Activation of Forkhead Box O Transcription Factors by Oncogenic BRAF Promotes p21<sup>cip1</sup>-Dependent Senescence

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Abstract

Oncogene-induced senescence (OIS) is a potent tumor-suppressive mechanism that is thought to come at the cost of aging. The Forkhead box O (FOXO) transcription factors are regulators of life span and tumor suppression. However, whether and how FOXOs function in OIS have been unclear. Here, we show a role for FOXO4 in mediating senescence by the human BRAF<sup>V600E</sup> oncogene, which arises commonly in melanoma. BRAF<sup>V600E</sup> signaling through mitogen-activated protein kinase/extracellular signal-regulated kinase resulted in increased reactive oxygen species levels and c-Jun NH<sub>2</sub> terminal kinase-mediated activation of FOXO4 via its phosphorylation on Thr<sup>223</sup>, Ser<sup>226</sup>, Thr<sup>447</sup>, and Thr<sup>451</sup>. BRAF<sup>V600E</sup>-induced FOXO4 phosphorylation resulted in p21<sup>cip1</sup>-mediated cell senescence independent of p16<sup>ink4a</sup> or p27<sup>kip1</sup>. Importantly, melanocyte-specific activation of BRAF<sup>V600E</sup> in vivo resulted in the formation of skin nevi expressing Thr<sup>223</sup>/Ser<sup>226</sup>-phosphorylated FOXO4 and elevated p21<sup>cip1</sup>. Together, these findings support a model in which FOXOs mediate a trade-off between cancer and aging. Cancer Res; 70(21); 8526–36. ©2010 AACR.

Introduction

Activating mutations in the Ser/Thr kinase BRAF are observed in ∼7% of all human tumors with high occurrence in thyroid carcinoma, colorectal cancer, ovarian cancer (1), and especially melanoma (∼70%; ref. 2). The predominant BRAF mutation present in these cases is a substitution of Val600 for Glu (BRAF<sup>V600E</sup>), which causes increased downstream signaling toward mitogen-activated protein kinase/extracellular signal-regulated kinase (ERK) kinase (MEK; ref. 2). Although BRAF-activating mutations initially stimulate proliferation, cell cycle progression is ultimately arrested through induction of senescence (3–5). Oncogene-induced senescence (OIS) can be facilitated through the individual activities of p16<sup>ink4a</sup> and p21<sup>cip1</sup> (6, 7), and also in case of BRAF<sup>V600E</sup>, these cell cycle inhibitors are thought to regulate senescence (4, 8, 9).

Reactive oxygen species (ROS) propagate cellular signaling induced by growth factors and thereby regulate a variety of cellular processes including proliferation (10, 11). However, when ROS levels increase above a certain threshold, sometimes called oxidative stress, ROS react with and damage the cellular interior. Additionally, excessive ROS can induce cellular senescence (12), and as such, they are considered to accelerate aging and age-related pathologies (13, 14). ROS are known to signal to a plethora of downstream targets, and it is currently elusive which of these regulate the induction of senescence.

Forkhead box O (FOXO) transcription factors are the mammalian orthologues of the <i>Caenorhabditis elegans</i> protein DAF-16, which functions as an important determinant of life span (15). FOXOs were originally identified as downstream components of insulin/insulin-like growth factor signaling through phosphoinositide 3-kinase (PI3K) and protein kinase B (PKB/AKT; refs. 16, 17). In mice, FOXOs act as functionally redundant tumor suppressors (18), and in cell systems, FOXOs can either mediate apoptosis or quiescence in response to growth factor deprivation (19). In contrast to insulin signaling, which represses FOXO activity, cellular ROS can activate FOXOs (20, 21). Regulation of FOXOs by ROS occurs through numerous posttranslational modifications (22), rendering FOXOs sensors of cellular ROS (23). Consequently, FOXO activation increases resistance to oxidative stress through transcription of enzymes as MnSOD (24) and catalase (25) through a negative feedback loop. Increased FOXO activity is associated with longevity in model organisms (15).
and humans (26), which lends credit to the hypothesis that excessive ROS accelerate aging. Thus, FOXOs are regulated by ROS, play a role in both tumor suppression and aging, and thereby provide an important paradigm to understanding the relation between aging and disease such as cancer.

Materials and Methods

Additional information is available in Supplementary Materials and Methods.

