A Novel AKT1 Mutant Amplifies an Adaptive Melanoma Response to BRAF Inhibition

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ABSTRACT

BRAF inhibitor (BRAFi) therapy leads to remarkable anti melanoma responses, but the initial tumor shrinkage is commonly incomplete, providing a nidus for subsequent disease progression. Adaptive signaling may underlie early BRAFi resistance and influence the selection pattern for genetic variants, causing late, acquired resistance. We show here that BRAFi (or BRAFi + MEKi) therapy in patients frequently led to rebound phosphorylated AKT (p-AKT) levels in their melanomas early on-treatment. In cell lines, BRAFi treatment led to rebound levels of receptor tyrosine kinases (RTK; including PDGFRβ), phosphatidylinositol (3,4,5)-triphosphate (PIP3), pleckstrin homology domain recruitment, and p-AKT. PTEN expression limited this BRAFi-elicited PI3K–AKT signaling, which could be rescued by the introduction of a mutant AKT1 (Q79K) known to confer acquired BRAFi resistance. Functionally, AKT1 Q79K conferred BRAFi resistance via amplification of BRAFi-elicited PI3K–AKT signaling. In addition, mitogen-activated protein kinase pathway inhibition enhanced clonogenic growth dependency on PI3K or AKT. Thus, adaptive or genetic upregulation of AKT critically participates in melanoma survival during BRAFi therapy.

SIGNIFICANCE: This study provides a mechanistic link between early, adaptive and late, acquired BRAF inhibitor resistance in melanoma, with early BRAFi-induced signaling alterations shaping the subsequent evolutionary selective pressure. These findings argue for upfront, combined targeting of the mutant BRAF genotype and a pervasive drug-adaptive, AKT-dependent tumor response. Cancer Discov; 4(1); 69–79. © 2013 AACR.

See related commentary by Solit and Rosen, p. 27.
disease progression caused by acquired drug resistance (4). It is unclear what adaptive signal(s) underlies initial incomplete tumor responses and whether a deficiency in such adaptive signaling might favor genetic selection for its upregulation. We have recently shown that a majority of melanomas with late or acquired resistance to a BRAFi display molecular or genetic alterations that lead to MAPK pathway reactivation (5–9). However, a significant minority of disease-progressing melanomas harbor genetic lesions that upregulate the phosphoinositide 3-kinase (PI3K)–PTEN–AKT pathway (9). These genetic alterations include nonsynonymous, gain-of-function mutations in positive regulators (PIK3CA, AKT1, and AKT3) and loss-of-function mutations (PIK3R2, PTEN, and PHLPPI) and gene deletion (PTEN) in negative regulators. While some somatic variants (e.g., PIK3CA<sup>E545G</sup>, AKT1/Q617K) harbor known mechanisms of action, the structure-functional consequences of others (e.g., PIK3R2<sup>N561D</sup>, AKT1<sup>Q79K</sup>, PTEN<sup>64134G</sup>) are novel.

Given that the landscape of mechanisms of acquired BRAFi resistance reflect the essential survival functions of MAPK and PI3K–PTEN–AKT signaling pathways in BRAF-mutant melanoma, we explored the roles of these pathways in acute or adaptive resistance. Recent works in cancer cell lines (10, 11) have demonstrated how targeted inhibition of the MAPK pathway can lead to adaptive alterations in signal transduction crosstalk/feedback and transcriptional output. Here, we show that in clinical melanoma biopsy specimens, MAPK pathway inhibition elicited a pervasive rebound in AKT activation. In cell line work, this rebound in AKT activation could be traced to enhanced phosphatidylinositol (3,4,5)-triphosphate (PIP<sub>3</sub>) generation and was antagonized by wild-type (WT) PTEN. Moreover, the pleckstrin homology domain (PHD) class of AKT mutants, including the novel AKT1<sup>Q79K</sup> mutant, displayed enhanced affinity for PIP<sub>3</sub>, dramatically amplified the BRAFi-induced upregulation of PI3K–AKT signaling in the presence of PTEN, and as such conferred BRAFi resistance in a cell context–dependent manner. These data thus reveal key insights into the dynamic evolutionary continuum of BRAFi resistance. Early adaptive events in response to MAPK inhibitors, which limit the initial efficacy, may shape subsequent mechanisms of acquired resistance, which further augment adaptive responses and lead to tumor regrowth.

