Loss of NF1 in Cutaneous Melanoma Is Associated with RAS Activation and MEK Dependence

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Abstract

Melanoma is a disease characterized by lesions that activate ERK. Although 70% of cutaneous melanomas harbor activating mutations in the BRAF and NRAS genes, the alterations that drive tumor progression in the remaining 30% are largely undefined. Vemurafenib, a selective inhibitor of RAF kinases, has clinical utility restricted to BRAF-mutant tumors. MEK inhibitors, which have shown clinical activity in NRAS-mutant melanoma, may be effective in other ERK pathway-dependent settings. Here, we investigated a panel of melanoma cell lines wild type for BRAF and NRAS to determine the genetic alteration driving their transformation and their dependence on ERK signaling in order to elucidate a candidate set for MEK inhibitor treatment. A cohort of the BRAF/RAS wild type cell lines with high levels of RAS-GTP had loss of NF1, a RAS GTPase activating protein. In these cell lines, the MEK inhibitor PD0325901 inhibited ERK phosphorylation, but also relieved feedback inhibition of RAS, resulting in induction of pMEK and a rapid rebound in ERK signaling. In contrast, the MEK inhibitor trametinib impaired the adaptive response of cells to ERK inhibition, leading to sustained suppression of ERK signaling and significant antitumor effects. Notably, alterations in NF1 frequently co-occurred with RAS and BRAF alterations in melanoma. In the setting of BRAF(V600E), NF1 loss abrogated negative feedback on RAS activation, resulting in elevated activation of RAS-GTP and resistance to RAF, but not MEK, inhibitors. We conclude that loss of NF1 is common in cutaneous melanoma and is associated with RAS activation, MEK-dependence, and resistance to RAF inhibition. Cancer Res; 74(8); 2340-50. ©2014 AACR.

Introduction

The mitogen-activated protein kinase (MAPK) signaling pathway is a critical regulator of cell growth and cell-cycle progression. Receptor tyrosine kinases (RTK), activated by extracellular mitogens, stimulate the RAS (H-, N-, and K-RAS) small GTPase proteins. RAS proteins are activated when guanine exchange factors facilitate binding to GTP and inactivated by GTPase activating proteins (GAP), such as NF1, that facilitate the hydrolysis of GTP to GDP (1). Active RAS facilitates dimerization (2) and activation of RAF (A-, B-, and CRAF/RAF1) kinases, which in turn activate the mitogen-activated protein kinase kinase 1/2 (MEK1/2) and extracellular signal-regulated kinase 1/2 (ERK1/2) kinases. Activated, phosphorylated ERK regulates the transcription of proteins such as cyclin D1 that promote cell-cycle progression, transcription factors that promote the transformed phenotype and a network of genes that negatively inhibit pathway output by regulating the activity of RTKs, RAS, and RAF (3).

Alterations resulting in aberrant activation of ERK can be found at almost every level of the MAPK pathway and are common in human tumors. BRAF mutations, particularly at codon 600, are found in many cancers, including approximately 50% of cutaneous melanomas (4). Selective inhibitors of RAF (vemurafenib, dabrafenib) have unprecedented clinical activity in patients whose melanomas harbor BRAF(V600E) mutations, and their use results in a prolongation of progression-free and overall survival (5). NRAS mutations, most commonly at codon 61, have been identified in another 15% to 20% of melanomas and occur in a mutually exclusive pattern with BRAF(V600E) (4, 6, 7). Treatment options remain limited for these patients and those whose tumors are wild type for BRAF and NRAS, and the prognosis of such patients is particularly grim with a median overall survival of less than 1 year (8).