Antibodies

The antibodies against FOXO4 (834), HA (12CA5), phosphorylated Thr447, and phosphorylated Thr317 have been described before (21, 27). The following antibodies were purchased: phosphorylated Thr298/Tyr351-c-Jun NH2 terminal kinase (JNK) and phosphorylated Thr227/Tyr204-ERK (Cell Signaling); Thr28-phosphorylated FOXO4 (Upstate); MnSOD (Stressgen); trimethyl-H3K9 and FOXO3α (Upstate); p27kip1 (BD Pharmingen); p16ink4a (ab-2; Neomarkers); p21cip1 (M19), BRAF (C19), FOXO4 (N19), FOXO1 (N18), proliferating cell nuclear antigen (PCNA; PC10), and p53 (DO-1; Santa Cruz); and tubulin (Sigma). Antibodies against phosphorylated Thr223 and phosphorylated Thr231/Ser236 were generated by immunizing rabbits with the keyhole limpet hemocyanin–conjugated peptides CKAPKKKPSVLPAPPEGA-pT-PSTPVG and CKAPKKPSVLPAPPEGA-pT-PTSPVG and CKAPKKPSVLPAPPEGA-pT-PT-pS-PVG, respectively, wherein pT and pS present phosphorylated threonine and serine. Produced antibodies were subjected to positive and negative affinity purification according to manufacturer’s protocol (Covance).

Constructs and RNA interference

The following constructs have been described before: pbabe-puro, pMT2-HA-FOXO4, and pRP261-GST-FOXO4-ΔDB (16); 6× FOXO DNA-binding element (DBE)–firefly luciferase, MnSOD–firefly luciferase, and TK–Renilla luciferase, MnSOD-firefly luciferase, and TK-Renilla luciferase (24); pEFm-BRAFV600E (2); and p2i1391 and p2i1391 (BD Pharmingen); p16ink4a (ab-2; Neomarkers); p21cip1 (M19), BRAF (C19), FOXO4 (N19), FOXO1 (N18), proliferating cell nuclear antigen (PCNA; PC10), and p53 (DO-1; Santa Cruz); and tubulin (Sigma). Antibodies against phosphorylated Thr223 and phosphorylated Thr231/Ser236 were used to immunize rabbits with the keyhole limpet hemocyanin–conjugated peptides CKAPKKKPSVLPAPPEGA-pT-PSTPVG and CKAPKKPSVLPAPPEGA-pT-PTSPVG and CKAPKKPSVLPAPPEGA-pT-PT-pS-PVG, respectively, wherein pT and pS present phosphorylated threonine and serine. Produced antibodies were subjected to positive and negative affinity purification according to manufacturer’s protocol (Covance).

Immunofluorescence, terminal deoxynucleotidyl transferase-mediated dUTP nick end labeling staining, and BrdUrd incorporation

Immunofluorescence was performed as described (27) using antisera against FOXO4 (834 and monoclonal antibody), HA (12CA5), PCNA, H3K9-Me(III), and pT223//S226. BrdUrd incorporation and terminal deoxynucleotidyl transferase-mediated dUTP nick end labeling (TUNEL) staining were performed according to the manufacturer’s protocols (Roche). For the mouse sections, anti-p21cip1 M19 was used.

Cellular ROS measurements with H2DCFDA

HEK293T cells were transfected with pcDNA3 or a plasmid encoding BRAFV600E (2 μg), in parallel with phage-puro (500 ng). At 16 hours posttransfection, cells were selected with 2 μg/mL puromycin for 36 hours and subsequently left untreated or pretreated for 24 hours with 4 mmol/L α-acetyl cysteine (NAC) or 10 μmol/L U0126, washed with PBS, and incubated for 10 minutes with 1 ml 10 μmol/L H2DCFDA (Invitrogen). Following recovery for 4 hours in medium with or without NAC or U0126, cells were pretreated with or without 200 μmol/L H2O2 for 45 minutes and collected by trypsinization. Centrifuged cells were incubated with 0.02 mg/mL propidium iodide (PI), and live cells were analyzed by FACS for DCF fluorescence. CHL and WM266.4 cells were treated similarly, but without puromycin and PI selection.

Colony formation assay and senescence-associated β-galactosidase staining

A14 or U2OS cells were transfected as indicated together with phage-puro (500 ng). At 24 hours posttransfection, cells were subjected to puromycin selection (2 μg/mL). Following 2.5 days of selection, one set of cells was lysed and analyzed by immunoblotting for protein expression. At 10 days posttransfection, cells were fixed in methanol and stained with 0.5% crystal violet in 25% methanol. Plates were dried, and colony formation was quantified by determining in 10% acetic acid and measuring absorbance at 560 nm. CHL, PMWK, Colo829, and A375 cells were treated similarly but transfected with 500 ng FOXO4 and 250 ng phage-puro. Senescence-associated β-galactosidase (SA-β-GAL) staining was performed 9 days posttransfection as described (30).

