hoc Fisher’s test showed P < 0.05 for the mutant BRAF group versus the other groups. H, drug combinations with the highest efficacy and selectivity toward RAS mutant melanomas included simvastatin with flavopiridol.
### Table 1. Summary of drug pairs overlapping for highest efficacy and synergy

<table>
<thead>
<tr>
<th>Drug 1</th>
<th>Drug 2</th>
<th>Average efficacy</th>
<th>Average synergy</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Mutant BRAF</td>
<td>Mutant RAS</td>
<td>wtBRAF/wtRAS</td>
</tr>
<tr>
<td>Mutant BRAF-selective</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Bosutinib</td>
<td>MK-2206</td>
<td>0.85</td>
<td>0.53</td>
</tr>
<tr>
<td>Laptinib</td>
<td>Dovitinib</td>
<td>0.84</td>
<td>0.51</td>
</tr>
<tr>
<td>Laptinib</td>
<td>MK-2206</td>
<td>0.81</td>
<td>0.32</td>
</tr>
<tr>
<td>Laptinib</td>
<td>PHA 665752</td>
<td>0.88</td>
<td>0.43</td>
</tr>
<tr>
<td>Laptinib</td>
<td>Tozasertib</td>
<td>0.86</td>
<td>0.46</td>
</tr>
<tr>
<td>MK-2206</td>
<td>PD173074</td>
<td>0.84</td>
<td>0.51</td>
</tr>
<tr>
<td>Obatoclax</td>
<td>PD173074</td>
<td>0.84</td>
<td>0.67</td>
</tr>
<tr>
<td>PD173074</td>
<td>Vorinostat</td>
<td>0.84</td>
<td>0.48</td>
</tr>
<tr>
<td>Simvastatin</td>
<td>BMS-536924</td>
<td>0.58</td>
<td>0.84</td>
</tr>
<tr>
<td>Simvastatin</td>
<td>CIP-1374</td>
<td>0.60</td>
<td>0.83</td>
</tr>
<tr>
<td>Simvastatin</td>
<td>Temozolomide</td>
<td>0.57</td>
<td>0.83</td>
</tr>
<tr>
<td>Simvastatin</td>
<td>Vinblastine</td>
<td>0.56</td>
<td>0.82</td>
</tr>
<tr>
<td>Simvastatin</td>
<td>17-DMAG</td>
<td>0.59</td>
<td>0.81</td>
</tr>
<tr>
<td>Simvastatin</td>
<td>JK 184</td>
<td>0.60</td>
<td>0.81</td>
</tr>
<tr>
<td>Simvastatin</td>
<td>PX 12</td>
<td>0.62</td>
<td>0.81</td>
</tr>
<tr>
<td>Simvastatin</td>
<td>Flavopiridol</td>
<td>0.60</td>
<td>0.80</td>
</tr>
<tr>
<td>Non-genotype-specific</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Statric</td>
<td>FAK Inhibitor 14</td>
<td>0.96</td>
<td>0.95</td>
</tr>
<tr>
<td>Obatoclax</td>
<td>Flavopiridol</td>
<td>0.95</td>
<td>0.89</td>
</tr>
<tr>
<td>Vorinostat</td>
<td>Flavopiridol</td>
<td>0.83</td>
<td>0.79</td>
</tr>
</tbody>
</table>

**NOTE:** Drug combinations overlapping for highest average synergy and effectiveness (GI80) with respect to a specific genotypic group (at least 15% higher growth inhibition than in the other 2 groups) or those without genotype selectivity. Average efficacy (percent as decimal) and average synergy values (percent as decimal over predicted Bliss additivity) of the 9 concentration combinations are shown for each drug pair. Drug pairs chosen for confirmation of cytotoxicity are bold-faced.

using a broader range of concentrations than those in cHTS confirmed the overall synergistic nature of these drug interactions, as determined by combination index calculations (Fig. 4A; Supplementary Table S9). Laptinib or bosutinib in combination with MK-2206 was highly synergistic on the representative mutant B*RAF* line YUMAC. Simvastatin with flavopiridol or 17-DMAG was also additive on the mutant N*RAS* line YUGASP at high concentrations, but synergistic at concentrations well below the range used in cHTS.

