Tumor and Stem Cell Biology

Oncogenic B-Raf\(^{V600E}\) Induces Spindle Abnormalities, Supernumerary Centrosomes, and Aneuploidy in Human Melanocytic Cells

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Abstract

Activating B-Raf mutations arise in 60% to 70% of human melanomas and are thought to play a vital role in tumorigenesis, although how this occurs remains poorly understood. Wild-type B-Raf is critical for normal mitosis of human somatic cells, suggesting that mutational activation of B-Raf might compromise mitosis. We examined this hypothesis by introducing oncogenic mutant B-Raf\(^{V600E}\) into established human melanoma cells, assessing the effects on mitosis and their possible relationship to extracellular signal–regulated kinase (ERK) pathway activation. Exogenous expression of this activated B-Raf mutant led to a high incidence of aberrant spindles and supernumerary centrosomes. These mitotic abnormalities were suppressed by expression of a B-Raf\(^{V600E}\)–mutant–specific shRNA or by the addition of the mitogen-activated protein/ERK kinase–specific inhibitor U0126. Mitotic abnormalities generated by B-Raf\(^{V600E}\) also caused missegregation of chromosomes leading to aneuploidy. Because activating B-Raf mutations are detected frequently in benign nevi, we extended our studies to primary human melanocytes. Remarkably, short-term expression of B-Raf\(^{V600E}\) was sufficient to induce aneuploidy in human melanocytes or in immortalized human mammary epithelial cells. Collectively, our studies identify a novel role for the B-Raf oncogene in driving aneuploidy in melanocytic cells. We propose that disruption of mitotic controls by oncogenic B-Raf has important implications for understanding melanoma tumor development. Cancer Res; 70(2); 675–84. ©2010 AACR.

Introduction

Raf kinases (A-Raf, B-Raf, and C-Raf) stimulate the mitogen-activated protein kinase (MAPK) cascade, which consists of mitogen-activated protein/extracellular signal–regulated kinase (MEK) and extracellular-signal regulated kinase (ERK). Of the three Raf kinase members, B-Raf is the most potent MEK activator (1), with prominent roles in cell growth, cell cycle progression, and survival (2, 3). In addition, mitotic roles for B-Raf in regulating spindle formation and activation of the spindle assembly checkpoint (SAC) have been shown recently in human somatic cells (4), which is consistent with mitotic functions of ERK (5–9). Mitotic activation of B-Raf requires Cdc2/cyclin B activity (10, 11), suggesting a regulatory mechanism that is distinct from Ras-mediated activation of Rafs during the G1 phase of the cell cycle. Therefore, B-Raf can promote cell proliferation by a variety of mechanisms throughout the cell cycle that extend to key roles at mitosis.

Activating B-Raf mutations arise somatically in 7% of human cancers, with a particularly high frequency (60–70%) in cutaneous melanomas (12–14). The V600E mutation accounts for at least 90% of all B-Raf mutations detected to date, which renders B-Raf constitutively active (12, 15). As such, B-Raf\(^{V600E}\) sustains 10-fold higher levels of ERK activity (16), which likely contributes to its oncogenic transforming activity shown in immortalized fibroblasts and mouse melanocytes in culture (12, 17, 18). In melanoma cells, B-Raf\(^{V600E}\) subverts adhesion-dependent controls (19, 20) and suppresses anoikis (21, 22). Targeting oncogenic B-Raf inhibits melanoma cell proliferation and survival in vitro and melanoma tumor growth and vascular development in vivo (17, 23, 24). Together, these findings underscore crucial roles for oncogenic B-Raf in tumorigenesis, yet the mechanism through which oncogenic B-Raf exerts its transforming properties remains poorly understood.