Results

Ectopic introduction of FOXO4 induces cellular senescence in BRAFV600E-expressing Colo829, A375, and SK-mel28 melanoma cells

To study the involvement of FOXOs in BRAFV600E-dependent cellular responses, we ectopically expressed FOXO4 in the human melanoma-derived cell line, Colo829, harboring an endogenous BRAFV600E mutation. This resulted in reduced colony formation along with diminished PCNA and BrdUrd positivity (Fig. 1A) but without significant TUNEL staining (Supplementary Fig. S1).

FOXOs repress oxidative stress (21), and increased oxidative stress is suggested to cause cellular senescence (12). Surprisingly, however, ectopic FOXO4 expression rendered Colo829 cells positive for SA-β-GAL activity (Fig. 1B). Also detection of two other independent markers of senescence (4, 31), senescence-associated heterochromatin foci (SAHF) and H3K9-trimethylation, was significantly enhanced by FOXO4 (Fig. 1C), suggesting that this indeed is a senescence response.

To exclude artifacts of a single cell type, we also expressed FOXO4 in other melanoma cell lines that express endogenous BRAFV600E. A375, and SK- Mel28, or wild-type BRAF, CHL, and PMWK. Whereas FOXO4 induced SA-β-GAL expression in A375 and SK-Mel28, no positivity was observed in CHL or PMWK cells (Supplementary Fig. S2 and data not shown).
Thus, in endogenous BRAFV600E-expressing Colo829, A375, and SK-Mel28 melanoma cells, expression of FOXO4 induces a growth arrest through cellular senescence.

BRAFV600E induces phosphorylation of FOXO4 on JNK target sites

The MEK-ERK pathway is a primary signaling output for normal and oncogenic BRAF. In addition to MEK-ERK signaling, BRAFV600E expression is reported to promote activation of JNK (32) which we confirmed (Supplementary Fig. S3). Previously, we showed that FOXO4 is a JNK target and identified Thr447 and Thr451 through mutation analysis as a subset of the phosphorylated acceptor sites (21). We therefore wondered whether BRAFV600E could signal through JNK toward FOXO4 to promote senescence. To fully address this question, we first determined all possible JNK sites of in vitro phosphorylated FOXO4 by liquid chromatography–tandem mass spectrometry analysis (Supplementary Data). In addition to the previously characterized Thr447 and Thr451, this revealed two novel residues, Thr223 and Ser226 (Supplementary Fig. S4). We generated phosphospecific antisera against these sites, including dually phosphorylated Thr223/Ser226. In vitro

Figure 1. FOXO4 induces cellular senescence in endogenous BRAFV600E-expressing Colo829 and A375 cells. A, ectopic FOXO4 expression reduces proliferation of Colo829 cells. Colo829 cells transiently expressing HA-FOXO4 were subcultured in puromycin containing selection medium and stained for colony outgrowth. Additionally, a set of cells were stained at 2.5 d posttransfection with anti-PCNA or analyzed for BrdUrd incorporation. Two hundred nontransfected and 50 transfected cells were quantified. Similar results were obtained in A375 melanoma cells. EV, empty vector. B, ectopic FOXO4 expression induces SA-β-GAL positivity in Colo829 cells. Colo829 cells expressing HA-FOXO4 were selected with puromycin and stained for colony formation or SA-β-GAL. Protein samples were obtained at 2.5 d posttransfection and analyzed by immunoblotting. Fifty colonies were quantified for positive cells. C, FOXO4 expression in Colo829 cells induces senescence. Colo829 cells were transfected as in A and at 5.5 d posttransfection stained with 4,6-diamidino-2-phenylindole (DAPI) to visualize SAHF formation in parallel with anti-H3K9-Me(III) for H3K9-trimethylation. One hundred cells were quantified, and the percentage of double-positive cells was indicated.
phosphorylation by JNK significantly increased detection of wild-type FOXO4 by these respective antisera, especially the newly discovered Thr223 and Ser226, whereas FOXO4-4A in which these residues are mutated to Ala (Fig. 2A) was not detected. This indicates that Thr223, Ser226, Thr447, and Thr451 are JNK-phosphorylated acceptor sites.

Because BRAFV600E signaling induces activation of both ERK and JNK, we next determined whether phosphorylation of the identified sites in cultured cells is mediated by either of these kinases. H2O2, which activates both, indeed resulted in the phosphorylation of Thr223 of FOXO4. Additionally, stimuli that exclusively activate either ERK [12-O-tetradecanoylphorbol-13-acetate (TPA) and epidermal growth factor] or JNK (anisomycin) showed that Thr223 phosphorylation correlates with activation of JNK, not ERK (Fig. 2B; Supplementary Fig. S5).