Laptinib and MK-2206 individually induced approximately 20% cell death each (normalized to vehicle control) by 3 days in the B*RAF* mutant line YUMAC (Fig. 4B and C). The combination of these 2 drugs at the same concentrations increased cell death by 50% (87% actual, 36% Bliss model prediction), consistent with their synergy seen in cHTS and isolobologram analyses. These agents alone or in combination lacked appreciable cytotoxicity in the mutant N*RAS* line YUGASP. Conversely, simvastatin paired with flavopiridol was more cytotoxic in YUGASP (80% actual, 63% predicted), compared with the B*RAF* mutant line YUMAC (36% actual, 35% predicted). The combination of simvastatin with 17-DMAG, or bosutinib with MK-2206, similarly resulted in genotype-selective cytotoxicity in the mutant R*AS* and B*RAF* lines, respectively (Fig. 4C; Supplementary Fig. S3F). The genotype-unbiased combination of vorinostat and flavopiridol was also cytotoxic to both R*AS* and B*RAF* lines at high concentrations.
Genotype-Selective Drug Combinations for Melanoma

Figure 4. Confirmation of synergy and cytotoxicity of genotype-selective drug pairs. A, formal assessment of synergy of lapatinib or bosutinib with MK-2206, and simvastatin with flavopiridol or 17-DMAG on representative BRAF mutant and RAS mutant melanomas, by Chou–Talalay isobologram analysis. Data are normalized, with connecting line at X and Y = 1 corresponding to the line of additivity. Datapoints falling below line are synergistic, along or near the line are additive, and above the line are antagonistic (see key). Data represent averages for 3 separate experiments. Combination indices and growth inhibition values can be found in Supplementary Table S9.

B, flow cytometry of Annexin-V and propidium iodide viability markers after lapatinib (2.5 μmol/L) and MK-2206 (5.0 μmol/L) treatment alone or in combination, or simvastatin (2.5 μmol/L) and flavopiridol (0.1 μmol/L) alone or in combination with representative lines YUMAC (BRAF mutant) or YUGASP (NRAS mutant). Numbers in the lower right quadrant correspond to early apoptotic cells, whereas numbers in the top right and left quadrants correspond to late apoptotic and necrotic cells, respectively. Flow cytometry for vehicle-only controls and other combinations are shown in Supplementary Fig. S3F.

C, percent viability for combinations tested by flow cytometry, as in B. N = 3 for all experiments. Error bars, mean ± SD. P values calculated by Student t test; *, P < 0.05.

D, evaluation of drug-class effects. Representative concentration-response curves of single agents or dual-agent combinations showing enhanced growth inhibition in mutant BRAF cells, using the EGFR inhibitor gefitinib with MK-2206 (top row) or atorvastatin with flavopiridol in mutant RAS cells (bottom row) in relation to the predicted Bliss independence model. See also Supplementary Fig. S4. For statin combinations with flavopiridol, top and bottom x-axes represent concentrations used for each drug with those same concentrations used in combinations. Same-concentration combinations were used for gefitinib and MK-2206.
Most target classes were represented by only one compound in eHTS, so we verified that the genotypo-selective effects produced by these combinations are related to their target classes. The EGFR inhibitors gefitinib or afatinib/BIIBW2992 paired with the AKT inhibitors MK-2206 or GSK692094 produced similar combination responses to lapatinib and MK-2206, and were more effective in mutant BRAF lines, including the line most intrinsically resistant to vemurafenib (YUKSI; Fig. 4D; Supplementary Fig. S4A). Likewise, the combination of statins, including lovastatin and atorvastatin, combined with the pan-CDK inhibitors flavopiridol and AT7519 produced similar responses that were somewhat effective in mutant BRAF lines, but more effective in HRAS mutant and HRAS mutant lines (Fig. 4D; Supplementary Fig. S4B).

