The Activation of MAPK in Melanoma Cells Resistant to BRAF Inhibition Promotes PD-L1 Expression That Is Reversible by MEK and PI3K Inhibition

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Abstract

**Purpose:** Selective BRAF inhibition (BRAFi) provides a paradigm shift for melanoma treatment. The duration of benefit is typically limited before resistance develops. Interest remains in combining targeted and immune therapies to overcome resistance and improve durability of clinical benefit. One mechanism of evading immune destruction is programmed death-1 ligand 1 (PD-L1) expression by tumors that results in potent antitumor immune suppression.

**Experimental Design:** BRAFi-resistant melanoma cells were examined for changes in PD-L1 expression by immunoblot and flow cytometry. Signaling pathways involved in altering PD-L1 expression were examined. Strategies to maximize the effect of the BRAFi therapy were studied including MEKi, MEKi combinations, and additional pathways including phosphoinositide-3 kinase (PI3K).

**Results:** Melanoma cells resistant to BRAFi exhibit increased MAPK signaling and promotion of PD-L1 expression. PD-L1 expression is transcriptionally modulated by c-Jun and augmented by STAT3. MEK inhibition (MEKi) regains downregulation of MAPK signaling and suppresses the production of PD-L1. MEKi in melanoma cells shows dual therapeutic effects with simultaneous suppression of PD-L1 expression and induction of apoptosis. By combining MEKi with BRAFi, an additive effect on the inhibition of PD-L1 expression results.

**Conclusions:** We report a novel mechanism that suppresses preexisting immune responses in patients with melanoma receiving BRAFi therapy. BRAFi resistance leads to increased expression of PD-L1 in melanoma cells, mediated by c-Jun and STAT3. MEKi may be feasible to counteract BRAFi resistance of MAPK reactivation and also for the additive effect of PD-L1 suppression. Potential therapeutic benefits of combining targeted inhibitors and immune modulation to improve patient outcomes should be investigated.

**Introduction**

Use of the selective BRAF inhibitor (BRAFi) vemurafenib (PLX4032/RG7204) has altered the paradigm for treating metastatic melanoma tumors with V600E mutations, showing high response rates and survival advantage over chemotherapy (1–3). However, the median progression-free survival to treatment with vemurafenib is approximately 7 months. As a result, an active area of investigation remains the identification of means to improve the durability of selective BRAFi treatment. The combination of BRAF plus MEK inhibition is currently being investigated as a means to overcome BRAFi resistance. In addition, the success of CTLA-4 blockade with ipilimumab at improving survival with a subset of patients experiencing durable benefit (4, 5) suggests that the combinations with immune therapy may provide significant improvement to BRAFi alone. As a result, improved understanding of the molecular interactions with immune regulation provides the basis for the development of rational combinations for patients.

Several mechanisms of resistance to vemurafenib have been identified as leading to downstream activation of mitogen-activated protein kinase (MAPK). These include: (i) deregulated receptor tyrosine kinase (RTK) activity, e.g., platelet-derived growth factor receptor-\(\beta\) (PDGR-\(\beta\)) or insulin-like growth factor 1 receptor (IGF1R; refs. 6, 7); (ii) mutational activation of NRAS and MEK1(8); (iii) switching among RAF isoforms (9). Taken together, these studies indicate the reactivation of the downstream kinases in the MAPK pathway as the mechanism of resistance...
The availability of the selective BRAF inhibitor vemurafenib and immune checkpoint blockade with ipilimumab has dramatically altered treatment for patients with metastatic melanoma in offering survival advantages. Overcoming resistance to BRAF inhibition in melanoma is currently a critical area of investigation. Furthermore, the integration of targeted therapies with immune therapies presents novel opportunities for patients. There remain many questions on how best to combine such therapies to improve patient outcomes. In the current study, we identify a molecular mechanism that provides the basis for BRAF inhibitor–resistant melanoma cells to evade the immune system via upregulation of the inducible ligand programmed death-1-ligand 1. Subsequently, we identify potential molecular means to reverse this through MEK inhibition. These findings have particular implications for therapeutic strategies in the development of targeted combinations as well as combinations of targeted small molecules and immune checkpoint blockade.