Given the high prevalence of BRAF and NRAS alterations in melanoma, we hypothesized that melanomas, including those wild type for both genes (BRAFWT/NRASWT), may exhibit a dependence on ERK pathway activation for maintenance of the...
transformed phenotype that may be exploited for therapeutic advantage (9, 10). Here, we performed a functional and genomic analysis of BRAFVT/NRASVT melanoma cell lines to determine whether occult MAPK pathway alterations are present in such cells. NF1 alterations that result in RAS activation and MEK dependence were identified in a subset of BRAFVT/NRASVT melanoma cell lines. However, NF1 alterations were not mutually exclusive with RAS and BRAF aberrations. Loss of NF1 in cells co-mutated for BRAF was sufficient to overcome the upstream negative feedback that results in suppression of RAS activation in BRAF(V600E) cells and was sufficient to confer resistance to vemurafenib. Furthermore, NF1 loss and corresponding relief of upstream ERK-dependent negative feedback attenuated the antiproliferative effects of the selective MEK inhibitor PD0325901 in NF1-null cells. In contrast, trametinib, an allosteric MEK inhibitor recently approved for use in patients with BRAF-mutant melanoma (11), attenuated the phosphorylation of MEK resulting from relief of upstream negative feedback and exhibited greater potency than PD0325901 in NF1-null melanoma cells. In summary, loss of NF1 expression in melanoma results in RAS activation and vemurafenib resistance even in the setting of BRAF mutation. Allosteric MEK inhibitors that impair the adaptive response of cells to ERK inhibition by blocking MEK phosphorylation should be studied in patients with melanoma whose tumors harbor NF1 loss.

Materials and Methods

Cell lines and culture conditions

"SK-Mel" cell lines were provided by Taha Merghoub and Alan Houghton (Memorial Sloan-Kettering Cancer Center, New York, NY), MeWo, Malme3M, A375, and SNF96.2 were purchased from the American Type Culture Collection. M308 was provided by Antoni Ribas (University of California Los Angeles, Los Angeles, CA) and WM3918 by Katherine Nathanson and Meenhard Herlyn (Wistar Institute, Philadelphia, PA). Other than A375 and SNF96.2 (grown in Dulbecco’s Modified Eagle Medium), all cell lines were grown in RPMI 1640 as previously described (12).

Genomic studies

Cellular DNA was extracted using the Qiagen DNeasy Tissue Kit. DNA was analyzed using a mass spectrometry-based fingerprinting assay to validate cell line identity as described previously (13). NRAS (G12A, G12D, Q61K, Q61R, Q61L), BRAF (V600E, V600K, V600R, K601E), and c-KIT (D816V) mutations were detected using a mass spectrometry-based assay (Sequenom) and validated by Sanger sequencing (13). Selected cell lines were screened for mutations and copy number alterations in 279 cancer-associated genes using the integrated mutation profiling of actionable cancer targets (IMPACT) assay as has been described (14) and viewed in the integrated genomics viewer (15). Genomic data from the TCGA melanoma project were derived from the cBioPortal for Cancer Genomics (http://cbioportal.org).

RNA-seq

RNA was extracted from cells using the RNeasy Mini Kit (Qiagen Inc.). Quality assessment, poly-A selection, and sequencing with an Illumina HiSeq 2000 were performed by the Genomics Core Laboratory at Memorial Sloan-Kettering Cancer Center. All samples had a minimum RNA integrity number (RIN) of 7.0 (16). Sequencing produced 40 to 120 million 75 bp reads per sample. FASTQ files were generated using CASAVA 1.8.2 software (Illumina). Low-quality bases and adapter sequences were removed with Cutadapt. Trimmed reads were aligned to human genome assembly GRCh37 using Tophat 2.0.8 (17, 18). Gene quantification and differential expression were calculated using Cufflinks 2.1.1 (19). Data visualizations were created with the gplots package for R.

Western blotting

Cells were collected, lysed, and blotted as previously described (12). Secondary antibodies were detected using Super Signal (Thermo) and chemiluminescence imaging using a Fuji LAS-4000 imager (GE Lifesciences). Anti-NF1 (SC-67), α-Tubulin (SC-17829), and actinin (SC-17829) were from Santa Cruz.
Biotechnology; anti-Ras (#1862335) from Thermo Scientific; and anti-pERK (#9102), pMEK (#9121), MEK (#9122), and p-CRAF S338 (#9427) from Cell Signaling Technology.