**Vemurafenib-Resistant Mutant BRAF Cells Regain Sensitization to Vemurafenib upon Concomitant Inhibition of EGFR and AKT**

We next assessed the interaction of vemurafenib-resistant BRAF and AKT mutations with MK-2206 or lapatinib alone or with MK-2206. Vemurafenib-resistant lines tested. The impact of these agents on MAPK and PI3K signaling in acquired vemurafenib-resistant lines (YULAC-R and YUCOT-R) was similar to that in primary vemurafenib-resistant lines. Vemurafenib or MK-2206 alone depleted or partially restored p-ERK levels, respectively (Fig. 5G; Supplementary Fig. S6C). In contrast, single-agent lapatinib treatment in acquired vemurafenib-resistant lines resulted in initial suppression, but subsequent elevation of p-ERK and p-AKT levels relative to baseline (Fig. 5G), whereas it had little impact on p-AKT and p-ERK in primary vemurafenib-resistant lines. Nevertheless, the 3 combined agents effectively suppressed both p-AKT and p-ERK levels in the vemurafenib-sensitive (Supplementary Fig. S6D and S6E) and vemurafenib-resistant lines tested.

Finally, we assessed the single-, dual-, and triple-agent treatments in preventing the long-term emergence of resistant colonies (Fig. 5H). As expected, the parental line YULAC readily formed colonies with lapatinib or MK-2206 alone or combined (data not shown). Dual-agent combinations with vemurafenib performed more effectively; however, a lower number of resistant clones did emerge. Only the vemurafenib/lapatinib/MK-2206 triple combination was found to impede the emergence of resistant colonies completely.