In agreement with JNK activation, BRAFV600E induced a significant increase in phosphorylation of all JNK sites, but
not on the PKB/AKT site Thr28 (Fig. 2C). Furthermore, treatment of cells with the JNK inhibitor SP600125 not only inhibited BRAFV600E-induced JNK autophosphorylation in a dose-dependent manner, but also Thr223 phosphorylation of FOXO4 (Supplementary Fig. S6). Together, these results indicate that BRAFV600E promotes JNK-mediated phosphorylation of FOXO4.

To address whether phosphorylation of FOXO4 on the JNK sites is required for FOXO4 to be able to induce senescence in BRAFV600E-expressing melanoma cells, we expressed the FOXO4-4A mutant next to wild-type FOXO4. FOXO4-4A neither significantly repressed colony formation nor induced SA-β-GAL positivity (Fig. 2D). In contrast, a mutant of FOXO4 that mimics phosphorylation on JNK sites, FOXO4-4E, induced a senescence response similar to wild-type FOXO4 (Fig. 2D). Altogether, these data indicate that FOXO4 is a downstream target of BRAFV600E through JNK-mediated phosphorylation and that phosphorylation on the JNK target sites is required for FOXO4 to promote senescence in response to BRAFV600E.

**BRAFV600E** signaling elevates cellular ROS levels, which promote FOXO4 phosphorylation by JNK

JNK activity is regulated through a large variety of signaling pathways, and we therefore next addressed the molecular mechanism through which BRAFV600E regulates JNK and thereby FOXO4 activity. Elevations in cellular ROS generated through H2O2 treatment of cells can directly invoke senescence (12), and senescence induction in, for instance, melanocytes has recently been correlated with increased ROS (33). Moreover, OIS can be bypassed by ROS scavenging compounds such as NAC (34, 35). Hence, we investigated the possibility that BRAFV600E signaling affects cellular ROS levels by loading cells with the ROS detecting probe H2DCFDA (DCF). BRAFV600E expression significantly increased cellular ROS levels as detected by DCF fluorescence (Fig. 3A). The BRAFV600E-induced increase in cellular ROS could be further increased by treatment with H2O2 (45 minutes, 200 μmol/L) but was impaired on preincubation with NAC. Downstream signaling through MEK seems at least partially required, because preincubation with the MEK inhibitor U0126 reduced DCF fluorescence. These data indicate that ectopic BRAFV600E expression leads to the generation of cellular ROS through downstream MEK signaling. In agreement herewith, melanoma cells expressing BRAFV600E showed higher basal ROS levels compared with wild-type BRAF-expressing cells (Supplementary Fig. S7). Elevations in ROS are sufficient for phosphorylation of FOXO4 by JNK, as treatment of cells with H2O2 resulted in a time-dependent increase of both JNK activation and Thr223 phosphorylation (Supplementary Fig. S8; Fig. 2B). Moreover, BRAFV600E-mediated JNK activation and FOXO4 phosphorylation were repressed on pretreatment of cells with NAC or U0126 (Fig. 3B).

Prolonged treatment with U0126 induces apoptosis in Colo829 cells (36), making it impossible to interpret the effect of this inhibitor on FOXO4-induced senescence. Therefore, Colo829 cells were treated with NAC to reduce cellular ROS. This resulted in reduced colony formation of Colo829 cells (Fig. 3C), most likely due to the fact that proliferation per se requires low amounts of ROS (14). Importantly, however, NAC impaired the ability of FOXO4 to induce senescence in these cells. Altogether, these data point to a pathway in which BRAFV600E induces FOXO4 phosphorylation by JNK through a MEK-regulated elevation of intracellular ROS, and in line with that, ROS are essential for FOXO4 to induce senescence in the presence of BRAFV600E.

**p21<sup>kip1</sup> mediates the cell cycle arrest and senescence response by BRAFV600E-FOXO4 signaling**

Next, we addressed the mechanism downstream of how FOXO4 promotes BRAFV600E-induced senescence. p27<sup>kip1</sup> is an important mediator of FOXO-induced G1 arrest and subsequent quiescence response in the absence of growth factors (19). Therefore, we reasoned a role for p27<sup>kip1</sup>. FOXO4-induced p27<sup>kip1</sup> expression, however, was counteracted rather than enhanced by coexpression of BRAFV600E (Fig. 4A; data not shown). Thus, we conclude that the FOXO4-mediated cell cycle arrest, in response to BRAFV600E signaling, is unlikely to be regulated through p27<sup>kip1</sup>.