The regulation of PD-L1 expression is likely complex and is regulated by multiple signaling pathways, some that have been investigated including MAPK (17), phosphoinositide 3-kinase/protein kinase B (PI3K/PKB), and the Janus kinase/signal transducers and activators of transcription (JAK/STAT; 18). Factors that influence PD-L1 expression may also be dependent on the cell type. In the current study, established BRAF-resistant melanoma cell lines were examined for relevant changes in PD-L1 expression. Further determination of molecular targets that influence PD-L1 expression in melanoma cells and potential rational combinations for improved efficacy were explored.

**Materials and Methods**

**Cell culture and mutational characterization**

Melanoma cell lines including K028, M34, and K029 were previously established and expanded from fresh tissues. Tumor samples were obtained from patients on Dana-Farber Cancer Institute/Harvard Cancer Center Institutional Review Board–approved protocols. Melanoma cell lines SK-Mel-5 and A375 were purchased from ATCC. Cell cultures were maintained in DMEM containing 10% fetal bovine serum (FBS). Mutational analyses of NRAS, BRAF, and MEK were done by direct PCR product sequencing (19). The selection of these cell lines in the study are based on detection of mutation at BRAFV600E before and after the establishment of BRAFi resistance, whereas no mutations of NRAS and MEK1 have been identified in all of BRAFi-resistant cell lines using direct PCR product sequencing on the mutated hotspots of these genes.

**Small interfering RNA transfections**

Cells were transfected with siRNAs (20 nmol/L) using Lipofectamine RNAiMAX reagent (Invitrogen) as per the manufacturer’s instructions. siRNA constructs were purchased from Dharmacon including RPS6, STAT3, c-Fos, human c-Jun, STAT5A, and STAT5B. siRNA constructs of ERK1/2, c-Jun-NH2-kinase (JNK), and p38 were purchased from Cell Signaling Technology, Inc. siRNA constructs were diluted in OPTI-MEM I reduced serum medium (GIBCO) to a final concentration of 20 nmol/L and mixed with Lipofectamine RNAiMAX reagent. Nontarget siRNA (QIAGEN) was used as a control.

**Drug treatment**

The following compounds and reagents were used: PLX4032 was provided by the laboratory of Dr. Nathaniel Gray at Dana-Farber Cancer Institute (Shanghai Haoyuan Chemexpress Co., Ltd.). STAT3 inhibitor Nifuroxazide was purchased from Santa Cruz Biotechnology. LY294002 and U0126 were purchased from Cell Signaling Technology. RAD001 was purchased from Selleck Chem. A stock solution was prepared in dimethyl sulfoxide (DMSO) or water at a concentration of 10 mmol/L or 10 mg/mL and maintained at −20°C. Drug was diluted in DMSO or water for working solutions and used at concentrations ranging from 0.1 nmol/L to 25 μmol/L for the treatment of cell lines.
Quantitative real-time PCR for relative RNA levels of PD-L1

Total RNA was extracted using the Rneasy Mini Kit (Qiagen), and reverse transcription reactions were conducted using the SuperScript First-Strand Synthesis System (Invitrogen). Real-time PCR analyses were conducted using the ABI 7300 real-time PCR machine (Applied Biosystems). The primers used for quantitative PCR (qPCR) were AGTGGTAA-GACCAACCACCAAT (forward) and TCATTGGAG-GATGTCCAGAGGT (reverse). To discriminate specific from nonspecific cDNA products, a melting curve was obtained at the end of each run. Data were normalized to β-actin levels in the samples in triplicates. Relative expression is calculated using the ΔΔCt method using the following equations: ΔCt (Sample) = Ct (Target) – Ct (Reference); relative quantity = 2^ΔΔCt.

Human phosho-MAPK array

The BRAFi-resistant melanoma lines M34 and K028 were plated in Dulbecco’s Modified Eagle’s Medium (DMEM) with 10% FBS and allowed to adhere overnight. Media was then exchanged containing PLX4032 at 2 µmol/L and incubated at 37°C in 5% CO2. The parental melanoma lines M34 and K028 treated with dimethyl sulfoxide (DMSO) served as controls. Cell lysates (300 µg total proteins per array) were applied following the manufacturer’s instructions (R & D Systems).