**Mechanistic and In Vivo Evaluation of the Mutant NRAS-Selective Simvastatin/Flavopiridol Combination**

Statins interfere with isoprenyl RAS modifications required for plasma membrane localization and activity (32–34). Indeed, membrane localization of NRAS was nearly eliminated with simvastatin treatment (Fig. 6A), confirming an association between loss of membrane-anchored NRAS and induction of cytotoxicity. Still, a large number of other proteins, including cancer-relevant RAC and RHO proteins, are also isoprenylated and may be concomitantly affected by statins. We therefore carried out RNA interference (RNAi)-mediated knockdown experiments to compare the effects of NRAS reduction with statin-induced NRAS inhibition. NRAS siRNA treatments resulted in nearly complete loss of mutant NRAS protein, greatly reduced p-ERK, and moderately reduced p-AKT (Fig. 6B). The combination of NRAS siRNA and flavopiridol treatment fully suppressed p-ERK levels and substantially increased BIM and PARP cleavage by 96 hours. This finding was associated with increased cytotoxicity relative to either treatment alone, as measured by flow cytometry (Fig. 6C). As with NRAS siRNA, repeated administration of lower concentration simvastatin reduced activity of the MAPK and PI3K pathways. This effect was enhanced in the presence of flavopiridol in NRAS mutant and HRAS mutant lines (Fig. 6D; Supplementary Fig. S7A and S7B), along with a significant reduction in viability and clonogenicity (Fig. 6E; Supplementary Fig. S7C and S7D). In contrast, cytotoxicity and clonogenic inhibition following
Figure 5. Combined targeting of EGFR and AKT re-establishes vulnerability to vemurafenib. A, representative 2D clonogenic (i), soft agar (ii), and flow cytometry (iii) assays on the YUKSI primary vemurafenib-resistant mutant BRAF line, which also shows marked resistance to lapatinib and MK-2206 used alone or combined. B, DMSO vehicle, L, lapatinib (1.5 μmol/L), M, MK-2206 (1.5 μmol/L). B, reproduced experiments as described in A for the primary-resistant lines YUKSI and YUKOLA, as well as acquired resistant line YULAC-R. Normalized clonogenic fraction refers to 2D clonogenic and soft agar assays, whereas normalized survival fraction refers to flow cytometry analyses. Lapatinib and MK-2206 both used at 1.5 μmol/L. C, immunoblotting to assess target engagement of EGFR and AKT by lapatinib and MK-2206, alone or combined. Increase of p-EGFR can be seen upon AKT inhibition by MK-2206. D, 2D clonogenic (i), soft agar (ii), and flow cytometry (iii) assays on the YUKSI line showing enhanced susceptibility to vemurafenib upon treatment with lapatinib and MK-2206 combination at 1.5 μmol/L each. E, reproduced experiments as in D for the vemurafenib-resistant lines YUKSI, YUKOLA, and YULAC-R. F, Molecular consequences of vemurafenib, lapatinib, and MK-2206 as single agents or as dual- or triple-agent combinations for downstream activity indicators of MAPK and PI3K pathways, including p-ERK and p-AKT. Primary vemurafenib-resistant YUKSI cells were treated with drugs for 24 hours before protein extraction. Concentrations of drugs in μmol/L are shown in parentheses after drug letter designations. G, p-ERK and p-AKT activity in the in vitro–selected vemurafenib-resistant YULAC-R line after 1- or 24-hour drug treatments. High levels of cleaved PARP could be detected clearly by 24 hours in the triple-agent combination in association with complete loss of p-ERK and p-AKT. F, full-length PARP; C, cleaved PARP. H, long-term 2D clonogenic assay on the parental YULAC line that was sensitive to vemurafenib. Cells were plated at 2 × 10^3 cells per well and treated every other day with fresh drug for 2 weeks, followed by 4 weeks of recovery. Only the triple-agent combination completely prevented the emergence of colonies.
Simvastatin sensitizes mutant NRAS cells to flavopiridol in vitro and in vivo. **A**, immunofluorescence on YUGASP mutant NRAS cells showing depletion of membrane-associated NRAS after simvastatin treatment at 5 μmol/L for 24 hours, or 1 μmol/L for 72 hours, with fresh drug added daily. **B**, NRAS knockdown by siRNA nearly depletes p-ERK protein and attenuates active AKT. Addition of flavopiridol at 0.1 μmol/L during the final 48 hours of siRNA treatment completely abrogated p-ERK and resulted in increased levels of proapoptotic BIM and cleaved PARP relative to siRNA or flavopiridol treatment alone. EL, L, and S mark the 3 BIM isoforms; F, full-length PARP; C, cleaved PARP. **C**, flow cytometry for viability confirmation in YUGASP mutant NRAS cells after NRAS knockdown with or without flavopiridol (FLAV) treatment at 0.1 μmol/L. SCR, scrambled siRNA control. (continued on following page)

Finally, we tested the impact of the simvastatin/flavopiridol combination in reducing tumor growth, using a preclinical xenograft model. YUGASP cells were injected subcutaneously into immunocompromised mice, and a dose-escalation study was conducted to ensure tolerability up to predefined maximum doses of the 2 drugs combined. No toxicity was observed with single agents or dual agents in the ranges of doses tested (data not shown). Simvastatin and flavopiridol modestly reduced tumor growth as single agents, with flavopiridol having a greater effect (Fig. 6F and G). The combination of simvastatin and flavopiridol significantly reduced tumor growth and resulted in initial tumor regression within the first week of treatment. The combination was well tolerated (Supplementary Fig. S7G), and histologic assessment at the 2-week mark indicated a trend toward increased cell death, as indicated by pyknotic cell index and reduced mitotic index in the combination treatment group relative to the single-agent and mock treatment arms (Supplementary Fig. S7H).

