Preclinical Development

Comprehensive Predictive Biomarker Analysis for MEK Inhibitor GSK1120212

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Abstract

The MEK1 and MEK2 inhibitor GSK1120212 is currently in phase II/III clinical development. To identify predictive biomarkers, sensitivity to GSK1120212 was profiled for 218 solid tumor cell lines and 81 hematologic malignancy cell lines. For solid tumors, RAF/RAS mutation was a strong predictor of sensitivity. Among RAF/RAS mutant lines, co-occurring PIK3CA/PTEN mutations conferred a cytostatic response instead of a cytotoxic response for colon cancer cells that have the biggest representation of the mutations. Among KRA5 mutant cell lines, transcriptomics analysis showed that cell lines with an expression pattern suggestive of epithelial-to-mesenchymal transition were less sensitive to GSK1120212. In addition, a proportion of cell lines from certain tissue types not known to carry frequent RAF/RAS mutations also seemed to be sensitive to GSK1120212. Among these were breast cancer cell lines, with triple negative breast cancer cell lines being more sensitive than cell lines from other breast cancer subtypes. We identified a single gene DUSP6, whose expression was associated with sensitivity to GSK1120212 and lack of expression associated with resistance irrelevant of RAF/RAS status. Among hematologic cell lines, acute myeloid leukemia and chronic myeloid leukemia cell lines were particularly sensitive. Overall, this comprehensive predictive biomarker analysis identified additional efficacy biomarkers for GSK1120212 in RAF/RAS mutant solid tumors and expanded the indication for GSK1120212 to patients who could benefit from this therapy despite the RAF/RAS wild-type status of their tumors. Mol Cancer Ther; 11(3); 720–9. ©2011 AACR.

Introduction

The RAS-RAF-MEK-ERK [mitogen-activated protein kinase (MAPK)] signaling pathway is one of the most activated and also most extensively studied pathways in cancer (1). Genetic alterations causing aberrant activation of members of the MAPK pathway are commonly observed in cancer. For instance, receptor tyrosine kinases such as epidermal growth factor receptor (EGFR), HER2, or c-MET are frequently activated as a result of DNA amplification or gain-of-function mutations (2–4). Activating mutations in RAF/RAS genes represent the most important tumor predictive biomarkers for sensitivity to MEK inhibitors (10, 11). However, there is clear variance in sensitivity even among the limited set of RAF/RAS mutant cell lines that have been profiled. Furthermore, early clinical data indicates that although RAF/RAS mutant tumors (e.g., melanoma) seem to be more sensitive, tumors with these mutations are not uniformly mutated in more than 40% of melanomas and is also mutated at lower frequencies in other tumor types such as colon cancer and ovarian cancer. Therefore, although mutations in MEK1 or MEK2 are rare, pathway activation caused by mutations in the RTKs, RAS, or RAF are mediated through MEK (MAP/ERK kinase) kinases, making inhibition of MEK an attractive cancer therapeutic strategy (1).

Targeted therapies rely on the phenomenon of oncogene addiction to attempt to inactivate a mutated oncogenic pathway, critical to survival of cancer cells while sparing normal cells, which do not carry the mutation and are not similarly addicted to the pathway (5, 6). Thus, predictive markers identifying the appropriate genetic background are crucial to the success of targeted therapies. Examples include translocations of BCR-ABL with imatinib and ERBB2 DNA amplification with trastuzumab and lapatinib (7–9). Various reports suggest that activating mutations in the RAS or BRAF genes represent the most important tumor predictive biomarkers for sensitivity to MEK inhibitors (10, 11). However, there is clear variance in sensitivity even among the limited set of RAF/RAS mutant cell lines that have been profiled. Furthermore, early clinical data indicates that although RAF/RAS mutant tumors (e.g., melanoma) seem to be more sensitive, tumors with these mutations are not uniformly
responsive (12, 13). In some cases, co-occurring genetic alterations presumably provide mechanisms of resistance. A more comprehensive profile of the genetic determinants of sensitivity and resistance may further increase response rates to MEK inhibitors and provide rational combination strategies. Furthermore, it may assist in identifying those tumors that are dependent on MAPK pathway activation but do not harbor a RAF/RAS mutation. Identifying RAF/RAS wild-type tumors that might be responsive to MEK inhibitor would enable more cancer patients to benefit from these inhibitors.