Next, we addressed the importance of another cyclin-dependent kinase (CDK) inhibitor, p16<sup>ink4a</sup>, which has been implicated in senescence. p16<sup>ink4a</sup> levels do not seem to increase on FOXO4 and BRAFV600E coexpression (Fig. 4A; data not shown). Also, in Colo829 cells in which FOXO4 induces senescence (Fig. 1), a premature stop mutation is present in the CDKN2A gene resulting in loss of p16<sup>ink4a</sup> expression (37). These data also argue against involvement of p16<sup>ink4a</sup> in FOXO4-mediated OIS driven by BRAFV600E.

Because p21<sup>cip1</sup> and p16<sup>ink4a</sup> seem functionally redundant in OIS (6, 7, 9), we next analyzed a role for p21<sup>cip1</sup>. Interestingly, BRAFV600E cooperated with FOXO4 to induce p21<sup>cip1</sup> expression (Fig. 4A), and in correlation with the induction of senescence, FOXO4 expression increased p21<sup>cip1</sup> expression in Colo829 cells (Supplementary Fig. S9). Similar effects were observed on p21<sup>kip1</sup> mRNA expression determined by quantitative real-time PCR. Moreover, BRAFV600E and FOXO4 expression resulted in a synergistic activation of a luciferase-reporter gene driven by the p21<sup>kip1</sup> promotor (Fig. 4B). This level of synergy was also observed using a construct under a different FOXO-responsive promoter (i.e., MnSOD) and a synthetic promoter encompassing six optimal FOXO DBEs (6× DBE; Supplementary Fig. S10), suggesting that the cooperative induction indeed reflects increased FOXO activity.

As HA-FOXO4-4A did not induce senescence in Colo829 cells, whereas HA-FOXO4-4E did, we also determined the ability of these mutants to induce p21<sup>cip1</sup> transcription. In line with the lack of senescence induction, HA-FOXO4-4A, but not HA-FOXO4-4E, was significantly less capable of driving p21<sup>kip1</sup> transcription (Fig. 4C). These data indicate that BRAFV600E activates FOXO4 through JNK-mediated phosphorylation to promote p21<sup>kip1</sup> transcription, which in Colo829 cells correlates with the induction of senescence.

To address to what extent p21<sup>kip1</sup> is required for the FOXO4-induced cell cycle arrest and senescence response to BRAFV600E signaling, we used short hairpin RNA (shRNA)-mediated knockdown of p21<sup>cip1</sup>. This impaired p21<sup>kip1</sup>
expression induced by BRAF<sup>V600E</sup> FOXO4 coexpression (Supplementary Fig. S11). Whereas BRAF<sup>V600E</sup> and FOXO4 together induced a strong G1 arrest as determined by FACS analysis, this effect was abolished on knockdown of p21<sup>cip1</sup> (Fig. 4D). Because p21<sup>cip1</sup> expression is elevated in FOXO4-induced senescence in Colo829 cells, we also addressed the effect of p21<sup>cip1</sup> knockdown on the induction of senescence. Strikingly, FOXO4 expression did not induce SA-<beta>-GAL staining in Colo829 cells on p21<sup>cip1</sup> knockdown (Fig. 4D), indicating that p21<sup>cip1</sup> is required in FOXO4-induced senescence in these cells. Altogether, these data show that FOXO4 is a downstream target of BRAF<sup>V600E</sup> that can facilitate a cell cycle arrest and OIS through regulation of p21<sup>cip1</sup>.

**BRAF<sup>V600E</sup> regulates p21<sup>cip1</sup> expression through MEK and ROS-dependent phosphorylation of FOXOs**

Following our observations that suggest BRAF<sup>V600E</sup> mediated JNK/FOXO4 activation runs through MEK-ROS signaling, we addressed the involvement of MEK and ROS in the regulation of p21<sup>cip1</sup> and cell cycle arrest by BRAF<sup>V600E</sup> and FOXO4. Pretreatment of cells with either NAC, to reduce ROS (Fig. 5A), or U0126, to inhibit MEK (Fig. 5B), repressed JNK activation by BRAF<sup>V600E</sup>, phosphorylation of FOXO4 on the JNK target site Thr<sup>223</sup>, and the cooperative induction of p21<sup>cip1</sup>. Furthermore, whereas ectopic expression of FOXO4 in Colo829 cells significantly enhanced p21<sup>cip1</sup> promoter activity, pretreatment of these cells with U0126 or NAC reduced this effect (Fig. 5C). This shows that JNK-mediated phosphorylation of FOXO4 and the concomitant activation of p21<sup>cip1</sup> transcription are dependent on MEK activity and elevations in cellular ROS.