RESULTS

Although AKT has been implicated in BRAFi resistance, the timing of its upregulation during BRAFi therapy is not clear. To determine whether MAPK pathway targeting results in a rebound increase in phosphorylated AKT (p-AKT) in the tumors of patients treated with a BRAFi (or BRAFi + MEKi), we assessed the p-AKT levels in melanoma tumors biopsied early on-treatment (days 4 to 25) relative to their patient-matched baseline (pretreatment) tumors by immunohistochemistry (IHC; Fig. 1A) using a validated antibody (Supplementary Fig. S1) and quantifying signals via image analysis (Supplementary Fig. S2). These early on-treatment biopsies took place during a period of time to objective tumor responses, before or at maximal tumor responses. Such patient-matched (and in most cases also tumor site–matched) melanoma samples (n = 9 patients; clinical data in Supplementary Table S1) are critical for this analysis because baseline p-AKT levels, assessed in parallel technically, varied over a considerable range among tumors from distinct patients. Importantly, in the majority of tumors biopsied early on-treatment (7 of 9), p-AKT increased upon treatment. We also examined the PDGFRβ expression by IHC, as this receptor tyrosine kinase (RTK) has previously been correlated with BRAFi resistance (5, 12). Induction of PDGFRβ expression upon treatment was observed in 5 of 7 tumors (Supplementary Fig. S3) that displayed a relative increase in p-AKT levels, but was not observed in the two tumors that did not display a relative p-AKT increase, consistent with our observations in cell lines (see below). Interestingly, as Patient #1 developed disease progression (via mutant NRAS) on BRAFi, he was treated with BRAFi + MEKi (BRIM7 clinical trial). This combinatorial treatment (day 15) was also associated with PDGFRβ induction (Supplementary Fig. S3). In preliminary work with five sets of transcriptomes for patient-matched pre- and early on-treatment (days 6–22; BRAFi or BRAFi + MEKi) melanomas, we observed PDGFR<sub>B</sub> mRNA induction by MAPK pathway inhibition in 5 of 5 patients (fold increase from 1.4 to 2.9, FDR adjusted P ≤ 0.05; unpublished data). Thus, inhibition of the MAPK pathway in BRAF<sup>V600E</sup>-mutant melanoma was associated with a tumor-associated rebound PDGFRβ and p-AKT induction in the majority of patients.

As in BRAF-mutant melanoma tumors, BRAF-mutant human melanoma cell lines displayed a wide range of basal p-AKT levels at exponential growth densities (Supplementary Fig. S4). We have previously shown that certain BRAF-mutant human melanoma sublines chronically treated with a BRAFi (or some cases of short-term cultures derived from BRAFi-resistant melanoma tissues in patients) upregulated the expression and tyrosine phosphorylation levels of two key RTKs, namely PDGFRβ and EGFR receptor (EGFR), as well as the levels of p-AKT. More recent work on triple-negative breast cancer cell lines uncovered a negative feedback of the MAPK pathway (via MYC-mediated transcriptional repression) on RTK expression (10). To assess the timing of p-AKT induction in response to BRAFi (or MAPK pathway) inhibition, we treated BRAF-mutant melanoma cell lines with a BRAFi ( vemurafenib), a MEKi (AZD6244), or an ERKi (FR180204). Inhibitor treatment for 48 hours consistently led to an induction of p-AKT (Thr308) levels, suggesting crosstalk at a level below ERK signaling (Fig. 1B). MAPK pathway inhibition (by BRAFi, MEKi, or ERKi) for 48 hours led to concomitant c-MYC downregulation, RTK/PDGFRβ (but not EGFR, see below) overexpression, and p-AKT and p-CRAF upregulation, correlating with an induction of PDGFR<sub>B</sub> but not EGFR mRNA levels (data not shown).

While EGFR tyrosine phosphorylation can transiently increase within hours of BRAFi treatment (13), its protein expression level was not induced until after prolonged (weeks) BRAFi treatment coinciding with drug-tolerant persisting (but slowly cycling; unpublished data) cell subpopulations entering a proliferative phase (Supplementary Fig. SSA and SSB). Interestingly, although BRAFi induced p-AKT levels in M229 cells at 48 and 72 hours, cotreatment with a PDGFRβ inhibitor, sunitinib, or an EGFR inhibitor, gefitinib, reduced (but did not completely abolish) this BRAFi-induced p-AKT level, with the strongest effect observed with the cotreatment...
Figure 1. MAPK pathway inhibition leads to rebound upregulation of AKT signaling in melanoma tumors and cell lines. A, BRAFi (vemurafenib or dabrafenib) or BRAFi + MEKi treatment led to increased p-AKT Ser473 levels in early on-treatment tumor biopsies (days #4 to 25) relative to the patient-matched, baseline (pretreatment) biopsies. p-AKT IHC of melanin-bleached tumor sections (×400; quantification shown as heat intensity). Rx, symbol for treatment. B, BRAF-mutant melanoma cell lines were treated with the indicated MAPK inhibitor (1 μmol/L) or dimethyl sulfoxide (DMSO) for 48 hours. Phospho- and total protein levels were then probed by Western blotting. Tubulin, loading control. C, lipids were extracted from the indicated cell lines (n = 3 per group) treated with vemurafenib (1 μmol/L) for increasing durations (h), and the PIP3 levels were detected by ELISA (average of biologic triplicates; error bar, SD). D, localization of WT PHD–GFP cells treated with vemurafenib (1 μmol/L) for increasing durations (h; scale bar, 20 μm). Note the cellular morphologic response to vemurafenib treatment in the surviving subpopulations. Photomicrographs representative of two independent experiments. Vemu, vemurafenib.
of BRAFi with both sunitinib and gefitinib (Supplementary Fig. S5C). This suggests that these RTKs either contribute independently to p-AKT induction or can compensate for each other’s kinase inhibition. After chronic vemurafenib treatment, drug-resistant, BRAF-mutant melanoma sublines (M229 R5, M238 R1), which overexpress both wild-type PDGFRβ and EGFR, could be re-sensitized to vemurafenib by cotreatment with sunitinib and gefitinib, suggesting a BRAFi-induced dependency on RTK activities (Supplementary Fig. S5D). Accordingly, BRAFi treatment induced apoptosis in M229 and M238 cell lines (Supplementary Fig. S6A) and the cell-surface expression of PDGFRβ (Supplementary Fig. S6B). In fact, cell-surface PDGFRβ expression was higher in the live subpopulations compared with the dead subpopulations (Supplementary Fig. S6C), and the live subpopulations over time were also more strongly enriched with PDGFRβ-positive cells (Supplementary Fig. S6D). These data suggest that BRAF inhibition specifically (and MAPK pathway inhibition in general) upregulates RTK expression, which contributes to adaptive AKT signaling. We then traced the BRAFi-induced p-AKT levels to an induction of lipid/membrane-associated PIP3 levels (Fig. 1C). This increase in PIP3 levels correlated with an increase in cell-surface recruitment of the PHD (Fig. 1D), as visualized by PHD-GFP fusion protein expressed at similar levels (Supplementary Fig. S7). Thus, BRAFi treatment led to rebound RTK upregulation, PIP3 membrane accumulation, PHD membrane recruitment, and AKT activation.