**Proliferation assays/FACS analysis**

Cell viability was measured by trypan blue incorporation using a Vi-CELL XR 2.03 (Beckman Coulter) as previously described (20). Percent growth was calculated using the equation 100 × [(Day 5 drug) − (Day 0)] / [(Day 5 DMSO) − (Day 0)]. FACS analysis was performed as previously described (21).

**RAS-GTP assay**

GTP-bound RAS was isolated via immunoprecipitation using recombinant RAS binding domain of RAF1 (RAF1-RBD; Active RAS Pull-down and Detection Kit; Thermo Scientific), according to the manufacturer’s instructions. The product was detected using total (pan-RAS) or isoform specific (H-, K-, N-) RAS antibodies.

**RNAi studies**

siRNA studies used ON-TARGET plus siNF1 SMARTpool and ON-TARGET plus nontargeting siRNA#2. shRNA studies were accomplished using GIPZ shNon-targeting RNA or TRIPZ inducible shRNA against NF1. shRNAs (shNF1 #2: CloneID V2THS-260806; shNF1 #4: CloneID V3THS-380114; shRNA#6: CloneID V3THS-380110) were induced with 2 μg/mL doxycycline daily for 1 week before vemurafenib studies.

**Results**

**NF1 expression is lost in a subset of RAS-activated BRAFWT/NRASWT cell lines**

To identify a cohort of BRAFWT/NRASWT melanoma cell lines for genomic and biologic characterization, 191 melanoma cell lines were genotyped for BRAF and NRAS mutations using a mass spectrometry–based (Sequenom) assay (13, 22). This screen identified 66 cell lines that lacked hotspot mutations in BRAF or NRAS (Fig. 1A and Supplementary Table S1). As this assay was designed to detect only the most common BRAF and NRAS mutations, we further performed Sanger sequencing of BRAF exons 11 and 15 and NRAS exons 2 and 3. This analysis identified BRAF mutations not present in the Sequenom assay in 2 cell lines (D594G in SK-Mel-264 and N581S in SK-Mel-215; Supplementary Table S2). Direct sequencing of KRAS and HRAS further identified activating mutations in KRAS in 2 and HRAS in 1 cell line, respectively (Supplementary Table S2). In summary, 61 cell lines were wild type for RAS and BRAF.

Given the high prevalence of ERK activation in melanoma (10), we hypothesized that a subset of the BRAFWT/RASWT cohort likely harbored occult alterations within the MAPK pathway that cause RAS to become refractory to negative feedback and thus confer activation of ERK. We thus measured levels of activated, GTP-bound RAS in a subset of the BRAFWT/RASWT cell lines as a surrogate of pathway activation. Similar to human tumors, KRAS- and NRAS-mutant melanoma cell lines exhibit high levels of RAS-GTP, whereas BRAF-mutant cell lines have low or undetectable levels of RAS-GTP (Fig. 1B; refs. 3, and 23). RAS was activated to varying levels in the BRAFWT/RASWT melanoma cells, with some expressing levels of activated RAS similar to those present in RAS-mutant cells (Supplementary Fig. S1).

The NF1 gene encodes a protein that functions as the predominant RAS GTPase activating protein (RAS GAP), which suppresses RAS activity and reduces RAS-GTP levels by promoting endogenous RAS GTPase activity. NF1 is inactivated in diverse human cancers (24–27) and would be predicted, if lost, to cause RAS to become refractory to negative feedback. We performed Western blot analysis to determine whether loss of NF1 protein expression occurred in, and was correlated with, elevated RAS-GTP levels in BRAFWT/RASWT melanoma cell lines. Complete loss of NF1 expression was noted in 5 of the BRAFWT/RASWT cell lines, all of which had high levels of RAS-GTP (Supplementary Fig. S1). Having previously performed high-resolution DNA copy number profiling (array CGH) on 92 melanoma cell lines (22), we identified a sixth NF1-null cell line that harbored homozygous NF1 gene deletion and concurrent NRAS(Q61R) mutation (SK-Mel-103).