Flow cytometry analysis

Cells were harvested and stained with APC-conjugated anti-human CD274 (Clone 29E.2A3, Biolegend), Annexin V-FITC (BD Pharmingen), or isotype-matched control antibody (BD Pharmingen). Samples were analyzed on a FACS Caliber Flow Cytometer using CellQuest (BD) using FlowJo (TreeStar) software. Standardized fluorescence intensities were calculated by dividing the median fluorescence intensities of specific antibodies by the median fluorescence intensities of isotype controls.

Immunoblot analyses

Cells were seeded in 6-well plates in DMEM containing 10% FBS. At 60% to 70% confluence, cells were then treated with the relative agent for 30 minutes to 72 hours at various concentrations. Cells were lysed in Cell Lysis Buffer (Cell Signaling Technology) containing protease inhibitor cocktail (Roche Diagnostics). Proteins were separated on 7.5% SDS-polyacrylamide gels. Immunoblot revealed that in the presence of 10% fetal calf serum (FCS) containing medium level concentration of PLX4032 (2 µmol/L), the BRAFi-resistant cell lines developed dramatic increased activation in MAPK signaling pathways at multiple levels including extracellular signal-regulated kinase (ERK1/2), c-Jun N-terminal kinase (JNK1, 2, and 3) and p38 (α-, β-, δ, and γ-isofoms; Supplementary

AP1 ELISA assay

The BRAFi-resistant melanoma lines A375, K028, M34, SK-Mel-5, and K029 were plated in DMEM with 10% FBS and allowed to settle down overnight. The cells were then changed to fresh DMEM with 10% FBS containing PLX4032 at 2 µmol/L and incubated at 37°C in 5% CO2 for 45 minutes. The parental melanoma lines without treatment of PLX4032 served as controls. The nuclear portions of protein were prepared using the nuclear extraction kit (Panomics). The AP1 activation was quantified using the transcription factor ELISA kit following the manufacturer’s instructions (Panomics).

Statistical analysis

Experiments were repeated in triplicate, with the exception of the comparisons of PD-L1 expression before and after knockdown of c-Jun, which had 2 replicates. Data are expressed as mean ± SD. Comparisons of group means were assessed using general linear models. For multiple pairwise comparisons against a control within a cell line, Dunnett correction was used to preserve the overall type-1 error. Statistical significance was defined as P < 0.05.

Results

PD-L1 expression is increased in melanoma cell lines resistant to PLX4032

A panel of melanoma cell lines harboring BRAF V600E mutations were analyzed by immunoblot for PD-L1 expression before and after the establishment of BRAFi resistance (Fig. 1A) and confirmed for cell surface expression by flow cytometry (Fig. 1B, C, and D). Although all of the parental melanoma lines showed detectable levels of mRNA for PD-L1, only one line (M34) expressed significant level of PD-L1 pretreatment (94.67% ± 4.99%). Following the establishment of resistance to PLX4032, all of the melanoma lines expressed significantly higher levels of PD-L1 than their parental line counterparts, 6.2-fold to 10.9-fold increase by the frequency of PD-L1–positive cells and 7.8-fold increase in the median fluorescence intensity for M34 cells (Fig. 1C and D). PD-L1 expression remained increased in the resistant cell lines in the absence of PLX4032 for up to 3 months following drug withdrawal.

Acquired BRAFi-resistant melanoma cell lines exhibit increased signaling of multiple pathways

We assessed status of signaling pathways in melanoma cell lines before and after establishment of BRAFi resistance. A combined analyses of the Phospho-MAPK Array and immunoblot revealed that in the presence of 10% fetal calf serum (FCS) containing medium level concentration of PLX4032 (2 µmol/L), the BRAFi-resistant cell lines developed dramatic increased activation in MAPK signaling pathways at multiple levels including extracellular signal-regulated kinase (ERK1/2), c-Jun N-terminal kinase (JNK1, 2, and 3) and p38 (α-, β-, δ, and γ-isoforms; Supplementary
In addition, further characterization of these BRAFi-resistant lines revealed c-Jun phosphorylation and phosphorylation of STAT3 and 5 enhanced compared with parental lines (Supplementary Fig. S1C and S1D).