These studies in melanoma tissues and cell lines (Fig. 1) support the notion that BRAF inhibition leads to early, adaptive AKT signaling. In a subset of melanoma tissues with late, acquired BRAFi resistance, we recently uncovered mutations, including gain-of-function AKT1 and AKT3 mutations, which upregulate the PI3K-AKT pathway and confer BRAFi resistance (9), identifying the PI3K-AKT pathway as another core drug escape pathway in addition to MAPK reactivation. In this setting of late, acquired BRAFi resistance, the detection of the presence of a gain-of-function AKT mutant, for instance, would lift this restriction via signal amplification. The mechanism of AKT1Q79K is based on its activation-associated phosphorylation (Fig. 2B). We then tested the structure prediction (9) that the mechanism of AKT1Q79K gain-of-function is based on its mutant PHD displaying enhanced PIP3 binding and membrane recruitment, as has been shown for the mutant PHD of AKT1E17K first described in breast cancer (14). In agreement with our structure-based prediction, an AKT1 PHD containing the Q79K mutation and fused to GFP localized to the cell surface independently of serum stimulation, in contrast to WT PHD-GFP and similar to a PHD-GFP fusion protein containing a known AKT1-activating mutation, E17K (Fig. 2C; ref. 14). Moreover, the increased recruitment of Q79K PHD-GFP to the cell surface was also less sensitive to PI3K inhibition by LY294002 when compared with the WT PHD-GFP in the presence of serum stimulation, suggesting that AKT1Q79K may be hyper-responsive to cell surface membrane recruitment by low levels of PIP3.

To assess the baseline (no BRAFi treatment) activation status of AKT1Q79K in the context of BRAF-mutant human melanoma cell lines with varying PTEN expression (Supplementary Fig. S4), we derived stable cell lines expressing either the vector or AKT1Q79K in a doxycycline-repressible manner (Fig. 2C). Upon induction of expression for 2 days, similar FLAG-tagged AKT1Q79K expression levels were achieved in all cell lines (Fig. 2C), resulting in an expression level of the FLAG-tagged AKT1 (top band) comparable with that of the endogenous AKT (bottom band). Notably, in the absence of BRAF inhibition, activation-associated phosphorylation of FLAG-AKT1Q79K (top band) was greater than that of the endogenous WT AKT1 (bottom band) in each cell line. This was most evident in the PTEN WT-expressing line M229, where the endogenous p-AKT level was very low, despite the total AKT levels being similar across all cell lines. The p-AKT1Q79K level was lowest in the cell line (M229) with the lowest basal endogenous p-AKT level, indicating that, although the AKT1Q79K mutant is more readily phosphorylated and activated compared with the WT, its maximal phosphorylation still requires upstream signal activation (i.e., PIP3 generation). Introduction of WT PTEN into the PTEN nonexpressing cell lines WM2664 and M249 (Supplementary Fig. S4) suppressed the endogenous p-AKT level (Fig. 2D; data not shown). Upon restoration of PTEN expression and under a lowered PIP3 environment, the AKT1 PHD mutants (E17K, Q79K) were much more activated than AKT1 WT, i.e., AKT1 PHD mutants were much more sensitive to limiting PIP3 levels (Fig. 2E).

We then hypothesized that BRAFi treatment, by increasing PIP3 levels, would provide the necessary upstream signal to maximally activate AKT1Q79K, enabling the mutant to rescue the negative effect of PTEN and to amplify the BRAFi-induced rebound p-AKT (Thr308) level. Consistent with prior experiments (Fig. 1B), treatment of M229 (low basal p-AKT), M238 (intermediate basal p-AKT), and WM2664 (high basal p-AKT) cells with the BRAFi vemurafenib induced endogenous p-AKT Thr308 in a time-dependent manner (followed up to 48 hours; Fig. 2F). The strength of this BRAFi-induced p-AKT rebound level was weakest in BRAF-mutant melanoma cell lines displaying the lowest basal level of p-AKT and WT PTEN expression, such as M229 cells. In contrast, BRAFi induced strong specific expression of the BRAFi target genes (Fig. S5).