GSK1120212 is a potent and specific allosteric inhibitor of MEK1/2 that is currently in phase II/III clinical development (14). It has shown clinical activity in tumors with activating mutations in BRAF (ASCO 2010). In this study, we conducted a comprehensive predictive biomarker study for GSK1120212 using 218 solid tumor cell lines covering different tissue types and subtypes. A comprehensive genetic characterization has been done in these cell lines. Our data confirm the association of a comprehensive genetic characterization has been done at the ATCC cell bank (short-tandem repeat, sequencing, single nucleotide polymorphism fingerprinting). DNA copy number profiling and transcriptomics profiling of these cell lines were described previously (15). Briefly, unless otherwise recommended, cell lines were cultured in RPMI-1640 supplemented with a final concentration of 10% FBS, 2 mmol/L GlutaMAX, and 1 mmol/L sodium pyruvate. Genomic DNA was extracted from each line using Mini DNeasy Kit (Qiagen, Inc.) and copy number data was profiled using Affymetrix 500K SNP Chip. RNA was isolated from exponentially growing cells by replacing the media with TRIzol and purifying the RNA using Qiagen RNeasy spin columns. The transcriptomics data from these cell lines were collected using the Affymetrix U133 Plus2 Gene Chips in triplicate. All the genomic data on these cell lines have been deposited in https://cabig.nci.nih.gov/caArray_GSKdata/. Mutation data of these cell lines for BRAF, KRAS, NRAS, HRAS, PIK3CA, and PTEN were mostly obtained from COSMIC database (v49 release, Wellcome Trust Sanger Institute, United Kingdom).

Cell line proliferation assay

Each cell line was seeded into 384-well microtiter plates at high and low cell densities, ranging from 300 to 3,600 cells per well, depending on cell line doubling rate. Cells were plated in triplicate and incubated at 37°C in 5% CO2 for 24 hours. Compound was added at 10 concentrations, ranging from 0.16 nmol/L to 5 μmol/L along with a dimethyl sulfoxide (DMSO) control. Cell numbers were measured using 4′,6-diamidino-2-phenylindole (DAPI) nuclei staining and quantitated with an InCell1000 High Content Analyzer (GE Biosciences). A zero-time value (D0) was measured for each cell line, at each seeding density, immediately after the addition of DMSO control. Cell numbers at day 3 (D3) were also measured using DAPI staining. A drug response curve was generated using model 205 of XLfit in Microsoft Excel. GI50 was defined as the drug concentration at which cell growth was inhibited at 50% compared with DMSO control. Compound cytotoxic effect was reached if the number of cells after 3-day drug treatment (D3) is smaller than that measured at D0 (i.e., cell number at D3 < cell number at D0) and compound cytostatic effect was reached if the number of cells did not decrease below the number measured at D0 following up to 5 μmol/L drug treatment. For hematologic lines, a 3-day proliferation assays was conducted using CellTiter-Glo (Promega).