**PI3K-mTOR-S6 signaling pathway influences PD-L1 expression in melanoma cells**

To assess the molecular pathways involved in PD-L1 expression in melanoma cells following BRAFi, we began to investigate the effects on PI3K signaling due to its potential influence on inducible cell surface receptors. Most of the BRAFi-resistant cell lines exhibited an increase of phosphorylation of S6 related to PI3K signaling (Supplementary Fig. S2A). We next sought a pharmacologic effect of PI3K inhibition on PD-L1 expression. Treatment of BRAFi-resistant melanoma lines with PI3K inhibitor LY294002 decreased pAKT in all lines as expected. Chemical PI3K inhibition also significantly decreased PD-L1 transcript abundance and protein expression in BRAFi-resistant cell lines (Supplementary Fig. S2B and S2C). These results have been further confirmed by immunoblot staining (Data not shown).

We then tested the effects of ribosome protein (S6) inhibition on PD-L1 expression. Treatment of the BRAFi-resistant melanoma cells with the mTOR inhibitor RAD001 did lead to substantial decrease of S6 phosphorylation in the 3 BRAFi-resistant lines K028PR, M34PR, and K029PR; however, such an inhibition failed to elicit any inhibitory effect on the expression of PD-L1 (Supplementary Fig. S2D). Furthermore, a completed depletion of S6 using siRNA did not inhibit PD-L1 expression (Supplementary Fig. S2E).

Taken together, while pharmacologic inhibition of PI3K partially reduces PD-L1 expression, inhibition downstream of PI3K by either pharmacologic inhibition of mTOR or siRNA knockdown of S6 fails to significantly reduce PD-L1 expression. This suggests that the PI3K-mTOR-S6 pathway...
Figure 2. The MAPK pathway influences changes in PD-L1 expression in PLX4032-resistant melanoma cells. A, the MEK inhibitor U0126 decreases PD-L1 expression at the mRNA level in melanoma cells. Both the high PDL1-expressing M34 parental line and the BRAFi-resistant lines K028, K029, and M34 were treated with U0126 (U; 20 μmol/L) for 4 hours. Cells were treated with DMSO (D) for controls. PD-L1 mRNA levels were analyzed by quantitative real-time PCR (qRT-PCR). The data are the average of 3 independent experiments. B, MEKi with U0126 inhibits PD-L1 expression at the protein level. PD-L1 frequencies were analyzed by flow cytometry at 72 hours as described in A. The data are the average of 3 independent experiments. C, effects on PD-L1 expression by knockdown of ERK1/2 alone, JNK alone, or the combination for 48 hours and analyzed by immunoblotting. JNK was not targeted for K028R as it was not seen to be upregulated in the kinase array. Cells were treated with nontarget siRNA (NT) as controls. The blot is representative of 3 independent experiments. Example of flow cytometric analyses of PD-L1 expression and apoptosis on melanoma cells following knockdown of ERK1/2 alone, JNK alone, or the combination (right). D, flow cytometry profiling of PD-L1 expression before and after knockdown of ERK1/2 alone, JNK alone, or the combination in parental M34 and PLX4032-resistant K028 and M34 cell lines. The data are the average of 3 independent experiments. NT, nontarget siRNA. Represented are percentage of cells staining positive for PD-L1 (left) and the percentage of cells positive for Annexin V evaluation for apoptosis (right). $P$ values are relative to NT for each cell line. ($^* P < 0.001$).
may not have significant impact in the modulation of PD-L1 expression in BRAFi-resistant melanoma cells.

**Increased activation of MAPK promotes PD-L1 expression in the BRAFi-resistant melanoma cells**

Having examined the PI3K-mTOR-S6 pathway involvement in PD-L1 expression, we next examined the possible contribution of the MAPK pathway. Treatment with the MEK inhibitor U0126 led to a prolonged decrease in mRNA level of PD-L1 lasting for 24 hours (Fig. 2A). Correspondingly, treatment of the BRAFi-resistant cells with U0126 led to the inhibition on phosphorylation of ERK1/2 (Supplementary Fig. S3), which resulted in significant decrease of PD-L1 expression (Fig. 2B).