NRAS mutations are significantly more prevalent than other RAS mutations in melanoma even though KRAS mutations are predominant in most other cancers (4). To determine which RAS isoforms were activated in NF1-null melanomas, we assayed activated KRAS, HRAS, and NRAS by performing immunoprecipitation with the RAS binding domain of RAF1 (RAF1-RBD; see Materials and Methods) followed by RAS isoform-specific immunoblots. All 4 NF1-null cell lines examined expressed high levels of total active RAS when compared with a BRAF(V600E) control cell line (Fig. 1B and Supplementary Fig. S1). NRAS(Q61K) SK-Mel-30 cells expressed high levels of GTP-bound NRAS, but no detectable levels of activated KRAS, similar to the NRAS(Q61R)/NF1-null SK-Mel-103 line. GTP-bound NRAS was also highly expressed in the other NF1-null cell lines, whereas only a subset had concurrent activation of KRAS, including SK-Mel-217, which harbored KRAS gene amplification. Elevated levels of GTP-bound KRAS and NRAS were also detected in the KRAS (G12C)-mutant SK-Mel-285 cell line. Levels of activated HRAS were low or undetectable in all the NF1-null melanoma cell lines (Supplementary Fig. S1).

To define the mechanistic basis for the loss of NF1 expression in the melanoma cell lines, we performed next-generation sequencing of 279 genes commonly mutated in human cancer using an exon capture-based approach (IMPACT assay; refs. 14 and 28). Two cell lines were found to harbor nonsense mutations in NF1 (Fig. 2A): MeWo, a hemizygous Q1336* mutation, and SK-Mel-286, L161* and Q282* mutations. The remaining 4 cell lines had deletions involving the NF1 gene locus: SK-Mel-
113, focal homozygous loss of the N-terminal domain; SK-Mel-103 and WM3918, focal homozygous loss of the C-terminal domain, and SK-Mel-217, broad monosomatic loss, as well as a focal, intragenic deletion in the second NF1 allele (Fig. 2B). In sum, genomic alterations sufficient to account for complete loss of NF1 protein expression were identified in all 6 NF1-null melanoma cell lines.

Although loss of NF1 was identified in the BRAFWT/RASWT cohort, it was not mutually exclusive with RAS alterations. Notably, concurrent alterations in the NF1 and RAS genes have also been noted in 2 recent whole-exome sequencing studies of melanoma tumors, including Hodis and colleagues and the melanoma study performed by the Cancer Genome Atlas (TCGA) working group (Fig. 2C; ref. 29). CDKN2A and/or TP53 were among the genes most commonly co-altered in the NF1-null melanoma cell lines and tumors, suggesting that these genes may cooperate with NF1 loss in promoting melanogenesis as has been reported in other cancer types, such as astrocytomas and malignant peripheral nerve sheath tumors (30). NF1-null cell lines are sensitive to MEK inhibitors that impair the adaptive response of cells to ERK inhibition

The growth of NF1-null cell lines derived from human malignant peripheral nerve sheath tumors (MPNST) and MPNSTs that arise in NF1−/− mice have been shown to be dependent on mTORC1 signaling and exquisitely sensitive to the mTORC1 inhibitor rapamycin (31, 32). To determine whether NF1-null melanomas were also mTORC1 dependent, we treated the NF1-null melanoma cell lines with rapamycin and compared their sensitivity with that of SNF96.2, a representative human NF1-null MPNST cell line (Fig. 3A). The NF1-null melanomas as a group were significantly less sensitive to rapamycin (IC50 ranging from 1 to 286 nmol/L) than SNF96.2 cells (IC50 = 0.05 nmol/L), suggesting that mTORC1 dependency is not a feature of all NF1-null cells. To probe the MEK dependence of NF1-null melanomas, we used PD0325901, a selective allosteric inhibitor of MEK1/2 (Kapp of 1 nmol/L for MEK1 and MEK2; ref. 33). The effect of PD0325901 on the proliferation and survival of 4 NF1-null melanoma cell lines was compared with that of a MEK inhibitor-sensitive BRAF(V600E) melanoma cell line (SK-Mel-239) and to a MEK inhibitor-resistant ERBB2-amplified breast cancer cell line (BT-474). The proliferation of all 4 NF1-null cell lines was inhibited by PD0325901, albeit with IC50 that were 10- to 20-fold greater than that of the BRAF(V600E) SK-Mel-239 cells (Fig. 3B).