Next, we investigated the role of endogenous FOXOs in signaling from BRAF<sup>V600E</sup> toward p21<sup>cip1</sup> transcription. High ectopic expression of BRAF<sup>V600E</sup> strongly induced p21<sup>cip1</sup> promoter activity (ref. 8; Fig. 5D). This induction was abrogated on shRNA-mediated simultaneous depletion of endogenous FOXO1, 3a, and 4, whereas add-back of a FOXO4
mutant insensitive to shRNA-mediated knockdown (FOXO4-SM) was sufficient to rescue BRAFV600E-induced transactivation of the p21cip1 promoter (Fig. 5D; Supplementary Fig. S12 and S13). Thus, endogenous FOXOs are essential for ectopic BRAFV600E to induce p21cip1 transcription.

**Endogenous BRAFV600E regulates FOXO4 phosphorylation and p21cip1 expression in cultured melanoma cells and in vivo**

To further investigate the endogenous regulation of FOXO4 by oncogenic BRAF, we used a distinct human melanoma-derived cell line WM266.4 (BRAFV600D; Fig. 6A). WM266.4 cells are tumorigenic yet express very high levels of p21cip1. This, we reasoned, made them suitable to investigate the entire endogenous signaling cascade from oncogenic BRAF toward p21cip1. Like Colo829 and in agreement with hyperactive BRAF signaling, WM266.4 cells expressed a significant amount of active ERK and JNK. As for Colo829 cells, expression of p16ink4a was not detectable in this cell line (Fig. 6A; ref. 38). Small interfering RNA (siRNA)–mediated knockdown of BRAF in WM226.4 cells reduced ERK and JNK activity and, importantly, resulted in diminished p21cip1 expression (Supplementary Fig. S14), arguing that the high p21cip1 level in WM266.4 cells is indeed driven by the oncogenic BRAF. Treatment of WM266.4 cells with U0126 inhibited MEK activity and subsequent JNK activation, indicating that, indeed also in these cells, MEK signaling is essential for JNK activation by oncogenic BRAF (Fig. 6B). Interestingly, next to impaired p21cip1 expression, the U0126-mediated repression of JNK reduced phosphorylation of endogenous FOXO4 on the JNK sites Thr223 + Ser226 and also siRNA-mediated knockdown of endogenous FOXOs reduced the p21cip1 expression (Fig. 6B). U0126 further enhanced this reduction, probably reflecting incomplete knockdown of FOXOs by these siRNAs. Together, these experiments indicate that oncogenic BRAF can regulate p21cip1 expression through phosphorylation of endogenous FOXOs by JNK, confirming the results we obtained in our overexpression studies.

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**Figure 4.** BRAFV600E–FOXO4 signaling induces transcription of p21cip1, not p27kip1 or p16ink4a. A, BRAFV600E and HA-FOXO4 coexpression results in increased p21cip1. Total lysates of puromycin selected HEK293T cells expressing HA-FOXO4 and BRAFV600E were analyzed by immunoblotting. B, BRAFV600E and FOXO4 cooperatively promote p21cip1 transcription. Quantitative real-time PCR for p21cip1 mRNA in HEK293T (left) and p21cip1-luciferase assay on A14 cell lysates (right), which transiently expressed HA-FOXO4 and BRAFV600E. C, mutation of the JNK sites in FOXO4 affects the ability to transactivate p21cip1 transcription. p21cip1-luciferase assay in Colo829 cells, using wild-type FOXO4, HA-FOXO4-4A, and HA-FOXO4-4E. D, p21cip1 is required for FOXO-mediated G1 arrest and senescence response in a background of BRAFV600E signaling. Left, U2OS cells (optimal for FOXO-mediated G1 arrest; ref. 19) were transfected with BRAFV600E and HA-FOXO4 in combination with a plasmid encoding a short hairpin against p21cip1 or a scrambled control. Right, SA-β-GAL staining after expression of HA-FOXO4 in combination with a plasmid encoding a scrambled or p21cip1 short hairpin in Colo829.
Ultimately, to study the biological relevance of our observations in vivo, we used a BrafV600E-Tyr:CreERT2/+ mouse model, which expresses BrafV600E in melanocytes off the endogenous Braf gene in a tamoxifen-inducible manner (39). As reported before, activation of BrafV600E signaling induced melanocytic nevi within the dermis, composed of nests of pigmented epitheloid cells intermingled with whorls of lightly pigmented and amelanotic spindle cells (Supplementary Fig. S15). At the periphery of these melanocytic nevi, we observed multiple patches of darkly pigmented, large polygonal cells, interpreted as neoplastic melanocytes. 
P21cip1 expression was significantly expressed within these neoplastic melanocytes at the periphery of the BrafV600E-induced nevi (Fig. 6C), and minor p21cip1 expression was detected in the less pigmented regions of the nevi and within epidermal layers. To investigate endogenous FOXO4 expression in the mouse skin, we developed novel monoclonal antisera. The antisera could immunostain ectopically expressed mouse HA-FOXO4 in Colo829 cells (Supplementary Fig. S16). When applied to the mouse skin sections, the antisera showed expression of endogenous FOXO4 in the mouse skin (Fig. 6C).