We further confirmed the role of ERK-MAPK pathway in modulation of PD-L1 expression using siRNA technology. With substantial depletion of ERK1/2, knockdown of ERK1/2 led to a decrease in PD-L1 expression in a K028-resistant line, 3.6-fold decrease in M34 parental line, and 1.7-fold decrease in M34 resistant lines, respectively (Fig. 2C and D). In the resistant cells, PD-L1 expression decreases by flow cytometry, specifically in the cells that are not undergoing apoptosis. These results, in line with inhibition of PD-L1 expression induced by treatment of melanoma cells with MEK inhibitor U0126, support the notion that ERK-MAPK signaling plays a critical role in modulation of PD-L1 expression in melanoma cells.

**c-Jun promotes PD-L1 expression in melanoma cells, which can be enhanced via cooperation of STAT3**

Having defined the significant role of MAPK signaling in modulation of PD-L1 expression in melanoma cells, factors involved in modulation of PD-L1 expression at transcriptional level was investigated next. The BRAFi-resistant melanoma cells had an increased activity of c-Jun (Fig. 3A), a transcriptional factor primarily driven by MAPK signaling. This suggested a role of c-Jun in modulation of PD-L1 expression. We further tested the effects of MEK inhibitor (U0126) on the activity of c-Jun. Treatment of the BRAFi-resistant cells with U0126 led to a significant inhibition of both the levels of phosphorylation and protein (Fig. 3B). Together,
Figure 4. STAT3 influences PD-L1 expression in conjunction with c-Jun. A, immunoblot analyses of STAT3 activity in BRAFi-resistant melanoma cell lines without treatment (DMSO, D) or in the presence of U0126 (U; 20 μmol/L) for 30 minutes. B, effects on PD-L1 expression by knockdown of c-Jun, STAT3, or the combination using siRNA. Both parental and BRAFi-resistant lines (M34) were treated with siRNA (10 μmol/L) targeting c-Jun alone, STAT3 alone, or the combination for 48 hours. Cells were treated with nontarget siRNA (NT) as controls. Immunoblot analyses of c-Jun and STAT3 (top left). The blot is representative of 3 independent experiments. Examples of flow cytometric analysis of PD-L1 expression as well as apoptosis (right). The flow cytometry profiles are representative of 3 independent experiments. Comparison of PD-L1 expression before and after knockdown of c-Jun alone, STAT3 alone, or the combination in parental and PLX4032-resistant M34 cell lines (bottom left). The data are the average of 3 independent experiments. Represented are percentage of cells that stain positive for PD-L1 and percentage of cells positive for Annexin V evaluation of apoptosis. C, pharmacologic suppression of STAT3 activity decreases PD-L1 expression in melanoma cells. Both parental and BRAFi-resistant cell lines (M34) were treated with nifuroxazide (5 μmol/L) for 30 minutes (immunoblot) or 72 hours (flow cytometry). Cells were treated with DMSO as a control. Immunoblot analysis of STAT3 activity (top). The blot is representative of 3 independent experiments. Flow cytometric analyses of PD-L1 expression as a function of drug exposure (bottom). The flow profile is representative of 3 independent experiments. D, the effect on PD-L1 expression by knockdown of STAT5 in melanoma cells. The same cell lines as described...
this evidence supported further investigation of c-Jun activity in the transcriptional regulation of PD-L1.

To test the role of c-Jun as the transcriptional factor of PD-L1 in the BRAFi-resistant melanoma cells, we knocked down c-Jun using siRNA (Fig. 3C) and determined the effects on PD-L1 expression (Fig. 3D and E). Knockdown of c-Jun led to significant decrease of PD-L1 in K028 resistant and parental M34 line, as well as near complete inhibition of PD-L1 expression in M34-resistant line (Fig. 3D and E).