Western blot analysis

After media was aspirated from the dishes, cells were rinsed once with cold PBS and were then scraped off plates in cold PBS and spun down. Cell pellets were lysed in M-PER lysis buffer (Thermo Scientific) supplemented with Protease inhibitors (Roche Diagnostics) and phosphatase inhibitors (Upstate). Cell lysates boiled in loading buffer were run on 4% to 12% gels (NuPage), transferred to polyvinylidene difluoride membrane, and probed with antibodies. The antibodies used in the studies are anti-phospho-ERK at 1:1,000 dilution (catalog no. 4376; Cell Signaling), anti-phospho-AKT at 1:1,000 dilution (catalog no. 9271; Cell Signaling), anti-cleaved PARP at 1:1,000 dilution (catalog no. 9541; Cell Signaling), anti-total ERK at 1:500 dilution (catalog no. sc-93; Santa Cruz), ERK at 1:500 dilution (catalog no. sc-93; Santa Cruz), anti-total AKT at 1:1,000 dilution (catalog no. 4691; Cell Signaling), anti-cleaved caspase-3 at 1:1,000 dilution (catalog no. 9661; Cell Signaling), and DAPI staining. A drug response curve was generated using model 205 of XLfit in Microsoft Excel. GI50 was defined as the drug concentration at which cell growth was inhibited at 50% compared with DMSO control. Compound cytotoxic effect was reached if the number of cells after 3-day drug treatment (D3) is smaller than that measured at D0 (i.e., cell number at D3 < cell number at D0) and compound cytostatic effect was reached if the number of cells did not decrease below the number measured at D0 following up to 5 μmol/L drug treatment. For hematologic lines, a 3-day proliferation assays was conducted using CellTiter-Glo (Promega).
anti-total AKT at 1:1,000 dilution (catalog no. 2967; Cell Signaling), anti-glyceraldehyde-3-phosphate dehydrogenase (GAPDH) at 1:5,000 dilution (catalog no. G8795; Sigma-Aldrich), anti-DUSP6 at 1:500 dilution (catalog no. sc-8599; Santa Cruz).

**Transcriptomics analysis for epithelial/mesenchymal features and breast cancer cell line characterization**

On the basis of Affymetrix U133_2 transcriptomics data from the cell lines (described previously), transcript abundance was estimated by normalizing all probe signal intensities to a value of 150 using the MAS5 algorithm in the Affymetrix MicroArray Analysis Suite 5.0. For subsequent analysis, the average probe intensity was used for sample triplicates. For determining epithelial or mesenchymal profile, 4 epithelial markers (CDH1, OCLN, DSP, and CLDN1) and 6 mesenchymal markers (S100A4, CDH11, VIM, CDH2, ACTA2, and FN1) were selected for analysis. The Affymetrix probes assaying each were interrogated. The probe with the highest expression values across the cell lines was selected, in which more than one probe existed for a gene, and the probes were further checked for specificity by BLASTing against the human genome. The selected probes identifiers were 201131_s_at, 203440_at, 200974_at, 212464_at. The intensity values (averaged across the triplicates) were Z-score normalized across all the cell lines. An average of the epithelial markers and mesenchymal markers were taken. If the epithelial average was higher than the mesenchymal average, the cell line was classified as epithelial and if the mesenchymal average was higher than the epithelial average across all the cell lines. An average of the triplicates. An average of the triplicates. The Z-score normalized across all the cell lines. An average of the epithelial markers and mesenchymal markers were taken. If the epithelial average was higher than the mesenchymal average, the cell line was classified as epithelial and if the mesenchymal average was higher, the cell line was classified as mesenchymal.

For breast cancer cell lines, basal and luminal cell lines were identified on the basis of hierarchical clustering. Basal breast cancer cell lines were differentiated from luminal cell lines on the basis of previously published signatures (16).

**Results**

**Sensitivity profiling of MEK1/2 inhibitor, GSK1120212, in solid cancer cell lines**

To identify predictive biomarkers for GSK1120212, 218 solid cancer cell lines encompassing different tissue of origins were profiled for sensitivity using a 3-day proliferation assay (Supplementary Table S1). Cell lines were defined as sensitive if GI50 was below 50 nmol/L and resistant if above 1 μmol/L, whereas if between 50 nmol/L and 1 μmol/L the sensitivity of the cell lines was considered intermediate. As shown for other MEK inhibitors, GSK1120212 showed increased activity against RAS or RAF mutant cell lines compared with cell lines wild type for these genes (Fig. 1A). When segregated into tissue types, tumor types known to carry high frequency of RAF/RAS mutations, such as pancreatic cancer, colon cancer, and melanomas showed generally increased sensitivity to MEK inhibitor GSK1120212 (Fig. 1B).

However, for certain tissue types known to carry low frequency of RAF/RAS mutations, a significant proportion of cell lines showed sensitivity to GSK1120212. Among these were breast, glioma, head and neck, kidney, and ovarian cancer. The biological determinants of the sensitivity of these RAF/RAF wild-type cell lines were further analyzed and discussed in subsequent sections.