To explore the basis for this differential sensitivity, we assessed the effects of drug exposure on downstream targets of MEK/ERK signaling as a function of concentration and time. Treatment of both BRAF(V600E) and NF1-null cells with 50 nmol/L PD0325901 resulted in decreased activation of phosphorylated ERK1/2 (pERK) by 1 hour (Fig. 3C and Supplementary Fig. S2). In BRAF(V600E) cells, suppression of pERK was durable and maintained at 6 and 24 hours and was accompanied by loss of cyclin D1 expression, accumulation of cells in G1 phase, and induction of apoptosis (Fig. 3C and D). In contrast, a partial rebound in pERK activation was apparent by 6 hours in NF1-null cells and was accompanied by a failure of the drug to potently suppress cyclin D1 expression. This rebound in pERK in the NF1-null cells was attenuated with use of a higher concentration of drug (500 nmol/L), leading to potent suppression of cyclin D1 expression, maximal accumulation of cells in G1 phase, and inhibition of proliferation (Fig. 3B–D). Together, these data suggest that cyclin D1 expression and cell-cycle progression are MEK-dependent in NF1-null melanoma cells, but that rapid rebound in ERK activity may account for the lower sensitivity of NF1-null cells to the MEK inhibitor PD0325901. Induction of cell death was not observed following treatment with the MEK inhibitor in any of the NF1-null cell lines (Fig. 3D). Furthermore, cotreatment with PD0325901 and the pan-AKT inhibitor MK2206 did not augment growth inhibition or induce apoptosis as has been shown in colorectal cells with RAS activation (Supplemental Fig. S5; ref. 34).

Resistance to allosteric MEK inhibitors can be induced by upstream pathway hyperactivation (35, 36). We have previously shown that treatment of BRAFWT but not BRAF (V600E) cells with PD0325901 leads to increased levels of phosphorylated MEK (pMEK), which results from relief of upstream ERK-dependent negative feedback (3). Consistent with these prior observations, treatment of NF1-null melanoma cells with PD0325901 resulted in increased pMEK (Fig. 3C).

As the induction of pMEK in the NF1-null melanomas paralleled the rebound in pERK activation, we further studied the effects of a second allosteric MEK inhibitor on MEK signaling and cellular proliferation. Trametinib (GSK1120212) has a similar in vitro affinity for MEK1/2 as PD0325901 (IC50 for MEK1 and MEK2 of 0.7 and 0.9 nmol/L, respectively), but in contrast to PD0325901, binding of trametinib to MEK blocks its phosphorylation at serine 217 (11). To compare the relative potencies of PD0325901 and trametinib in vivo, we first exposed BRAF(V600E) SK-Mel-239, and NF1-null SK-Mel-113 cells to increasing concentrations of both drugs and assessed the effect of drug treatment on pERK activation at 1 hour. In BRAF(V600E) SK-Mel-239 cells, both drugs were equipotent in their ability to suppress ERK activation at 1 hour (Fig. 4A). In contrast, in NF1-null SK-Mel-113 cells, trametinib was considerably more potent in its ability to suppress pERK activation than either PD0325901 or 2 additional allosteric MEK inhibitors currently in clinical testing (AZD6244 and MEK162; Fig. 4A and Supplementary Fig. S4; refs. 37–39). Treatment of NF1-null melanoma cells with either PD0325901 or trametinib resulted in hyperactivation of RAS consistent with relief of upstream negative feedback following inhibition of ERK (Fig. 4B). However, relief of upstream feedback following MEK inhibition was accompanied by a significant increase in pMEK levels in PD0325901-treated NF1-null cells, which was attenuated in cells treated with trametinib (Fig. 4B and Supplementary Fig. S4). This attenuation of MEK phosphorylation was unique to trametinib and was not observed with PD0325901, AZD6244, or MEK162 (Supplementary Fig. S4). Furthermore, the resistance of MEK to upstream hyperactivation by RAS in trametinib-treated cells was accompanied by a more durable downregulation of pERK and more potent inhibition of genes whose transcription is dependent upon...
ERK, including CCND1 (cyclin D1), ETV1, MYC, and SPRY4, as compared with PD0325901 (Fig. 4B and D). Consistent with these biologic differences among the MEK inhibitors, the antiproliferative effects of trametinib were similar in BRAF (V600E) and NF1-null cells, whereas BRAF (V600E) cells exhibited greater sensitivity than NF1-null cells to PD0325901 (Fig. 4C and Supplementary Fig. S4).