We first confirmed that both AKT1 mutants are associated with upregulated levels of activation-associated phosphorylation (Fig. 2B). We then tested the structure prediction (9) that the mechanism of AKT1Q79K gain-of-function is based on its mutant PHD displaying enhanced PIP3 binding and membrane recruitment, as has been shown for the mutant PHD of AKT1E17K first described in breast cancer (14). In agreement with our structure-based prediction, an AKT1 PHD containing the Q79K mutation and fused to GFP localized to the cell surface independently of serum stimulation, in contrast to WT PHD-GFP and similar to a PHD-GFP fusion protein containing a known AKT1-activating mutation, E17K (Fig. 2C; ref. 14). Moreover, the increased recruitment of Q79K PHD-GFP to the cell surface was also less sensitive to PI3K inhibition by LY294002 when compared with the WT PHD-GFP in the presence of serum stimulation, suggesting that AKT1Q79K may be hyper-responsive to cell surface membrane recruitment by low levels of PIP3. We then hypothesized that BRAFi treatment, by increasing PIP3 levels, would provide the necessary upstream signal to maximally activate AKT1Q79K, enabling the mutant to rescue the negative effect of PTEN and to amplify the BRAFi-induced rebound p-AKT (Thr308) level. Consistent with prior experiments (Fig. 1B), treatment of M229 (low basal p-AKT), M238 (intermediate basal p-AKT), and WM2664 (high basal p-AKT) cells with the BRAFi vemurafenib induced endogenous p-AKT Thr308 in a time-dependent manner (followed up to 48 hours; Fig. 2F). The strength of this BRAFi-induced p-AKT rebound level was weakest in BRAF-mutant melanoma cell lines displaying the lowest basal level of p-AKT and WT PTEN expression, such as M229 cells. In contrast, BRAFi induced strong specific expression of the BRAFi target genes (Fig. S5).
MAPK Inhibition Elicits a Widespread, AKT-Dependent Adaptive Response in Melanoma

**RESEARCH BRIEF**

**Figure 2.** AKT1E17K and AKT1Q79K displayed upregulation of activation-associated phosphorylation. Indicated constructs were transfected into human HEK293T cells, and levels of phospho- and total proteins were probed by Western blotting. Tubulin, loading control. **C,** AKT1 PHD containing the E17K or Q79K mutations localized to the cell surface independently of serum stimulation (10% FBS, 1 hour), and serum-induced cell-surface localization of mutant PHD (vs. WT PHD) was less sensitive to a PI3K inhibitor (20 μmol/L LY294002, 1 hour). PHD of AKT1 was fused to GFP, expressed stably in M229 cells and visualized (scale bar, 20 μm). **D,** melanoma cell line stably expressing vector or doxycycline-repressible FLAG-tagged AKT1Q79K (doxycycline withdrawal, 48 hours) were probed for endogenous and exogenous p-AKT and indicated total protein levels. **E,** stable expression of PTEN WT and FLAG-AKT1 WT and mutants (vs. vector) in M249 revealed stronger PIP3 signal-amplifying effects of AKT1 PHD mutants with PTEN WT reexpression. **F,** indicated melanoma cell lines were treated with vemurafenib (1 μmol/L) for increasing durations (h) without change of media. Protein lysates were probed for levels of endogenous p-AKT (vector) versus exogenous p-AKT (AKT1Q79K) and indicated phospho- and total protein levels.
phosphorylation of exogenous AKT1Q79K in M229 cells, to an extent similar to the endogenous p-AKT levels induced by BRAFi treatment in WM2664 cells. Thus, consistent with our hypothesis, AKT1Q79K amplified a weak BRAFi-induced signal upstream of AKT. Taken together, BRAFi treatment leads to rebound RTK upregulation, PI3K, membrane accumulation, PHD membrane recruitment, and AKT activation. In addition, the AKT1E17K mutant, which can confer acquired BRAFi resistance (9), produces a signaling phenotype dependent on the cell context, which is related to the basal p-AKT level or PTEN status, and BRAFi inhibitor treatment.

It is likely then that the AKT1Q79K mutant would confer a BRAFi resistance phenotype in a cell context-dependent manner such that the greatest impact would be observed where the mutant AKT1 most robustly amplifies an adaptive response. To test this prediction, we treated multiple cell lines of varying PTEN genetic and protein expression status (Supplementary Fig. S4) with either dimethyl sulfoxide (DMSO) or increasing vemurafenib concentrations for 3 days (Fig. 3A, left) or 10 days (Fig. 3A, right). From both short- and long-term drug treatment regimens, AKT1Q79K expression conferred vemurafenib resistance robustly in M229 cells but weakly in M238 and WM2664 cells (as well as M263 and M249 cells; Supplementary Fig. S8). In M229 cells, where AKT1Q79K and AKT1E17K expression conferred a two-log increase in BRAFi resistance, the expression of AKT1 WT led to no significant change in BRAFi sensitivity. PTEN knockdown in M229 cells increased the basal p-AKT (Thr308) level and further boosted the BRAFi-elicted p-AKT level rebound (Fig. 3B). PTEN knockdown in M229 cells conferred resistance to vemurafenib but rendered the AKT1 PHD mutants incapable of conferring further vemurafenib resistance (Fig. 3C). These observations are consistent with the notion that WT PTEN activity limits the BRAFi-elicted adaptive response and that PHD, gain-of-function AKT1/3 mutants counteract this negative effect of WT PTEN to provide survival benefits under BRAFi- or MAPK-inhibited conditions.