**GSK1120212 caused a cytostatic, rather than cytotoxic, response on RAF/RAS mutant tumors encoding co-occurring PI3K or PTEN mutations**

On the basis of GI50, more than 80% of RAF/RAS mutant lines would be considered sensitive to MEK1/2 inhibitor GSK1120212 (GI50 < 50 nmol/L). However, because drug sensitivity in preclinical studies commonly overpredicts the observed clinical response (17), we attempted to further refine the sensitivity determinant for tumors harboring RAF or RAS mutations. To that end, an additional criteria to GI50 was added in which cell line response to GSK1120212 was categorized as cell killing (cytotoxic = cell number at D3 < D0) or cell growth inhibition (cytostatic...
KRAS mutant cell lines with a mesenchymal expression pattern are less sensitive to GSK1120212

Analysis of GSK1120212 sensitivity of cell lines with MAPK pathway mutations showed that although most BRAF mutant cell lines respond with single digit nmol/L GI50 values, KRAS mutant cell lines exhibited a wider range of sensitivity (Fig. 3A). To further define the determinants of KRAS mutant cell line sensitivity to GSK1120212, additional genetic and transcriptomic analysis were carried out. At the genetic level, we observed a trend for KRAS mutant cells with co-occurring PIK3CA or PTEN mutations to be less sensitive to GSK1120212 (Fig. 3A). However this is not statistical significant (t test). Epithelial-to-mesenchymal transition (EMT) has been implicated in resistance to multiple cancer therapies including EGFR inhibitors (20). Furthermore, Singh and colleagues (21) showed that KRAS mutant cell lines sensitive to RNA interference (RNAi)-mediated KRAS depletion had higher levels of E-cadherin protein, an epithelial state marker, than KRAS mutant lines insensitive to KRAS RNAi depletion. The process of EMT was studied using transcriptomics analysis for the KRAS mutant cell lines. A 10–gene transcript signature designed to assay epithelial and mesenchymal status was derived and used to correlate with response of KRAS mutant cell lines to GSK1120212. Using this gene transcript signature, we showed that cell lines with increased mesenchymal features showed higher GI50 values (less sensitive) than KRAS mutant cell lines sensitive to RNA interference (RNAi)-mediated KRAS depletion.
cell lines with increased epithelial features (t test $P = 0.00162$; Fig. 3B). The gene expression levels from which the EMT prediction was derived are represented in the heatmap at bottom of Fig. 3B. Exclusion of PIK3CA/PTEN mutant cell lines from this analysis improved the significance of this association ($P = 0.000902$; Fig. 3C), suggesting that epithelial-like (by transcriptional analysis) KRAS mutant cell lines wild-type for PIK3CA/PTEN are more sensitive to GSK1120212. Interestingly, despite the high sensitivity of most BRAF mutant lines

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\begin{array}{cccc}
& \text{KRAS mutant, PIK3CA/PTEN wildtype (26)} & \text{KRAS mutant, PIK3CA/PTEN mutant (12)} \\
\text{GI50 (nmol/L in log scale)} & 3,162 & 1,000 & 316 & 100 & 32 & 10 & 3 & 1 \\
\end{array}
\]

Figure 3. GI50 values for GSK1120212 are represented on the y-axis and individual cell lines on the x-axis. A, KRAS mutant, PIK3CA/PTEN mutant lines are colored red, showing a slight tendency for these lines to have higher GI50 values than KRAS mutant, PIK3CA/PTEN wild-type lines (not statistically significant, t test). B, KRAS mutant lines are colored for their epithelial/mesenchymal transcriptional signature; green lines denote higher average expression of the epithelial marker genes CLDN1, DSP, OCLN, and CDH1 than the mesenchymal marker genes, FN1, ACTA2, CSH2, VIM, CDH11, and S100A4. Orange lines denote higher average expression of the mesenchymal marker genes compared with the epithelial marker genes. Lines with a mesenchymal signature tend to have higher GI50 values ($P = 0.00162$). Below the bar chart is a heatmap showing the Z-score–normalized expression values of the markers genes in a heatmap. Higher expression is denoted by green, lower expression by red, and the median by blue. C, KRAS mutant, PIK3CA/PTEN wild-type lines are colored for their epithelial/mesenchymal transcriptional signature. Lines with a mesenchymal signature tend to have higher GI50 values ($P = 0.000902$). D, BRAF mutant lines are colored for their epithelial/mesenchymal transcriptional signature. Sensitive lines have both epithelial and mesenchymal signatures. The 3 most resistant lines have mesenchymal signatures.
Predictive Biomarker for MEK Inhibitor