NF1 loss and resulting RAS activation in BRAF(V600E) melanoma cells confers resistance to RAF inhibition

Levels of GTP-bound RAS are low in BRAF(V600E) melanomas as a result of high levels of ERK-dependent negative feedback (23). It was unclear whether loss of NF1 function in this context would be sufficient to overcome the feedback-mediated suppression of RAS activity in BRAF(V600E) cells. We therefore screened a panel of 10 BRAF(V600E) melanoma cell lines for loss of NF1 expression and activation of RAS-GTP. Nine of the 10 BRAF(V600E)–mutant melanoma cell lines expressed low to undetectable levels of RAS-GTP (Fig. 5A). A single BRAF(V600E) cell line (M308) had high levels of RAS-GTP similar to that of an NRAS(Q61K) cell line, and notably, M308 was devoid of NF1 expression by immunoblot (Fig. 5A). Genomic analysis by IMPACT confirmed the presence of a nonsense mutation in the NF1 gene (Q1070/C3) as the basis for the loss of NF1 protein expression in M308 cells (Supplementary Fig. S5). To determine whether NF1 loss desensitizes BRAF(V600E) cells to RAF inhibition, we assessed the sensitivity of M308 [BRAF(V600E)/NF1-null] cells to vemurafenib. Vemurafenib treatment of SK-Mel-239 and SK-Mel-113 cells expressing NF1 had a greater effect on cell growth than vemurafenib treatment of M308 cells (Supplementary Fig. S6A).

**Figure 3.** NF1-null melanoma cell lines are MAPK pathway dependent. A, cells were treated with increasing concentrations of rapamycin for 5 days. Results are percent cell growth as a function of drug concentration (nmol/L). B, cells were treated with increasing concentrations of the MEK inhibitor PD0325901 for 5 days. Results as in A. C, cells were treated with 50 or 500 nmol/L PD0325901 for 0, 1, 6, and 24 hours. Phospho- and total levels of MAPK pathway components were determined by immunoblot. D, cells were treated for 24 hours with 50 or 500 nmol/L PD0325901 before undergoing FACS analysis for cell-cycle distribution. Error bars, SEM; n = 3.
239 [BRAF(V600E)/NF1WT] cells resulted in potent downregulation of phosphorylated MEK and ERK and inhibition of cell growth (Fig. 5B). In contrast, vemurafenib had little effect on levels of phosphorylated MEK and ERK in BRAF (V600E)/NF1-null M308 cells and no effect on cell proliferation (Fig. 5B and C).

RAS activation is sufficient to induce vemurafenib resistance in BRAF(V600E) cells (Supplementary Fig. S6). To determine whether NF1 loss activates RAS sufficiently to overcome ERK-dependent negative feedback and induce vemurafenib resistance, we knocked down NF1 expression in BRAF(V600E) mutant A375 cells and assessed levels of RAS activation in the presence and absence of vemurafenib. siRNA and shRNA mediated knockdown of NF1 resulted in induction of RAS-GTP and decreased sensitivity to vemurafenib (Supplementary Fig. S6). These data suggest that loss of NF1 function in BRAF (V600E) mutant cells is sufficient to induce RAS-GTP activation and, as a consequence, vemurafenib resistance (Fig. 5A–C and Supplementary Fig. S6).