**DISCUSSION**

Resistance to therapies in cancer is a major clinical hurdle, creating a compelling need to discover more effective combinations of agents that are currently available. We present results from a drug combinatorial screen designed to probe positive drug interactions in mutation-defined subgroups of cancer. This screen has identified previously undescribed drug interaction patterns and several combinations with potential for high efficacy in melanoma (Table 1). Among these, statins with CDK inhibitors were validated as selective for NRAS and HRAS mutants, and a triple combination consisting of vemurafenib, EGFR, and AKT inhibitors was selective for BRAF mutant lines, including those with primary or in vitro–selected resistance to vemurafenib.
Genotype-Selective Drug Combinations for Melanoma

In patient-derived BRAF mutant melanomas with vemurafenib resistance, the EGFR inhibitors gefitinib, lapatinib, and afatinib were minimally cytotoxic when used alone, as were the AKT inhibitors MK-2206 and GSK692094, but more effective when combined at high concentrations than at lower concentrations. Yet, combinations of lapatinib and MK-2206 at reduced concentrations still effectively sensitized resistant cells to vemurafenib, giving credence to the idea that the major targets of these agents are critical mediators of vemurafenib resistance.

Cross-pathway feedback control between the MAPK and PI3K pathways is an important feature of many cancers (35, 36). In all vemurafenib-sensitive or -resistant BRAF mutant lines tested, we found an increase in ERK activity upon AKT inhibition with MK-2206. These effects were robust enough in primary lapatinib and MK-2206 at reduced concentrations still effectively sensitized resistant cells to vemurafenib, giving credence to the idea that the major targets of these agents are critical mediators of vemurafenib resistance.

In increased MAPK signaling, potentially through receptor kinases.

Melanomas with primary vemurafenib resistance were found to have higher baseline EGFR levels, similar to those in colorectal cancers insensitive to this agent (37, 38). In contrast to these studies, we found that combined EGFR and mutant BRAF inhibition was not effective for primary vemurafenib-resistant melanoma cells, or in preventing the emergence of resistant clones in vemurafenib-sensitive cells. Previous work in breast cancer showed upregulation of multiple RTKs, including EGFR, upon AKT inhibition with MK-2206 (36). Thus, it is plausible that primary-resistant melanomas will require AKT inhibition as a prerequisite for enhancing reliance upon MAPK signaling through RTKs and mutant BRAF. In addition, the partial reduction in p-ERK with EGFR inhibition seen in these cells may increase sensitivity to further MAPK inhibition by vemurafenib treatment. More generally, this idea suggests that combinations of specific RTK inhibitors with AKT inhibitors could likewise resensitize acquired vemurafenib-resistant lines to vemurafenib, and indeed, we found

**Figure 6. (Continued)** D, Western blot for p-ERK and p-AKT levels after treatment with simvastatin, flavopiridol, or both in mutant NRAS cells. The dual-agent combination reduced p-ERK and p-AKT levels more effectively than single agents. E, YUGASP cells were treated with simvastatin at 1 μmol/L, flavopiridol at 0.1 μmol/L, or the combination. Viability (left) and clonogenicity (right) assessed by flow cytometry and 2D clonogenic assay, respectively. F, tumor weights of xenografted tumors grown in immunocompromised mice and treated with simvastatin, flavopiridol, or both, or mock-treated with drug vehicle for 2 weeks. Kruskal–Wallis 1 way ANOVA, P < 0.0001; Asterisks over brackets indicate significant differences between 2 treatment groups. **, P < 0.001; ***, P < 0.0001, by Dunn multiple comparison test. G, tumor volume over time plot for those treatments as in F. ***, P < 0.001 by 1-way ANOVA followed by Bonferroni multiple comparison test for endpoint tumor volumes. All pairwise group comparisons showed significant differences, with the exception of mock-treated versus simvastatin alone. qod, every other day.
that the triple-agent combination was superior in these cases. Moreover, this regimen also blocked the long-term development of resistant clones in parental vemurafenib-sensitive cells, suggesting a route for prevention of vemurafenib resistance, which otherwise develops over a period of months (8, 9).