Regardless of PIK3CA/PTEN mutation or mesenchymal-like features (Supplementary Table S3; Fig. 3D), 3 BRAF (V600E) mutant sarcoma cell lines (GCT, A673, and SW-725) were not sensitive. Sarcomas typically arise from transformed mesenchymal cells, and the 3 cell lines have a mesenchymal-like gene signature.

**Basal or triple negative breast cancer cell lines showed increased sensitivity to GSK1120212 compared with other breast cancer subtypes**

Although breast cancer cell lines carry low frequency of RAF/RAS mutations, a significant number were sensitive to GSK1120212 (Fig. 1B). To better understand the determinants of breast cancer cell line sensitivity to GSK1120212, we correlated the HER2, ER, and PR status as well as basal or luminal status defined by published transcriptomics signature (16) to sensitivity to GSK1120212, as shown in Fig. 4. A total of 9 of 12 (75%) of more sensitive cell lines were of the basal subtype, whereas only 2 of 9 (22%) resistant lines were basal ($P = 0.029$). Notably, 3 of 4 (75%) of ERBB2-amplified cell lines were less sensitive, and 9 of 11 (82%) of triple negative (HER2, ER, and PR negative) cell lines were more sensitive, suggesting the triple negative subtype may preferentially respond to GSK1120212. Although basal breast cancers are not equivalent to triple negative breast cancers, they largely overlap in the clinic (22).

**DUSP6 expression is a predictive biomarker of MEK inhibitor sensitivity**

Although multiple gene signatures have been derived to predict MAPK pathway activation or response to MEK inhibitor (10, 23, 24), the technical difficulty to clinically measure these multiple transcripts has hindered their utility and usage. Our search to narrow the number of transcripts to predict cellular response to GSK1120212 led to identification of DUSP6 as single transcriptional marker of MEK inhibitor sensitivity. Of special interest is the fact that presence or absence of DUSP6 expression seems to be associated with MEK inhibitor sensitivity, not just degree of expression. DUSP6 is a cytoplasmic phosphatase inactivating PERK2 and is transcriptionally upregulated following activation of the MAPK pathway (25). Transcriptomics profiling of DUSP6 expression revealed that its expression was associated with sensitivity to GSK1120212 (Sensitivity: 79%; specificity: 82%; $P = 0.0027$; Fig. 5A).

Notably, among head and neck (H&N) cancer cell lines, none of the 5 sensitive cell lines carry RAF/RAS mutations. However, they all express high levels of DUSP6 (Supplementary Table S1 and Supplementary Table S2), and the only H&N cancer cell line not expressing DUSP6 was resistant to GSK1120212. Moreover, among the 7 tested cervical cancer cell lines, the 4 cell lines that do not express DUSP6 were all resistant to GSK1120212, and the remaining 3 cell lines expressing DUSP6 showed an intermediate response to GSK1120212. Among ovarian cancer cell lines, RAF/RAS mutation status alone would correctly predict 3 of 4 sensitive cell lines. A2780 had a sensitive response to GSK1120212 with $G_{1/2}$ of 28 nmol/L, and although it is wild type for RAF/RAS, it has a high expression of DUSP6. None of the 3 resistant ovarian cell lines express DUSP6 (MASS signal below background of 100; Supplementary Table S2; Fig. 5B). Western blot against DUSP6 was done on cell extracts from 7 ovarian cancer cell lines and showed that levels of DUSP6 protein correlated with that of DUSP6 mRNA levels and sensitivity to MEK GSK1120212 inhibitor (Fig. 5C). In addition, treatment of a sensitive cell line OVCA5 with GSK1120212 led to dose- and time-dependant protein expression decrease of DUSP6 (Fig. 5D), suggesting that DUSP6 has the potential to be simultaneously a predictive (high endogenous level) and pharmacodynamic (decreased expression upon drug treatment) marker of GSK1120212 sensitivity.