Most human tumors exhibit abnormal chromosomes numbers, known as aneuploidy, which is associated with tumor progression and poor prognosis (25, 26). Aneuploidy results from chromosome segregation errors that often arise due to faulty spindle checkpoint controls and centrosome amplification (see reviews in refs. 27, 28). Because B-Raf serves normal roles at mitosis in mediating proper spindle formation and activation of the SAC (4), we investigated whether expression of the constitutively active B-Raf\(^{V600E}\) mutant, present in most melanomas, might have detrimental
effects at mitosis. Here, we showed that introducing the B-RafV600E mutant into wild-type B-Raf melanoma cells resulted in supernumerary centrosomes, aberrant spindles, and aneuploidy. Similarly, aneuploidy was rapidly induced by B-RafV600E in primary human melanocytes and hTERT-immortalized epithelial cells. From these results, we propose that the B-Raf oncogene may be a key contributor to aneuploidy in melanoma.

Materials and Methods

Retroviral constructs and viral production. pBabe-puro and pBabe-puro-B-RafV600E retroviral vectors were a generous gift from Dr. Daniel Peeper (The Netherlands Cancer Institute, Amsterdam, the Netherlands). pSUPER-retro-B-Raf shRNA Mut-A was kindly provided by Dr. David Tuveson (Cambridge Research Institute/Cancer Research UK, Cambridge, United Kingdom) and used to selectively knock down the V600E mutant form of B-Raf as previously described (17). Retroviral vectors were transfected into HEK 293T replication-defective packaging cells for retrovirus production.

Cell lines and primary melanocytes. Human melanoma cell lines SK-MEL-5, SK-MEL-28, and A375 were obtained from the American Type Culture Collection and maintained in DMEM supplemented with 10% fetal bovine serum (FBS). SK-MEL-5 cells used in this study are wild type for B-Raf (12, 29), which was also confirmed by DNA sequencing analysis for exon 15, performed by the Moffitt Molecular Biology core facility (Supplementary Fig. S1). SK-MEL-28 and A375 cells carry B-RafV600E mutations (12). Sbc2 melanoma cells, originally derived from early radial growth phase primary melanomas, were obtained previously from M. Herlyn (Wistar Institute, Philadelphia, PA). Sbc2 cells are wild type for B-Raf (16, 30) and were grown in 2% tumor medium (4:1 mix of MCD153/L15 medium, 2% FBS, 5 μg/mL insulin, 1 mmol/L CaCl2). To further assess functional B-RafV600E mutations in melanoma cell lines, phospho-ERK levels were determined by immunoblot analysis after switching to low serum for 24 h. SK-MEL-5 and Sbc2 melanoma cells switched to 0.25% FBS exhibited minimal ERK activity, whereas SK-MEL-28 and A375 (both containing B-RafV600E mutations) cells showed robust levels of phospho-ERK (data not shown). Primary human epidermal melanocytes were obtained from ScienCell Research Laboratories and cultured in their Melanocyte Medium.

Human mammary epithelial cells immortalized with human telomerase (hTERT-HME) were generously provided to us by the laboratory of Dr. Huntington Potter at the Johnnie B. Byrd Alzheimer’s Center and Research Institute (University of South Florida, Tampa, FL). hTERT-HME cells were cultured in mammary epithelial cell growth medium from Lonza.

Retrovirus infections and DNA plasmid transfections. Sbc2 cells were infected with pBabe-puro or pBabe-B-RafV600E retroviruses as described (31) and selected in puromycin (0.8 μg/mL) for 8 to 10 d. Puromycin-resistant colonies were pooled and checked for ectopic B-RafV600E expression by immunoblot analysis. Transient gene expression in SK-MEL-5 cells was done by transfection of pEBG plasmids containing an NH2-terminal glutathione S-transferase (GST) tag fused to full-length human B-RafWT or V600E, as previously described (30); transfection efficiency was routinely in the range of 80% to 90% based on immunostaining with a GST antibody. Human melanocytes or hTERT-HME cells were transfected using the Nucleofector system from Amamaxa. Transfection efficiencies were estimated to be ~90% based on cotransfection with green fluorescent protein.