Given that AKT1Q79K expression in M229 cells amplified BRAFi-induced p-AKT (Thr308) and conferred vemurafenib resistance, we tested whether AKT1Q79K expression would render cell survival more dependent on AKT signaling in the presence of a BRAFi. First, we showed that vemurafenib-induced p-AKT (and the downstream substrate p-GSK3β) could be downregulated by cotreatment with the AKTi MK2206 in a dose-dependent manner (using 1 hour treatment to gauge on-target inhibition; Fig. 3D). M229 cells expressing AKT1Q79K exhibited reduced sensitivity to vemurafenib alone (as compared with M229 vector) but only slightly increased sensitivity to MK2206 alone (Supplementary Fig. S9). Importantly, the combination of BRAFi + AKTi was more effective than either agent alone in reducing the clonogenic growth of M229 cells expressing AKT1Q79K (Fig. 3E), consistent with BRAF inhibition leading to an increase in MAPK-redundant, AKT-dependent survival. In additional PTEN-treating, BRAFi-mutant melanoma cell lines (e.g., M238, M395; Fig. 4 and Supplementary Fig. S4 and S10) that are relatively insensitive to an AKTi alone (compared with a BRAFi or MEKi alone), the combination of BRAFi + AKTi (or MEKi + AKTi) was also more effective than either agent alone in reducing the clonogenic growth. Previous studies have suggested that the lack of PTEN expression correlated with cancer cell line sensitivity to AKT inhibition (15). Consistently, PTEN nonexpressing, BRAF-mutant melanoma cell lines (e.g., WM2664, M249, M397) were exquisitely sensitive to AKT inhibition alone (vs. BRAFi or MEKi inhibition alone; Fig. 4 and Supplementary Fig. S4 and S10). Thus, the intrinsic sensitivity of a subset of melanoma cell lines (those with no PTEN activity) to AKT inhibition and the BRAFi-induced sensitivity of another subset of melanoma cell lines (those with PTEN activity) to AKT inhibition rationalize the combination of PI3K–AKT and MAPK pathway inhibition to maximally suppress melanoma survival signaling.

We further tested the efficacy of combinatorial PI3K–AKT and MAPK pathway targeting using small-molecule inhibitors (either in clinical use or in development) to suppress adaptive BRAFi resistance relative to the efficacies of single target/pathway targeting and dual targeting of the MAPK pathway (i.e., BRAFi + MEKi). We measured adaptive escape from drug-induced cell death by long-term clonal assays, visualizing and quantifying the growth of survival fractions after repeated drug treatments. For drug treatments, we selected doses sufficient to induce complete on-target inhibition (p-ERK for the MAPK pathway inhibitors; p-AKT for the PI3K inhibitor BKM120; p-AKT and p-GSK3β for the AKT inhibitors MK2206 and GSK2141795) at 1 hour after treatment (Fig. 3D and Supplementary Figs. S11 and S12; data not shown for the AKTi GSK2141795). The MAPK pathway inhibitors studied include the ATP-competitive BRAFi vemurafenib (PLX4032) and the allosteric MEK inhibitors AZD6244 and GSK1120212. In these long-term survival assays, BRAFi treatment alone (vs. DMSO) was used as the “reference” (Fig. 4). Dual-target MAPK pathway inhibition (BRAFi + MEKi) was more potent than single-target MAPK pathway inhibition, consistent with the clinical data demonstrating an improvement in response rate with the combination of dabrafenib and trametinib compared with dabrafenib alone (16). Notably, single-target MAPK pathway inhibition combined with PI3K or AKT inhibition (Fig. 4A-C and Supplementary Fig. S10) led to similarly efficacious or even more profound suppression of clonal growth escape than dual MAPK pathway inhibition. This is consistent with the notion that PI3K–AKT signaling provides either mutant BRAF-independent survival or BRAFi-induced compensatory survival. In addition, triple treatment with BRAFi + MEKi + AKTi led to the most profound suppression of clonogenic growth regardless of PTEN expression status (Supplementary Fig. S10). It is important to note that the drug treatment duration of these clonogenic assays mostly measured the slow growth of drug-tolerant persisters (Supplementary Fig. S5A).