**Among hematopoietic malignancies cancer cell lines from AML and CML showed increased sensitivity to GSK1120212**

GSK1120212 was profiled against 81 cancer cell lines from hematologic malignancies (Fig. 6). As with the solid tumor lines, activating mutations in RAF/RAS were predictors of sensitivity to GSK1120212, with 12 of 22 sensitive cell lines encoding mutations in NRAS, KRAS, HRAS, or BRAF (Supplementary Table S4). Interestingly, majority of AML lines tested showed sensitivity to GSK1120212 (11 of 12 cell lines), which can only be partly explained by RAF/RAS activating mutations (6 of 12 lines with RAF/RAS mutation). Similarly, the majority (4 of 6) of CML lines tested were sensitive to GSK1120212, but none encoded activating mutations in RAF/RAS. In both cases,

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**Figure 4.** Proliferation response, measured by $G_{1/2}$, for GSK1120212 in 21 breast cancer cell lines indicates that basal breast cancer cells are more responsive than luminal cell lines (depicted in blue and pink bars, respectively). A total of 9 of 12 (75%) of more sensitive cell lines were of the basal subtype, whereas only 2 of 9 (22%) resistant lines were basal ($P = 0.029$). ERBB2 amplification, ER positivity, and PR positivity (by RNA levels) are denoted for each cell line. Notably, 3 of 4 (75%) of ERBB2-amplified cell lines were less sensitive, and 9 of 11 (82%) of triple negative (HER2, ER, and PR negative) cell lines were more sensitive.
sensitivity to GSK1120212 in the absence of RAF/RAS mutations may be explained by other commonly occurring oncogenic events (BCR-ABL translocation in CML and FLT3 internal tandem duplications in AML) that have been previously shown to signal through the MAPK pathway (26, 27). Whereas AML and CML lines tested were predominantly sensitive to GSK1120212, the majority of B cell lymphoma lines [Burkitt, Hodgkin’s, non-Hodgkin’s lymphoma (NHL), and various other subtypes], acute lymphocytic leukemia (ALL; B cell or B cell precursor), multiple myeloma, T-cell derived ALL, and cutaneous T-cell leukemia (CTL) cell lines were resistant to GSK1120212. Somewhat surprisingly, although 4 of 7 T-cell derived ALL lines had activating mutations in KRAS or NRAS, only one line was sensitive to GSK1120212. Taken together, these data showed that AML and CML cancer cell lines are more sensitive to GSK1120212 than other hematopoietic cancer cell lines, in which sensitivity correlates weakly with RAF/RAS mutational status.

Discussion

Clinical response has been seen with GSK1120212 in BRAF and RAS mutant tumors (ASCO 2010). However, only a subset of BRAF and RAS mutant tumors responded to the MEK inhibitor GSK1120212 (ASCO 2010). These results are reminiscent of the clinical response to Herceptin, in which only a subpopulation of HER2-amplified breast cancers show benefit with treatment (28). On the basis of these data, it is imperative that additional biomarkers to BRAF/RAS mutation be identified to improve the clinical success rate and benefit to patients. On the other hand, it is also important that we discover predictive markers that can identify sensitive patients with...
wild-type RAF/RAS tumors, broadening the therapeutic benefit of MEK inhibitors.

With these goals in mind, we conducted a comprehensive predictive biomarker analysis using response data for GSK1120212 from approximately 300 cancer cell lines. As with previously characterized MEK inhibitors (10, 11), we observed that activating RAF/RAS mutations were the predominant predictors of sensitivity. Consequently, tumor types known to carry high frequency of RAF/RAS mutations (melanoma, pancreatic, and colon cancers), thus particularly depend on MEK pathway activation for growth, showed the highest rate of response (Fig. 1B). Among RAF/RAS mutant colon cancer cell lines, cell lines encoding both RAF/RAS and PI3K/PTEN mutations tend to have a cytostatic (inhibition of cell growth) rather than a cytotoxic (cell death) response (Fig. 2A). This observation was further confirmed with RKO colon cancer cell line (BRAF/PI3K dual mutant), showing significant cell death only following treatment with both MEK and PI3K inhibitors but with neither agent alone (Fig. 2B).