Previous studies have shown that c-Jun acts as enhancer to modulate the expression of their targets forming a complex with its co-factor STAT3 (20). Along with the inhibition of c-Jun activity by MEK inhibition, treatment of the BRAFi-resistant melanoma cell lines by U0126 also led to dephosphorylation of STAT3 at sites of both of Tyr705 and Ser 727 (Fig. 4A). We then examined the role of STAT3 in modulation of PD-L1 expression in the BRAFi-resistant melanoma cells. Knockdown of STAT3 alone induced significant decreases of PD-L1 expression in both of the parental M34 cells (3.3-fold decreased) and the BRAFi-resistant M34 cells (6.6-fold decreased; Fig. 4B). Moreover, combined with knockdown of c-Jun, knockdown of STAT3 led to a synergistic inhibition of PD-L1 expression in the parental M34 lines and the BRAFi-resistant M34 line. Treatment of the BRAFi-resistant cells with the STAT3 inhibitor nilfuroxazide also led to significant decrease of PD-L1 expression (Fig. 4C). These data indicated that STAT3 may be involved in the modulation of PD-L1 with cooperation of c-Jun. Both knockdown of STAT5 or pharmacologic inhibition of STAT5 failed to decrease the expression of PD-L1 in both parental and resistant lines (Fig. 4D).

Discussion

Accumulating evidence suggests that reactivation of signaling downstream to RAF in the MAPK pathway is a major mechanism of resistance to BRAF inhibition in melanoma therapeutics (21, 22). In the present study, we found that the reactivation of MAPK leads to increased expression of the inducible ligand PD-L1. This upregulation involves c-Jun and STAT3 signaling as a consequence of BRAFi resistance. This is the first evidence that shows that reactivation of MAPK signaling is not only essential to BRAFi resistance, but also provides an additional mechanism of therapeutic resistance via modulation of host immune responses. Because fully human monoclonal antibodies to PD-1 and PD-L1 have shown significant clinical efficacy that seems to be associated with tumor expression of PD-L1 as a biomarker (23–25), interventions that alter PD-L1 expression may have additional implications for immune therapy.

In addition to enhanced activation of ERK-MAPK that occurs in BRAFi-resistant melanoma cells (6, 9, 26–29), JNK-MAPK and P38-MAPK signaling were also enhanced. The role of these 2 sub-MAPK pathways in BRAFi resistance remains poorly defined. While ERK-MAPK is generally involved in the control of cell proliferation, JNK signaling usually mediates responses to various forms of cellular stresses, such as damage repair mechanism, cell growth arrest, and cell death (30). Indeed, upon substantial dephosphorylation of ERK1/2 or JNK, a single knockdown is sufficient to elicit significant apoptosis, especially in the melanoma cells with BRAFi resistance. Furthermore, synergistic induction of apoptosis is able to be reached upon combined knockdown of ERK1/2 with JNK, suggesting an important role for these sub-pathways in melanoma cell survival. Interestingly, both ERK1/2 and JNK are direct kinases that modulate the activity

in A were treated with siRNAs (10 nmol/L) targeting STAT5. Cells treated with nontarget siRNA (NT) were used as controls. Immunoblot analysis of STAT5 (top). The blot is representative of 3 independent experiments. Flow cytometric analysis of PD-L1 expression before and after knockdown of STAT5 in parental and PLX4032-resistant M34 cell lines (bottom right). The data are the average of 3 independent experiments. Represented are the percentage of cells that stain positive for PD-L1 and percentage of cells positive for Annexin V evaluation for apoptosis. (*, P < 0.001).
of c-Jun, an inducible transcription factor that directs changes of gene expression such as PD-L1 (31), suggesting that these 2 kinases may be involved in the modulation of PD-L1 in response to multiple extracellular stimuli. Either the inhibition of activity of its upstream kinase MEK with MEKi (U0126) or the physical knockdown of ERK1/2 or JNK are able to reduce PD-L1 expression in melanoma cells (32–35). Taken together, these data suggest both ERK1/2 and JNK may modulate PD-L1 expression, especially the de novo upregulation of PD-L1 induced by BRAFi via the paradoxical activation of MAPK. In agreement with this observation, the present study has shown that depletion of ERK1/2 and JNK synergistically suppresses PD-L1 expression, but fails to induce similar effect on the induction of apoptosis.