In summary, we have shown that melanoma therapy based on MAPK pathway suppression can frequently unleash a rebound increase in PI3K–AKT pathway signaling in the tumors of treated patients. In cell lines, this signal crossstalk varied in strength, and one factor limiting the extent of a BRAFi-induced rebound in PI3K–AKT signaling was PTEN expression or activity. Interestingly, a novel PHD mutant of AKT1 (Q79K), which was detected in melanoma with acquired (late) BRAFi resistance, could counteract PTEN’s negative effect, amplify this BRAFi-elicted rebound level of AKT activation (by enhancing its cell-surface recruitment...
Figure 3. AKT PHD mutants confer vemurafenib resistance in a PTEN context-dependent manner. A, indicated stable melanoma cell lines were withdrawn from doxycycline (48 hours), treated with indicated concentrations of vemurafenib (vemu) for 72 hours, and survival (relative to DMSO-treated controls; mean ± SEM, n = 5) measured by the MTT (left; dashed line, 50% inhibition) or clonogenic assays (right). Media and vemurafenib at indicated concentration were replenished every 2 days for 10 days, starting 2 days after doxycycline withdrawal. B, the levels of vemurafenib-induced p-AKT in M229 cells without or with PTEN knockdown as shown by Western blotting. C, the effects of AKT1 PHD–mutant expression on vemurafenib sensitivity (MTT) in the context of PTEN WT expression or its knockdown. D, M229 cells stably expressing AKT1Q79K were treated with DMSO or vemurafenib (1 μmol/L, 48 hours) with and without increasing concentrations of the AKT1/2/3 inhibitor MK2206 (1 hour), and the lysates probed for the indicated phospho- and total protein levels. E, M229 cells stably expressing vector or AKT1Q79K were withdrawn from doxycycline (48 hours), seeded, treated with vemurafenib (1 μmol/L), and/or MK2206 (5 μmol/L) every 2 days (four treatments, 9 day drug exposure), fixed/stained, and quantified (% survival relative to DMSO).
Figure 4. Suppression of clonogenic melanoma growth via cotargeting of the PI3K-AKT and MAPK pathways regardless of PTEN status. A, M229 vector or M229 AKT1Q79K stable cell lines (2 days after doxycycline washout). M238, and WM2664 were treated with DMSO or indicated inhibitor(s) every day. BRAFi (vemurafenib), MEKi-AZD6244, and PI3Ki were used at 1 μmol/L (except for WM2664, 0.4 μmol/L), MEKi-GSK was used at 0.01 μmol/L (except for WM2664, 0.004 μmol/L). All cultures were fixed and stained with crystal violet (results shown are representative of two experiments). B, BRAFi (vemurafenib), MEKi-GSK (GSK1120212), and AKTi (MK2206) were used at 1, 0.01, and 5 μmol/L for M229 vector and M229 AKT1Q79K cells and at 0.5, 0.005, and 2.5 μmol/L for M238, and WM2664 cells. C, quantification of clonogenic growth in A and B expressed as percentage growth inhibition (relative to DMSO). MAPK inhibition (at BRAF or MEK) indicated in gray; PI3K or AKT inhibition in red. D, model showing that BRAFi treatment of BRAF-mutant melanoma can lead to a context-dependent, adaptive RTK–PI3K–AKT upregulation. BRAFi (or MAPKi) treatment derepresses RTK upregulation, resulting in activation of PI3K–AKT, and CRAF. With WT PTEN activity, this BRAFi-induced, rebound AKT upregulation is weak. In this context, AKT-activating mutants can counteract the effect of WT PTEN and amplify PIP3 signaling. Brown, mutated; blue, wild-type.

despite limiting PIP3 levels), and confer BRAFi resistance (Fig. 4D). This BRAFi-induced, PI3K-AKT-dependent adaptive response, along with the intrinsic sensitivity of PTEN nonexpressing, BRAF-mutant melanoma cells to AKT inhibition, helped to explain the efficacy of combined PI3K-AKT and MAPK pathway targeting. Taken together, these findings provide key insights into the common clinical observation of partial initial tumor responses to BRAFi or BRAFi + MEKi therapy and a strong rationale for combinatorial, upfront targeting of both the PI3K-AKT and MAPK melanoma survival pathways.

DISCUSSION

Strategies to deter acquired BRAFi resistance in melanoma have been based on the frequent occurrence of mechanisms that reactivation the MAPK pathway or the phenomenon of drug addiction displayed by the tumor cells with acquired resistance. These strategies have been either validated clinically or proposed to be tested clinically by the combination of BRAFi + MEKi or its intermittent dosing, respectively (16, 17). However, although the combination of BRAFi + MEKi likely achieves more profound pathway inhibition (compared
with BRAFi or MEKi alone) and hence a higher rate of initial clinical responses, the prolonged durability of response is still cut short by the late acquisition of resistance, strongly suggesting that a strategy based solely on MAPK pathway inhibition would be missing another essential melanoma survival pathway. This is even more evident when patients who progressed on vemurafenib were then treated with the combination of BRAFi + MEKi; the secondary response rates were low and, if seen, the durability short (18). This work on adaptive BRAFi resistance and our recent study of the landscape of acquired BRAFi resistance mechanisms (9) strongly support upregulation of the PI3K–AKT pathway as a critical event during the early and late evolution of resistance to MAPK pathway inhibition in patients.

Early and late resistance could potentially be mechanistically linked. In other words, the effects of BRAFi inhibition on melanoma signaling may influence and shape the evolutionary selective pressure on the residual tumor cells. We propose that, just as potent mutant BRAFi inhibition provides strong selective pressure for MAPK reactivation, a potent BRAFi-induced AKT upregulation would attenuate selective pressure for gain-of-function lesions in the PI3K–AKT pathway. On the basis of our data, we surmise that BRAFi-induced AKT upregulation during the first month of treatment may be widespread as an adaptive response. In those tumors in which this adaptive response was attenuated (e.g., by wild-type PTEN activity), genetic alterations upregulating the PI3K–PTEN–AKT pathway would distinctly confer growth and/or survival advantage. In fact, in the setting of acquired or late BRAFi resistance, our data support the notion that BRAFi inhibition can select for amplification of the early adaptive response driven by stable, genetic alterations, leading to dramatically enhanced survival dependency on the PI3K–PTEN–AKT pathway.