To assess the MEK dependence of the M308 melanoma cells, we determined the effects of PD0325901 and trametinib treatment on ERK activation and cellular proliferation. Analogous to the results seen with these inhibitors in BRAF(V600E)/NF1-null melanoma cells, exposure of M308 cells to 50 nmol/L PD0325901 was insufficient to durably suppress ERK signaling and cell proliferation (Fig. 5D and E). In contrast, treatment of M308 cells with trametinib resulted in durable suppression of pERK activation, potent downregulation of cyclin D1

Figure 4. Trametinib durably inhibits ERK activation and proliferation in NF1-null melanoma cell lines. A, cells were treated with increasing concentrations of PD0325901 or trametinib for 1 hour. pERK was measured by immunoblot. B, cells were treated with 50 nmol/L PD0325901 or 50 nmol/L trametinib for 0, 1, 6, and 24 hours. RAS-GTP was quantitated as described in Materials and Methods. Phospho- and total levels of MAPK pathway components were determined by immunoblot. C, cells were treated with increasing doses of PD0325901 or trametinib for 5 days. Results are percent cell growth as a function of drug concentration (nmol/L). D, NF1-null SK-Mel-113 cells were treated with dimethyl sulfoxide (DMSO) or 50 nmol/L PD0325901 or trametinib for 1, 6, or 24 hours. RNA levels were quantitated by RNA-seq. Shown are relative mRNA expression levels as a function of duration of drug exposure for selected ERK output genes.
expression, and potent inhibition of cellular proliferation (Fig. 5D and E).

Discussion

Neurofibromatosis Type I is a hereditary disorder caused by germline mutation of the NF1 gene (350 kb genomic DNA; 60 exons; 2,818 amino acids). This syndrome is characterized by the formation of benign neurofibromas as well as pigmented cafe-au-lait spots and Lisch nodules. Individuals with neurofibromatosis are at risk of developing malignant neoplasms at a young age, most commonly optic gliomas, malignant peripheral nerve sheath tumors, and juvenile myelomonocytic leukemia (40). Only recently have somatic alterations in the NF1 gene been implicated in malignancies, including gliomas, breast cancers, and leukemias (24–27). The prior underestimation of the prevalence of NF1 alterations in human tumors is likely attributable to the technical challenges previously inherent in sequencing large genes with tumor suppressive function in which mutations throughout the coding region are potentially oncogenic. With the advent of massively parallel next generation sequencing methods, many of these technical challenges have now been overcome.

Here, we report that a significant subset of melanoma cell lines, including those wild type for BRAF and RAS, exhibit total loss of NF1 protein expression. In all cases, a mutation and/or focal deletion of the NF1 gene, rather than posttranscriptional regulation (41) could be identified as the basis for NF1 loss. In contrast to prior reports (42, 43), all the NF1-null
splice site mutation in NF1 melanomagenesis and suggest that this cooperativity results, which NF1 is inactivated in mutation. This result indicates that the lineage context within null melanomas were dependent on ERK pathway activation observed that in contrast to NF1-null MPNSTs (31, 32), NF1-maintenance of transformation (Supplementary Fig. S8). We to target the pathways downstream of RAS responsible for constitutive RAS activation, including those with loss of NF1, is likely required to maximally elevate RAS-GTP expression, as a heterozygous splice site mutation in NF1 in A375 cells (45) was not accompanied by NF1 loss or increased RAS-GTP levels (Supplementary Fig. S7). These results suggest that loss of NF1 in BRAF(V600E) melanoma cells may provide a selective advantage, even in the absence of RAF inhibitor exposure, by diminishing the oncogene-induced suppression of RAS mediated by ERK-dependent negative feedback. A secondary consequence of this co-mutation pattern is that such tumors exhibit intrinsic resistance to selective RAF inhibitors. Our studies suggest that partial loss of NF1 function may result in a more pronounced and rapid restoration of RAS signaling following RAF inhibitor therapy. This could result in an attenuation of drug response sufficient to promote the emergence of drug-resistant clones.