The increased activity of c-Jun in melanoma cells with BRAFi resistance is closely related to the levels of PD-L1. Moreover, knockdown of c-Jun is necessary and sufficient to suppress expression of PD-L1 on melanoma cells either sensitive or resistant to Braf inhibition. We further observed that a combined depletion of c-Jun and STAT3 resulted in a synergistic inhibition of PD-L1, whereas a single knockdown of either c-Jun or STAT3 only led to partial inhibition, indicating a cooperation of these 2
in melanoma cells without established BRAFi resistance. A similar transcriptional synergy of c-Jun and STAT3 was also observed in the BRAFi-resistant cells; however, in this case, a single knockdown of c-Jun is sufficient to inhibit PD-L1 expression, suggesting that the BRAFi-resistant melanoma cells are more dependent on c-Jun for PD-L1 expression.

In the present study, we have identified that enhanced phosphorylation of STAT3 at Tyr 705 as well as Ser 727 are induced in the BRAFi-resistant melanoma lines. How the activity of STAT3 is elevated in BRAFi-resistant melanoma cells requires further investigation. Interestingly, the knockdown of c-Jun alone or STAT3 alone is sufficient to reduce PD-L1 expression in both parental and BRAFi-resistant melanoma cells. However, this failed to induce significant apoptosis.

The role of the PI3K-AKT/PKB-mTOR pathway in BRAFi resistance has been previously studied. Jiang and colleagues (36) reported that activation of the PI3K/AKT pathway accounts for, at least in part, the MEK-independent survival of the BRAFi-resistant melanoma cells. The increased PI3K/AKT activation is the result of extracellular stimuli in some cases. Previous reports in glioma, breast, and prostate carcinoma (37, 38) suggest that the expression of PD-L1 is dependent on the PI3K-AKT-mTOR-S6K1 pathway. In the present study, we found that blockade of this pathway either by PI3Ki (LY94002), mTORi (RAD001), or by depletion using siRNA has moderate effects on PD-L1 expression both in melanoma cells sensitive or resistant to BRAFi.

An important model of tumor homeostasis incorporates host immune surveillance to prevent tumor outgrowth during the earliest stages of tumor growth (39, 40). Prolonged immunosuppression is associated with high occurrence of secondary malignancies (e.g., immunosuppressive treatment not only fosters growth of preexisting tumors but also promotes incidences of secondary cancers in kidney transplant recipients; ref. 39). One of the adverse effects of selective BRAF inhibition treatment in melanoma is the development of secondary squamous cell carcinomas (SCC; keratoacanthoma-type) of the skin. These lesions harbor preexisting H-RAS mutations that upon driving of the paradoxical activation of MAPK lead to accelerated growth of the lesions and squamous cell carcinomas (41). It would also be of interest to investigate a potential role of PD-L1 expression via the above mechanism in the formation of secondary neoplasms. In agreement with this possibility, Cao and colleagues found that overexpression of PD-L1 promotes carcinogenesis in a methylcholanthrene-induced model of SCC, and that blockade of PD-1/PD-L1 signaling reverses the incidence of the secondary SCC (42, 43).

The expression of PD-L1 has been associated with MAPK signaling in other tumor types. PD-L1 expression was found to be regulated by MEK/ERK signaling in anaplastic large cell lymphoma and Hodgkin lymphoma (35). In acute myeloid leukemia, protection of blasts from cytotoxic T cells can be reversed by MEK inhibition (44). The importance of molecularly driven expression of PD-L1 is further exemplified through 9p24.1 amplification in nodular sclerosing Hodgkin lymphoma and primary mediastinal large B-cell lymphoma that result in increased expression of PD-L1 and induction by JAK2 (45). This strongly suggests that the oncogenic drivers for malignant transformation also result in expression of the inducible ligand PD-L1 as a generalizable principle to the development of the malignant phenotype.