To determine the phosphorylation status of FOXO4 on the JNK target sites in the BrafV600E-expressing skin samples, we used p1223/226 antisera. Detection with the p1223/226 antisera showed nuclear staining in unstimulated cells, including Colo829 (Supplementary Fig. S17; data not shown). Knockdown of endogenous FOXO4 reduced, although not abolished, the signal, showing the extent of specificity of this antisera for endogenous FOXO4. Importantly, endogenous Thr223/Ser226 phosphorylation of FOXO4 was specifically enriched in the areas of the nevi that also showed p21cip1 staining (Fig. 6C). Thus, in line with the cell culture data, in vivo activation of oncogenic BRAF promotes nevi formation, i.e., senescence in vivo, which harbor phosphorylation of FOXO4 on the JNK target sites Thr223/Ser226 and elevated p21cip1 expression within similar compartments.

**Discussion**

Here, we describe a role for FOXO4 in BrafV600E-induced senescence. BrafV600E activates FOXO4 through a MEK-ROS-JNK signaling cascade to induce p21cip1 expression.
and senescence (Fig. 6D). Senescence represents a barrier for tumor formation, and consequently, the melanoma-derived cells we have used de facto have bypassed this barrier. Irrespective, in cell culture active FOXO represses this barrier, suggesting that FOXO inactivation is one of the requirements for senescence bypass. This conclusion is supported by data showing that, in mice, loss of PTEN and consequently reduced FOXO activity synergizes with BRAFV600E to induce melanoma (40). Despite limitations in studying senescence in melanoma cell lines in culture, our histochemical analysis of lesions from BRAFV600E mice clearly suggests that in vivo FOXO and p21⁠^{cip1} indeed function in the senescence response induced by BRAFV600E.

Oncogenes induce senescence through various mechanisms. Although HRAS is an upstream regulator of RAF, HRASG12V expression in primary melanocytes induces senescence through the ER-associated unfolded protein response, whereas oncogenic (B)RAF does not (32). This difference between RAS and RAF is also reflected in mice models in which BRAFV600E induces both melanocyte senescence and

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Figure 6. Endogenous BRAFV600E regulates p21⁠^{cip1} transcription through FOXO4 phosphorylation on the JNK target sites. A, characterization of WM266.4 (BRAFV600E) cells. CHL (wt BRAF), Colo829 (BRAFV600E), and WM266.4 (BRAFV600E) cells were lysed and analyzed by immunoblotting. Endogenous FOXO4 expression was determined after immunoprecipitation. B, left, U0126 abrogates JNK signaling, endogenous phosphorylation of FOXO4 on Thr223 + Ser226 and p21⁠^{cip1} expression in WM266.4 cells. WM266.4 cells were untreated or treated for 24 h with 10 μmol/L U0126 and analyzed as in (A). The phosphorylation status of endogenous FOXO4 was determined after immunoprecipitation. HC, heavy chain. Right, endogenous FOXOs regulate p21⁠^{cip1} expression in WM266.4 cells. Lysates of WM266.4 cells transfected with scrambled siRNA or siRNA against FOXO1,3a and 4 (siFOXO) and untreated or treated for 24 h with 20 μmol/L U0126 were analyzed by immunoblotting. C, expression of p21⁠^{cip1}, total FOXO4, and Thr223/Ser226-phosphorylated FOXO4 is elevated in neoplastic regions of BRAFV600E-induced nevi. Top, skin sections of tamoxifen-treated Braf+/LSL-V600E; Tyr::CreERT2+/o mice were analyzed for background signal (second antibody only), p21⁠^{cip1} expression, total FOXO4, and Thr223/Ser226-phosphorylated FOXO4. Higher magnifications of the nevus (arrowheads) are shown in the bottom. The top right shows undifferentiated nevi. The bottom right represents a magnification of epidermal staining from the bottom left. Untreated tissue did not typically show positive staining. D, model on the regulation of FOXO4 by BRAFV600E, resulting in p21⁠^{cip1}-mediated senescence. BRAFV600E signaling activates MEK. In turn, MEK induces elevations in cellular ROS levels, thereby promoting activation of JNK. JNK subsequently phosphorylates FOXO4 and thereby promotes specific transcription of p21⁠^{cip1}, rather than p27⁠^{kip1} or p16⁠^{ink4a}, and triggers a senescence response.
melanoma (39), whereas HRAS^{G12V}, but not NRAS^{G12K}, induces senescence and only melanoma if combined with loss of tumor suppressors p16^{ink4a} or p19^{Arf} (41). Interestingly, senescence in general, including melanocyte senescence (33), frequently correlates with elevated levels of ROS and OIS can be bypassed by ROS scavenging compounds (34, 35). BRAF^{V600E} chronically increases cellular ROS, which, as we showed, is required for activation of FOXO4, p21^{cip1} transcription, and subsequent senescence. Together, these and our data suggest that, besides oncogene-specific pathways, increased ROS direct part of the senescence program, which may be more generic. Recently, RAS-induced senescence was shown to require a RAS-dependent negative feedback loop repressing P13K-PKB/AKT activity (42). As ROS, reduced PKB/AKT activity also activates FOXO, suggesting that activation of FOXO is the general event in senescence rather than the ROS/JNK signaling mechanism. Interestingly, the idea that FOXO activation will be a general component of senescence onset is in agreement with the current notion that the reverse, i.e., FOXO inactivation, represents a general component of tumor onset (18).