In this context, recent studies (19-21) and our own unpublished data place partial or complete genetic inactivation of PTEN at 10%–30% of BRAFi-mutant melanoma tumors or short-term cultures. It is not yet clear how frequently loss of PTEN function occurs as a result of epigenetic (DNA methylation, small non-coding RNAs, etc.), transcriptional, and posttranslational modification mechanisms in BRAFi-mutant melanomas. Presumably, the subgroup of BRAFi-mutant melanomas with wild-type and functional PTEN expression (i.e., the low p-AKT cohort) would mount the weakest AKT-dependent adaptive response when treated with a MAPK pathway inhibitor. Interestingly, recent clinical data suggest that BRAFi-mutant, p-AKT–low melanomas are more likely to regress in response to treatment with the MEKi selumetinib (AZD6244) than BRAFi-mutant, p-AKT–high melanomas (22). The relative lack of responses of the BRAFi-mutant, p-AKT–high melanomas may be explained by redundant survival pathways and/or a robust, AKT-dependent adaptive response. Another prediction from the current study is that the subgroup of BRAFi-mutant, wild-type PTEN-expressing melanomas, when treated with a MAPK-targeted therapy, would be susceptible to the development of acquired resistance driven by genetic amplifiers of the PI3K–PTEN–AKT pathway.

The AKT-dependent adaptive melanoma response is likely an early event in a set of coordinated, stereotypic reprogramming of growth and survival signaling. Our data indicate that this AKT upregulation is likely accompanied by a certain degree of MEKi–ERK reactivation driven by CRAFi, which is relatively much weaker compared with that driven by, for instance, NRAS mutations detected later during late or acquired resistance. This weaker form of MAPK reactivation occurring during the adaptive phase likely also constrains the initial efficacy of BRAFi and results from BRAFi-induced loss of ERK-dependent negative feedback, which normally suppresses ligand/RTK-driven RAS/MAPK signaling via BRAFi-insensitive RAF dimers (11). Data presented here and our unpublished work show that certain RTKs (e.g., PDGFRB, EGFR) are overexpressed and ligand-stimulated in a specific temporal order along the evolutionary continuum of adaptive resistance, spanning from an early period of maximal cell death induction, to an (overlapping) phase characterized by a surviving but slow-cycling subpopulation of drug-tolerant persisters (DTP), and then another transition marked by renewed proliferative clonal escape (i.e., drug-tolerant proliferating persisters or DTTP). These transitions could be marked by significant cellular morphologic and gene expression alterations (5). Subsequent to the DTTP stage, further clonal outgrowth can occur due to enhanced growth and proliferative fitness driven by specific genetic variants (e.g., NRAS mutations, mutant BRAFi amplification, AKT1/3 mutations; ref. 9). Thus, late acquired resistance mechanisms not only mirror but also augment adaptive resistance mechanisms.

Melanoma therapeutics has entered the era of combinatorial approaches. It has become evident recently that about 20% of BRAFi-mutant metastatic melanomas harbor readily screenable genetic alterations that upregulate the PI3K–AKT–PTEN pathway. Our studies show that melanomas can adaptively upregulate the PI3K–PTEN–AKT pathway early during MAPK-targeted therapy to compensate for MAPK pathway inhibition and, with further evolutionary selection, acquire genetic lesions to further enhance PI3K–AKT signaling for growth and survival. Thus, upfront, combinatorial targeting of both the PI3K–PTEN–AKT pathway and the MAPK pathway would be expected to curtail innate (lack of initial responses; ref. 23), adaptive (limited initial responses), and acquired (cessation of responses) resistance to MAPK-targeted therapies.

**METHODS**

**Cell Culture, Infections, and Drug Treatments**

Cells were maintained in Dulbecco’s Modified Eagle Medium with 10% FBS and glutamine. The melanoma cell lines were established at UCLA with Institutional Review Board approval and routinely authenticated by mitochondrial DNA sequencing. A375, SK, and WM cell lines were obtained from MSKCC and the Wistar Institute via Material Transfer Agreements and were not further authenticated except for verification of the BRAFi-mutant status. WT PHD, E17K PHD, and Q79K PHD of AKT1 fused to GFP as well as FLAG-tagged full-length AKT1, AKT1E17K, and AKT1Q79K were subcloned into the doxycycline-repressible lentiviral vector pLVX-Tight-Puro (Clontech, Inc.); viral supernatants generated by cotransfection with three packaging plasmids into HEK293T cells; and infections carried out with protamine sulfate. Stocks and concentrations of small-molecule kinase inhibitors were made in DMSO. Cells were quantified using CellTitre-GLO Luminescence (Promega) or crystal violet staining followed by NIH Image J quantification.
RESEARCH BRIEF