Much of the characterization of the mechanisms of the BRAFi resistance in melanoma suggested that targeting downstream effects of MAPK may prove effective, such as the targeting of MEK. This has led to a number of clinical investigations administering a MEK inhibitor following a BRAF inhibitor, or giving the combination of a MEK inhibitor and BRAF inhibitor to improve clinical outcomes over BRAF inhibition alone. Interestingly, the present study reveals that inhibition of ERK-MAPK by MEKi not only suppresses PD-L1 expression but also induces apoptosis on the melanoma cells. This suggests that MEK inhibition may not only have an effect on tumor cell death, but also strongly influences PD-L1-inducible ligand that would make it more susceptible to immune destruction. This not only supports the further study of BRAF inhibition plus MEK inhibition in BRAF-mutated tumors, but also suggests a role of MEKi in immune modulation that deserves further exploration. There remains concern of the effects of these small-molecule inhibitors on immune cell function. Investigators have suggested a dual role to these inhibitors.
Specifically, vemurafenib may improve T-cell function through the paradoxical activation of MAPK. It has been shown that vemurafenib at least preserves the viability and function of lymphocytes (10). There is greater concern that MEKi may be more detrimental to T-cell–specific immune function. The dual roles of these inhibitors in modulating tumor cell expression of PD-L1 and T-cell function require further clinical investigation. Further clinical exploration of combinatorial approaches of BRAFi and/or MEKi with blockade of the PD-1/PD-L1 pathway is also warranted.

The influences of c-Jun and STAT3 on PD-L1 expression reveal the importance of signaling pathways in determining the immune evasion potential of a cancer cell. As a mechanism, these findings further support the observations of AP-1–dependent enhancer for PD-L1 expression and the JAK3/STAT3-dependent PD-L1 promoter. AP-1–dependent PD-L1 expression in Hodgkin lymphoma was recently described whereby constitutive AP-1 activity in the presence of Epstein–Barr virus (EBV) infection induces PD-L1 expression (31). In addition, amplification of 9p24.1 in subtypes of non-Hodgkin lymphoma results in increased JAK2 expression and associated PD-L1 promotor activity (45). The enhancer/promoter elements of inducible immune regulatory ligands may play a critical role in cancer immune evasion. Furthermore, MEK/ERK signaling has been previously described to regulate PD-L1 expression in anaplastic large cell and Hodgkin lymphoma (35). MEK inhibition has also been shown to reverse PD-L1–mediated inhibition of cytotoxic T-cell function against acute myeloid leukemia cells (44). These observations along with the current report confirm the generalized importance of MAPK signaling in influencing PD-L1 expression. As a result, molecular mechanisms for immune evasion by tumor cells and subsequent contribution to the immunosuppressive tumor microenvironment can be established.

In melanoma, the significance of therapeutically targeting the oncogenic driver mutation BRAF has dramatically altered treatment for patients (1, 3). Selective BRAF inhibitor has been shown to enhance T-cell recognition of melanoma (11) as well as induce a brisk infiltration of T lymphocytes into metastatic deposits (12). In the current study, the development of BRAFi resistance results in the melanoma cell avoiding destruction through immune evasion by increasing PD-L1 expression. It will be important to characterize this phenomenon further to examine the relationship of PD-L1 and PD-1 in those infiltrates. It has also been reported that BRAF (V600E) expression in melanoma further induces immune suppression by the induction of IL-1 in stromal fibroblasts (46). The current study adds to the fundamental understanding of the molecular mechanisms involved in tumor immune evasion within the tumor microenvironment. Importantly, as significant numbers of pharmacologic tools now exist to alter these signaling pathways, such influence must be appreciated to engineer better combinatorial therapeutic approaches.

In summary, we have identified a novel mechanism that contributes to clinical resistance of BRAFi in patients with metastatic melanoma. Molecular resistance to BRAFi as exemplified by increased MAPK signaling prompts PD-L1 expression via enhancing the activity of c-Jun and its cofactor, STAT3. On the basis of these findings, molecular induction of PD-L1 in tumors may have dramatic effects on clinical efficacy. Appreciating the dual roles of small-molecule inhibition on tumor cell survival as well as immune recognition will be an important basis for future clinical investigation strategies for combination of small molecules and combinations of small molecules with immune checkpoint blockade to improve patient outcomes.

Disclosure of Potential Conflicts of Interest
F.S. Hodi is a consultant/advisory board member in Genentech/Roche and has clinical trial support to his institution from Genentech/Roche, Bristol-Myers Squibb, and Merck. Dr. Hodi has served as a non-paid consultant to Genentech/Roche. No potential conflicts of interest were disclosed by the other authors.

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