The effects of the vemurafenib/lapatinib/MK-2206 combination were minor on mutant NRAS cells, reaffirming its selectivity for lines with BRAF mutations. Generally, RAS mutant melanomas were resistant to most single-agent and dual-agent treatments in comparison with mutant BRAF melanomas and melanomas with WT BRAF and RAS, which is consistent with the slightly poorer clinical prognosis associated with NRAS mutation (22). Many drug combinations that were synergistic in mutant BRAF cells tested in cHTS, including RTK inhibitor combinations, were more often antagonistic in mutant RAS cells. This finding likely reflects the greater pleiotropy of RAS-dependent signaling, as RAS activates a variety of effector pathways, including MAPK, JAK-STAT, RAL-GDS, and PI3K signaling (20, 34).

Mutant RAS-selective combinations detected in cHTS often involved the HMG-CoA reductase simvastatin. Clinical studies have not supported use of statins as cancer monotherapies (39), and epidemiologic studies have not conclusively substantiated reduced cancer risk in individuals chronically treated with statins at the somewhat lower concentrations used for hypercholesterolemia control (39, 40). Still, it remains to be seen if statins are more functional for the specific prevention or treatment of RAS mutant cancers.

Here, we find that the impact of statins on NRAS mutant melanomas may be mediated through direct interference with the function of NRAS, as we confirmed that it is relocalized from the plasma membrane under these conditions, an important component of RAS signaling (41). Moreover, NRAS knockdown yielded biologic phenotypes similar to those with statin treatment, both alone and in combination with flavopiridol. Nonetheless, NRAS knockdown was more effective in suppression of p-ERK than simvastatin; and it is possible that the myriad proteins reliant on isoprenoid modifications—including additional GTP-binding proteins important in cancer, such as RAC and RHO—and more global effects on lipid metabolism contribute to these differences.

Concentrations of statins used in combinations to elicit complete cytotoxicity were by themselves only partially cytotoxic. Moreover, tumor growth inhibition with simvastatin alone in preclinical xenografts was not remarkable. RNAi-mediated knockdown of oncogenic NRAS elicited only partial cytotoxicity, similar to results seen with KRAS mutant cancers and mutant NRAS melanomas with or without activating BRAF mutations (14, 42–44). However, cHTS identified multiple second agents combined with simvastatin that were more effective in mutant RAS melanomas. Thus, these data show that loss of mutant NRAS, whether induced by small-molecule agents or by synthetic oligonucleotides, is mainly a critical priming event for cytotoxicity induced by a second agent such as an HSP90, MEK, or CDK inhibitor.

The pan-CDK inhibitor flavopiridol alone was not selective for mutant RAS melanomas, so this drug in combination with statins presumably works to forestall residual cell-cycle activation through RAS-dependent pathways or through pathways acting in parallel (45). In support of this idea, synthetic lethality has been shown elsewhere with combinatorial knockdown of mutant KRAS and CDK4 in non–small cell lung cancer mouse models (46). One phase II trial of flavopiridol as monotherapy in patients with stage IV melanoma resulted in stable disease in approximately half of patients, for up to half a year or more (47). Candidate oncogenic drivers were not evaluated, and so the efficacy of CDK inhibition in conjunction with oncogenic driver blockade, such as mutant RAS, remains unknown in humans. Our in vivo mouse studies show the tolerability and enhanced efficacy of flavopiridol in combination with simvastatin for mutant NRAS melanoma. This combination may also prove superior for preventing or treating vemurafenib-resistant BRAF V600* melanomas that acquire de novo mutations in RAS (14, 48).

Over the past 2 decades, the discovery of novel targeted agents that inhibit the oncogenic drivers of cancers has paved the way for more favorable patient outcomes and, importantly, more tolerable therapies. However, even the most precisely targeted therapies when used alone are limited in their ability to promote cytotoxicity in some cancer cells (30). Cancers associated with poor prognoses, such as advanced-stage melanomas, will require combination therapies to obstruct the outgrowth of resistant cells (49). Combinatorial drug screening has allowed for the discovery and experimental confirmation of a number of effective combination regimens that in the correct genotypic setting may prove more effective and tolerable in patients while avoiding selection for resistance through inadequate dosing.