Mechanisms of senescence induction also greatly differ between cell types. In cell culture, melanocyte senescence differs from fibroblast senescence (discussed in ref. 43). Human melanocytes deficient in INK4a show an impaired senescence response, but INK4a-deficient human fibroblasts senesce normally. Because a number of families with inherited predisposition to melanoma showed loss of p16^{ink4a} (44, 45), these and other data suggest that INK4a-dependent senescence is especially important in melanocytes. However, loss of p16^{ink4a} is not very common in early-stage melanomas (46), and in oncogenic BRAF-positive human and mouse nevi, examples of cellular senescence in vivo p16^{ink4a} expression are mosaic (47, 48). Also recently, we showed in the Braf^{+/LSL-V600E}, Tyr::CreERT2^{+/o} mouse model that loss of p16^{ink4a} does not affect BRAF^{V600E}-induced nevus formation (39). Furthermore, in these mice, BRAF^{V600E}-induced melanoma showed nuclear p16^{ink4a} staining in agreement with clinical data showing significant nuclear p16^{ink4a} expression in primary melanoma (30%–85%) as well as metastatic melanoma (15%; ref. 48). Thus, although p16^{ink4a} fulfills an important role in the suppression of melanoma progression, it seems not to be essential for establishing senescence (see also ref. 4). Here, we show firstly that, in the absence of p16^{ink4a}, FOXO4 can induce senescence, and secondly, this requires p21^{cip1}. This confirms the earlier suggestion that p21^{cip1} may facilitate melanocyte senescence in the absence of p16^{ink4a} (5). Thus, in BRAF^{V600E} signal-

ing, p21^{cip1} and p16^{ink4a} seem to regulate two independent cell cycle inhibitory responses that are functionally redundant to the induction of BRAF^{V600E}-induced senescence.

Besides INK4a, the requirement for FOXO further defines differences between fibroblasts and melanocytes in senescence induction. In contrast to our observations with respect to OIS in melanoma cells and melanocytes in vivo, in fibroblasts loss of FOXO3a rather than activation of FOXO has been implicated in replicative senescence (49). Recently, a differential requirement for FOXO has been suggested in tumor progression (50), and it will be of interest to see whether a similar differential requirement applies to the various stages at which cellular senescence can be induced.

FOXOs function as tumor suppressors (18), and senescence induction by FOXO as shown here provides one mechanism for this function of FOXO. Importantly, although a mechanism of tumor suppression, it is argued that cellular senescence is also causative to organismal aging (51, 52). OIS may therefore represent a trade-off between tumor suppression and life span. Interestingly, both lack of growth factor signaling and increased ROS result in FOXO activation. However, the absence of growth factor signaling can impose a reversible p27^{kip1}-mediated G_{1} cell cycle arrest and/or quiescence, which may be used to repair, for example, cellular damage (24). In this manner FOXO may positively affect life span and importantly with little cost to the organism. However, in response to BRAF^{V600E}-induced ROS, FOXOs protect against tumorigenesis through induction of senescence, and unlike the former, this protection is not without cost. Our findings underline the pivotal role that FOXOs play in mediating the role of ROS in normal signaling as well as aging, and it will be of interest to see whether, for example, age in return affects the ability of FOXO to mediate senescence.

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No potential conflicts of interest were disclosed.

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Activation of Forkhead Box O Transcription Factors by Oncogenic BRAF Promotes p21<sup>cip1</sup>-Dependent Senescence

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