AKT/PI3K and MAPK are the 2 most important cancer pathways downstream of most tyrosine kinase receptors. Cross-talk between these 2 pathways has been reported (29), and it is conceivable that for cell lines with mutations in both pathways, activated AKT can confer survival signal upon MEK pathway inhibition, whereas simultaneous inhibition of both pathways causes cancer cell death. This observation not only suggests combination studies using a PI3K inhibitor and a MEK inhibitor but also carries significance in further stratifying colon cancer patients for response. Approximately 40% of tumors of colon cancer patients have BRAF or RAS mutations, and half of these tumors would have concomitant PI3K/PTEN mutations, whereas the other half would be wild-type for PI3K/PTEN and would have greater probability to respond to single-agent MEK inhibitor (30, 31).

Mutant KRAS can activate multiple downstream effector pathways (29) besides the MEK pathway. As a result, the consequence of inhibiting MEK pathway in RAS mutant tumors can be influenced by the activity of other pathways downstream of RAS. In contrast, MEK pathway seems to be the only physiologically relevant pathway activated in BRAF mutants (32). Therefore, cells with mutant BRAF would presumably be truly addicted to MEK pathway activation. In an earlier study using CI-1040, it was reported that only BRAF mutation predicted sensitivity to MEK inhibition but not RAS mutation (11). Using GSK1120212, we found that overall cell lines with RAS mutations tend to be more sensitive (Fig. 1A). However, among 27 BRAF V600E mutant cell lines (the non-V600E mutations are known to have less activity), most were highly sensitive with GI50 of 5 nmol/L or below (20 of 27, 74%) regardless of PI3K/PTEN status. On the contrary, only 13 of 40 (32.5%) KRAS mutant cell lines gave GI50 values of 5 nmol/L or below, and a wider range of response was observed (Supplementary Table S5).

Because there is potential for some, but not all, patients with RAS mutant tumors to benefit from MEK inhibitor therapy, it is important to identify predictive biomarkers in the RAS mutant background. Even with GI50 alone, there seemed to be an association between PI3K/PTEN mutation and higher GI50, although this is not statistically significant (Fig. 3A). A previous study using RNAi to knockdown KRAS in K Ras mutant cell lines showed that not all KRAS mutant cell lines require KRAS to maintain cell viability (21). The gene signature derived from this study to predict true KRAS dependency was associated with epithelial phenotype. Through analyzing mRNA expression patterns, we found that KRAS mutant tumors with an expression pattern suggesting more mesenchymal features tended to be more resistant (Fig. 3B and C). This relationship may be mirrored in the observation that the only BRAF V600E mutant cells lines that showed even moderate resistance were derived from sarcomas, a mostly mesenchymal tumor type. In a recent publication on predictive biomarkers for another MEK inhibitor AZD6244, the authors observed an association between Wnt pathway and resistance in KRAS mutant colon cell lines (24).

Both MAPK and Wnt pathway activation are known to play an important and interconnected role in EMT transition in cancer, maybe through Rkip (33) or BMP4. However, despite this observed relationship between epithelial or mesenchymal expression pattern and MEK sensitivity, the underlying mechanism is not clear. EMT transition has been shown to be an acquired resistance marker to chemotherapy (20) and EGFR inhibitors (34) in multiple epithelial cancers (20). It could be that more advanced tumors tend to have undergone EMT and also to have gathered more upregulated growth pathways, which may compensate for MEK inhibition. Another possible explanation is that the MAPK pathway is an epithelial lineage pathway and, perhaps, as cells progress through EMT and become more mesenchymal, they also become less dependent on the MAPK pathway. This would suggest that RAF/RAS mutation would not be a route to oncogenesis in hematologic malignancies. RAF/RAS mutations are less common but certainly not absent from this class of cancers.