**METHODS**

**Melanoma Cell Cultures**

Patient-derived melanoma lines, with the exception of 501Mel, were collected as previously described (24). Cell lines were derived directly from human melanoma metastases using a Yale Institutional Review Board–approved protocol with informed consent. Tumor lines were further confirmed by expression profiling and Sanger sequencing for BRAF and NRAS mutational status (Supplementary Table S2) and compared with the independent clinical genetic evaluation of the pathologic resection specimens in many cases. These studies served to validate that the short-term cultures expressed melanoma markers and were of the correct designated genotype. Cell lines were cultured in basal medium (OptiMEM (Invitrogen) supplemented with 10% FBS and 1% penicillin/streptomycin (P/S)) and maintained in a 37°C incubator maintained at 5% CO2. Acquired vemurafenib-resistant lines (YUCOT-R and YULAC-R) were generated by exposing parental lines to 3 μmol/L vemurafenib every 2 days for approximately 10 to 12 weeks.

**Single- and Dual-Agent Screening**

Cells were deposited into 384-well microtiter plates at 750 cells per well using a multidrop dispenser (Thermo) in 20 μL basal medium. Drug stock plates for 1,000x single agents were created by serial 1:2 dilution, typically from 10 mmol/L (Supplementary Table S1), using an expandable multichannel pipette (MatrixTechCorp). A PlateMate Plus automated instrument (MatrixTechCorp) was used for pin transfer of 20 nL drug volume from drug stock plates into 384-well microtiter cell plates. A total of 0.1% and 20% DMSO was used as negative and positive controls, respectively. For dual-agent screens, 96–deep well plates were used for single-agent concentration stocks, and pairwise combinations of drugs were generated...
using hit-picking automation (Freedom EVO, Tecan). Each of 780 unique drug pairs at 9 concentration combinations was generated spanning twenty-two 384-well microtiter stock plates. All experiments were carried out in triplicate at the Yale Center for Molecular Discovery (YCMD, New Haven, CT). Cells were exposed to drug for 72 hours, followed by growth inhibition measurement with the CellTiter-Glo ATP detection assay (Promega) based on amenability for HTS (50). Only experiments with high Z-factor quality indices (>0.5) were analyzed.

**Statistical Analyses**

Data were compiled into a relational database using PostgreSQL RDBMS (PostgreSQL.org). Statistics were computed with built-in functions of PostgreSQL or with R (R-project; http://www.r-project.org).

In single-agent studies, concentration–effect curves were computed using Michaelis–Menten or 4-parameter logistic curve fitting in R. GI values were only interpolated. Maximum GI and GI50 effects achieved with single agents were hierarchically clustered by the Ward method based on Euclidean distance using R. The Kruskal–Wallis test was used to compare genotype groups with regard to efficacy differences. For dual-agent efficacy, unsupervised hierarchical clustering was conducted with heatmap2 function from the gplots library in R. For synergy and antagonism studies, unsupervised clustering was conducted and analyzed by ANOVA and Tukey–Kramer pairwise testing. Identification of drug synergy was assessed with the Bliss independence model (30) or the Chou–Talalay method (31) using normalized isobologram analyses.

**Flow Cytometry**

Cells were plated at $1 \times 10^5$ cells per well in 6-well format and allowed to adhere overnight. Lifted cells were combined with adherent cells harvested by trypsinization. Repeated administration of agents was conducted every other day for 3 total treatments using fresh medium and drugs, and analyzed by flow cytometry the following day. Cells were stained using the BD Pharmingen Apoptosis Detection Kit II according to the manufacturer’s protocol (BD). Samples were analyzed with the BD LSRII flow cytometer, with recording of at least 10,000 events per sample. Cells were analyzed by doublet discrimination, and compensation was applied for each experiment. Each line was treated independently, and gates were fixed based on negative control signals. Plots were generated using FlowJo 7.6.5.