Drug Sensitivity, Protein, and PIP3 Detection

Cell proliferation experiments were performed in a 96-well format (3 replicates) and drug treatments initiated at 24 hours after seeding for 72 hours. Stocks and dilutions of PLX4032 (Plexikon), LY294002, MK2206, AZD6244, BKM120, GSK1120212, GSK2141795, and GSK2118436 (Selleck Chemicals) were made in DMSO. In these short-term assays, surviving cells were quantified using CellTiter-GLO Luminescence (Promega) following the manufacturer’s recommendations. Clonogenic assays were performed by plating cells at single-cell density in 6-well plates and providing fresh media, doxycycline (if applicable), and vemurafenib (vs. DMSO) every day or every other day. In these long-term assays, surviving clonogenic colonies were fixed by 4% paraformaldehyde and stained with 0.05% crystal violet. Cell lysates for Western blotting were made in radioimmunoprecipitation assay buffer (Sigma) with protease (Roche) and phosphatase (Santa Cruz Biotechnology) inhibitor cocktails. Western blots were probed with antibodies against p-AKT (Ser473), p-AKT (Thr308), AKT, p-GSK3β (Ser9), GSK3β, p-ERK1/2 (T202/Y204), ERK1/2, PTEN, m-ATG, PDGFRβ, p-CRAF (Ser338), CRAF, EGFR, GFP, Cell Signaling Technology, and FLAG, Tubulin (Sigma). Samples in the same figure subpanels were run, transferred, blotted, and developed (with the same exposure time) together.

In IHC experiments, after deparaffinization and rehydration, all sections from tissue series with extensive microscopic or macroscopic melanin deposits in any tumor were first subjected to a bleaching step using 3% H2O2 for 2 hours at 55°C. Tissue sections were then antigen-retrieved with a vegetable steamer at 95°C for 30 minutes, and immunostaining with anti-p-AKT (Ser473) or anti-PDGFRβ (Cell Signaling Technology) was then performed following a standardized streptavidin-biotin complex technique with horseradish peroxidase (HRP) and DAB chromogen (Vector Labs). After mounting, stained slides were scanned in their entirety with Scaner Scope CS section scanner (Aperio) at x40 magnification, and the images analyzed by Tissue Studio 2.0 (Definiens). PIP3 measurement was performed by competitive PIP3 Mass ELISA (Echelon K-2500). Briefly, the acidic lipids of each sample were extracted by the TCA/chloroform/methanol method, and samples were normalized on the basis of protein concentration. Cellular PIP3(3,4,5)P3 quantities were calculated by comparing the values from the wells containing PIP3(3,4,5)P3 extraction products to the values in the standard curve.

Fluorescent Microscopy

Melanoma cell lines expressing GFP-AKT PHD or PHD mutants were cultured in 6-well plates over cover slides. Serum-starved cells were treated with serum or a small-molecule inhibitor for indicated durations. Cells were fixed with 4% paraformaldehyde and mounted with VECTASHIELD Mounting Media (Vector Lab). GFP signal was photographed with a Zeiss microscope (AXIO Image A1) mounted with a charged-coupled device camera (Retiga EXi QImaging), and the images captured by Image-pro plus 6.0.

Apoptosis Analysis

 Cultures of indicated melanoma cell lines were treated with PLX4032 (at different time points) for increasing durations of time, fixed (at the same time point), permeabilized, and treated with RNase (QIAGEN). Cells were then stained with Annexin V-FITC (BD Pharmingen) for 15 minutes at room temperature and mixed with 7-AAD before sample loading (LSR II Flow Cytometry, BD Bioscience). Flow cytometry data were analyzed by the FACs Express V2 software.

Data Quantification

Clonogenic assays were stained with 0.05% crystal violet and photographed, and colonies were quantified by NIH Image J (NIH, Bethesda, MD). Stained immunohistochemical slides were scanned with Scan Scope CS section scanner (Aperio) with ×40 magnification, and analyzed by Tissue Studio 2.0 image analysis software (Definiens). Briefly, tumor-rich regions were selected as regions of interest (ROI), and the software was trained to recognize tumor cells by hematoxylin and DAB intensity, nuclear size, and nuclear morphology. Cell morphology was simulated per parameter 5.

Disclosure of Potential Conflicts of Interest

R.A. Scolyer has received honoraria from the speakers’ bureau of Roche and is a consultant/advisory board member of GlaxoSmithKline. R.F. Kefford has received honoraria from the speakers’ bureaus of Roche and Novartis and is a consultant/advisory board member of Roche, GlaxoSmithKline, and Novartis. A. Ribas has ownership interest (including patents) in Entrogen. G.V. Long is a consultant/advisory board member of GlaxoSmithKline and Roche.

Authors’ Contributions

Conception and design: H. Shi, A. Hong, R.F. Kefford, R.S. Lo Development of methodology: H. Shi, X. Kong, R.C. Koya, T. Chodon, R.F. Kefford, R.S. Lo Acquisition of data (provided animals, acquired and managed patients, provided facilities, etc.; H. Shi, A. Hong, X. Kong, R.C. Koya, C. Song, G. Moriceau, C.C. Yu, C. Ng, T. Chodon, R.A. Scolyer, R.F. Kefford, A. Ribas, G.V. Long, R.S. Lo Analysis and interpretation of data (e.g., statistical analysis, bioostatistics, computational analysis); H. Shi, A. Hong, X. Kong, C. Song, G. Moriceau, W. Hugo, R.F. Kefford, G.V. Long, R.S. Lo Writing, review, and/or revision of the manuscript; H. Shi, R.C. Koya, R.A. Scolyer, R.F. Kefford, G.V. Long, R.S. Lo Administrative, technical, or material support (i.e., reporting or organizing data, constructing databases); H. Shi, X. Kong, W. Hugo, C.C. Yu, G.V. Long, R.S. Lo Study supervision: R.S. Lo

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