We decided to profile cell lines derived from many different tissue types and found tumor types that are known to have a low frequency of RAF/RAS mutations but unexpectedly showed sensitivity toward GSK1120212. Predictive biomarkers identifying tumors without mutations in RAF/RAS gene that still respond to MEK inhibition offer the opportunity to allow more patients to benefit from GSK1120212. All the available mutation data for the RAF/RAS wild-type cell lines was collected from Sanger database in hope of finding some other mutations that can explain the observed sensitivity. However no statistically significant association was observed, probably because most of the mutations occur at low frequency. Among breast cancer subtypes, triple negative breast cancer is considered to be EGFR driven and requires MEK pathway activation (35). Indeed, triple negative breast cell lines showed higher sensitivity toward GSK1120212 compared to GSK1120212 alone.
with breast cell lines from other subtypes (Fig. 4). For other tumor types, we investigated expression of MEK pathway genes downstream of RAF/RAS to identify tumors that have an activated MEK pathway but not identifiable with a RAF/RAS mutation. Multiple transcriptomics signatures have been reported either for RAF/RAS mutations or sensitivity toward MEK inhibitors (10, 23, 24). Most of these signatures include a DUSP6 gene, a family of dual-specificity phosphatases that regulate the MEK pathway.

We found that a single gene DUSP6, a DUSP that specifically dephosphorylates and inactivates ERK2, predicts response to GSK1120212 with sensitivity of 79% and specificity of 82% \( (P = 0.0027, \text{ Fig. 5}) \). DUSP6 is known to be involved in a feedback loop with ERK2 at the transcriptional level via ETS2 (25). Presumably its expression would reflect ERK2 activity and thus MAPK pathway activation status. In fact, it is among the genes identified by Prattas and colleagues to be the transcriptional output of MEK pathway (36). Indeed, when the MAPK pathway was inhibited by treatment with GSK1120212, a sharp reduction in DUSP6 level was also observed (Fig. 5D). Measuring a single gene instead of a group of genes in the clinical samples requires less tumor material. The fact that in cell lines DUSP6 transcription expression is usually below detection (in resistant cells) or significantly expressed (in sensitive cells) makes the assay almost binary. This has a significant advantage translating to clinical specimens when cellular heterogeneity of tumors complicates the interpretation of multifactorial gene signatures. In cell lines, the protein level of DUSP6 correlated well with mRNA level (Fig. 5C), making it a possibility to use immunohistochemistry to measure DUSP6 levels. With the sharp reduction of DUSP6 expression upon GSK1120212 treatment, it also has the potential to be used as a pharmacodynamic marker, as well as a predictive marker.

Among hematologic malignancies, the growth of the majority of myelogenous lines (AML and CML) was inhibited at low concentrations of GSK1120212 with \( G_{50} \) values of less than 50 nmol/L. These sensitive lines included RAF/RAS mutant and wild-type AML, whereas all of the CML lines were RAF/RAS wild type. Among these tumors, other frequent oncogenic events including BCR-ABL translocation and FLT3 internal tandem duplications can lead to alternative routes to constitutive RAS activation and MAPK pathway dependency (26, 27).

Overall, we have conducted a comprehensive, in-depth predictive biomarker study for the MEK inhibitor GSK1120212 in solid tumor cell lines as well as cell lines from hematologic malignancies. This work has identified additional predictive biomarkers in cancer cell lines with a RAF/RAS mutant background, as well as biomarkers that would identify RAF/RAS WT tumors that might respond to GSK1120212. The ultimate validation of these data will be the analysis of these biomarkers in cancer patients who have received GSK1120212.

Disclosure of Potential Conflicts of Interest

Y. Degenhart received other commercial support from and has ownership interest in GlaxoSmithKline.

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Received July 8, 2011; revised October 12, 2011; accepted November 10, 2011; published OnlineFirst December 14, 2011.

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Molecular Cancer Therapeutics

Comprehensive Predictive Biomarker Analysis for MEK Inhibitor GSK1120212

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doi:10.1158/1535-7163.MCT-11-0505

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