**Immunofluorescence**

Cells were plated on 8-chamber culture slides (BD Falcon) at 1,000 cells per well and allowed to adhere overnight before drug treatments. Cells were fixed using 4% paraformaldehyde at room temperature for 15 minutes, followed by quenching with 100 mmol/L glycine and permeabilization with 0.1% Triton X-100/PBS, and blocked with 5% bovine serum albumin (BSA)/phosphate-buffered saline with Tween 20 (PBST) for 30 minutes at 37°C. The anti-NRAS antibody (Santa Cruz Biotechnology; clone F155), which recognizes both mutant and WT NRAS, was used at 1:100 in 100 μL media (final siRNA concentration, 50 nmol/L). Fresh siRNA/transfection reagent mixture was added again 24 hours later, as described above, and cells were collected for protein or flow cytometry after 96-hour total exposure to siRNA. Flavopiridol (0.1 μmol/L) was added 48 hours before protein or cell collection, where indicated.

**Xenografts**

A total of $5 \times 10^6$ cells were resuspended in basal medium and injected subcutaneously into both flanks of 5- to 6-week-old NCr nude mice (Taconic). Tumors were grown until palpable at 200 mm3 before treatments. Simvastatin was slowly dissolved in prewarmed PBS and delivered daily by oral gavage at 10 mg/kg. Flavopiridol was dissolved in prewarmed 0.1% saline solution and delivered intraperitoneally every other day. Tumors were measured by digital caliper every other day, and volume was estimated using the equation $V = (width)^2 \times length/2$.

**Disclosure of Potential Conflicts of Interest**

No potential conflicts of interest were disclosed.

**Authors’ Contributions**

Conception and design: M.A. Held, C.G. Langdon, T. Graham-Steele, M.W. Bosenberg, D.F. Stern

Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.): M.A. Held, C.G. Langdon, A. Koo, J.W. Haskins

Analysis and interpretation of data (e.g., statistical analysis, biostatistics, computational analysis): M.A. Held, C.G. Langdon, J.T. Platt, Z. Liu, M.W. Bosenberg, D.F. Stern

Writing, review, and/or revision of the manuscript: M.A. Held, C.G. Langdon, Z. Liu, M.W. Bosenberg, D.F. Stern

Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases): J.T. Platt, Z. Liu, A. Koo

Study supervision: M.W. Bosenberg, D.F. Stern

Provided cell lines: A. Bacchiocchi, M.W. Bosenberg

Acknowledgments

The authors thank Ruth Halaban for her leadership of the Yale SPORE in Skin Cancer, and her generosity in providing materials for this study. The authors also thank Harriet Kluger, Mario Sznol, Karen Anderson, Yung-Chi Cheng, Gil Mor, Rick Bucala, and members of the Stern lab for helpful discussions and generous provision of some agents used in this work. Special thanks to the Yale Center for Molecular Discovery for HTS expertise.

Grant Support

This work was supported by a grant from an Anonymous Foundation to M.W. Bosenberg and D.F. Stern, the Harry J. Lloyd Charitable Trust (to M.A. Held, C.G. Langdon, J.T. Platt, and D.F. Stern), USPHS R01CA45708 (to D.F. Stern), T32GM07223 (to J.W. Haskins), and the Yale SPORE in Skin Cancer, funded by the National Cancer Institute (P50 CA121974; R. Halaban, Principal Investigator).

Received September 5, 2012; revised October 12, 2012; accepted October 16, 2012; published OnlineFirst December 13, 2012.

REFERENCES


Genotype-Selective Combination Therapies for Melanoma Identified by High-Throughput Drug Screening


Cancer Discovery  Published OnlineFirst December 13, 2012.

Updated version
Access the most recent version of this article at:
doi:10.1158/2159-8290.CD-12-0408

Supplementary Material
Access the most recent supplemental material at:
http://cancerdiscovery.aacrjournals.org/content/suppl/2012/11/02/2159-8290.CD-12-0408.DC1

E-mail alerts
Sign up to receive free email-alerts related to this article or journal.

Reprints and Subscriptions
To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.

Permissions
To request permission to re-use all or part of this article, contact the AACR Publications Department at permissions@aacr.org.