Efforts to develop clinically useful direct inhibitors of RAS have been unsuccessful to date (46). One alternative pharmacologic strategy for the treatment of tumors with constitutive RAS activation, including those with loss of NF1, is to target the pathways downstream of RAS responsible for maintenance of transformation (Supplementary Fig. S8). We observed that in contrast to NF1-null MPNSTs (31, 32), NF1-null melanomas were dependent on ERK pathway activation and not TORC1 for cell-cycle progression and cell proliferation. This result indicates that the lineage context within which NF1 is inactivated influences the downstream effector pathways that facilitate RAS-mediated transformation and thus likely dictates the potential utility of targeted pathway inhibitors.

Although NF1-null melanomas were dependent upon MEK-ERK activation for cell proliferation, we observed stark differences in the relative potency of allostERIC, non-ATP-competitive MEK inhibitors in the NF1-null cohort (11). Specifically, trametinib, which attenuates phosphorylation of MEK by RAF at Serine 217, had greater antitumor effects than PD0325901. Monophosphorylated MEK has only partial activity (11) and the ability of trametinib but not PD0325901 to abrogate the hyperphosphorylation of MEK resulting from relief of upstream negative feedback was associated with more durable inhibition of pERK and cyclin D1 expression and greater antiproliferative effects. A similar lack of potency was also noted in NF1-null melanoma cells with AZD6244 (Supplementary Fig. S4), a second non-ATP-competitive MEK inhibitor incapable of abrogating RAF phosphorylation of MEK. The inability of AZD6244 to block MEK phosphorylation likely accounts for the partial resistance to MEK inhibition observed following NF1 knockdown in a prior study (47). Our data are also consistent with a recent study suggesting that differences in the cellular potency of MEK inhibitors in KRAS-mutant cells can result from differences in the strength of hydrogen bonding with S212 in MEK, which is critical for blocking feedback induced MEK phosphorylation by wild-type RAF (48). In sum, the data imply that MEK inhibitors that block the phosphorylation of MEK by RAF may have greater clinical activity in tumors with activated RAS, including those with loss of NF1 function. Such inhibitors may, however, have a narrow therapeutic index in patients, as they would be predicted to potently inhibit RAS-dependent ERK signaling in normal tissues.

In summary, NF1 loss is common in cutaneous melanomas. Loss of NF1 is associated with RAS activation, MEK dependence and, in the setting of concurrent BRAF mutation, vemurafenib resistance. Upstream hyperactivation of RAS and RAF resulting from loss of negative feedback following ERK pathway inhibition can result in an attenuation of the antitumor activity of allostERIC MEK inhibitors. Inhibitors that prevent RAF-mediated phosphorylation of MEK abrogate this adaptive resistance to MEK inhibition and have greater antitumor activity in NF1-null cells. With the recent approval of trametinib by the U.S. Food and Drug Administration for the treatment of BRAF-mutant melanomas, these findings have potential therapeutic implications for patients with melanoma and others tumor types with NF1 alterations.

Disclosure of Potential Conflicts of Interest
P.B. Chapman is a consultant/advisory board member of Glaxo-Smith-Kline and Roche-Genentech. R. Yaeger is a consultant/advisory board member of GlaxoSmithKline Advisory Board—Combination therapies for BRAF mutant CRC. N. Rosen is a consultant/advisory board member of Astrazeneca, Chugai, and Novartis. D.B Solit is a consultant/advisory board member of Pfizer.

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Grant Support

This work was supported by the NIH; the Melanoma Research Alliance; Mr. William H. Goodwin and Mrs. Alice Goodwin and the Commonwealth Foundation for Cancer Research, and the Experimental Therapeutics Center of Memorial Sloan-Kettering Cancer Center; and the StARR Foundation; and a Stand Up To Cancer - Melanoma Research Alliance Melanoma Dream Team Translation Research Grant (SU2C-AACR-DT0612). Stand Up To Cancer is a program of the Entertainment Industry Foundation administered by the American Association for Cancer Research.

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Received September 11, 2013; revised January 30, 2014; accepted January 30, 2014; published OnlineFirst February 27, 2014.
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Cancer Res 2014;74:2340-2350. Published OnlineFirst February 27, 2014.

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doi:10.1158/0008-5472.CAN-13-2625

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