Immunofluorescence staining and microscopy. To assess mitotic spindles and centrosome numbers, melanoma cells were subjected to immunostaining with α-tubulin (Sigma) and γ-tubulin (Sigma) antibodies, respectively, as previously described (30). Immunostained cells were mounted with Prolong Gold containing 4′,6-diamidino-2-phenylindole (DAPI; Molecular Probes) to detect chromosomes. Microscope images of mitotic cells were viewed with a fully automated, upright Zeiss Axio-Imager Z.1 microscope (Carl Zeiss MicroImaging, Inc.) using 63×/1.40 numerical aperture (NA) and 100×/1.3 NA oil-immersion objectives and DAPI, FITC, and Texas red filter cubes. High-resolution images were captured using the AxioCam MRm charge-coupled device (CCD) camera and deconvoluted using Axiovision version 4.5 software or a Leica DMi6000/TCS SPS confocal microscope equipped with a 100×/1.40 NA Plan Apochromat oil-immersion objective, as previously described (30). All images were transferred into Photoshop v8.0 (Adobe) and saved as Tiff files.

Fluorescence in situ hybridization analysis and metaphase chromosome spreads. Cells were treated with 1 μg/mL colchicine for 2 h, harvested by trypsinization, and washed with PBS. Cells were swollen in 65 mmol/L KCl for 5 min at 37°, fixed in cold acetic acid/methanol for 5 min at 4°, dropped onto slides, and dried at room temperature. For metaphase spreads, cells were then stained with DAPI and viewed with a Nikon E800 fluorescence microscope with a 60×/1.40 NA Plan Apo oil-immersion objective. Images were captured with a Roper Coolsnap HQ CCD camera and processed with Metamorph 5.0 and Adobe Photoshop 8.0 softwares. For interphase fluorescence in situ hybridization (FISH) analysis, slides were stained with CytoCell enumeration probes against chromosomes 2 and 8 (for Sbc2 cells) or chromosomes 3 and 10 (for human epidermal melanocytes and hTERT-HME cells) conjugated with FITC or Cy3.5 (Rainbow Scientific). Staining was carried out according to the manufacturer’s protocol. FISH samples were viewed with a fully automated, upright Zeiss Axio-Imager Z.1 microscope with a 20× objective and DAPI, FITC, and Rhodamine filter cubes. Images were produced using the AxioCam MRm CCD camera and Axiovision version 4.5 software suite. P values were calculated using a two-sample test for equality of proportions with continuity correction.

Western blot analysis. Adherent melanoma cells, washed with cold PBS, were scraped into cell lysis buffer [50 mmol/L Tris-HCl (pH 7.5), 150 mmol/mL NaCl, 5 mmol/L EGTA, 0.5% NP40] containing protease inhibitors (10 μg/mL aprotinin, 10 μg/mL leupeptin, 25 mmol/L NaF, 1 mmol/L sodium vanadate) and centrifuged at 14,000 rpm for 15 min at 4°C to pellet insoluble cell debris. Protein concentrations of supernatants were determined using the detergent-compatible

Cancer Res; 70(2) January 15, 2010

Cancer Research
protein assay (Bio-Rad). Equal amounts of protein were resolved by 10% SDS-PAGE, electrophoretically transferred onto polyvinylidene fluoride membranes (Millipore Corporation), and subjected to immunoblot analysis. Primary antibodies used include rabbit anti–B-Raf (H-145) and anti–phospho-p44/42 MAPK (Thr 202/Tyr204; E10) monoclonal antibodies (Cell Signaling) and mouse anti-ERK1 (BD Transduction Laboratories). Secondary antibodies, alkaline phosphatase–conjugated AffiniPure goat anti-mouse IgG or anti-rabbit IgG-alkaline phosphatase antibodies (Sigma), were incubated for 1 h at room temperature and then processed for chemiluminescence detection using the CDP-Star reagent (Roche).

Results

Oncogenic B-Raf<sup>V600E</sup> induces spindle abnormalities and supernumerary centrosomes. Mitotic roles for B-Raf in human somatic cells have been previously shown by our laboratory (4). Because activating B-Raf mutations are detected in a high proportion of human cutaneous melanomas, we postulated that its constitutive activity may adversely affect mitosis. To test this possibility, we ectopically expressed the oncogenic B-Raf<sup>V600E</sup> mutant in human melanoma cells (SBcl2 and SK-MEL-5) that are wild type for B-Raf. Moderate expression of recombinant B-Raf<sup>V600E</sup> over endogenous wild-type B-Raf levels was confirmed by Western blot analysis (Fig. 1A) and, as predicted, resulted in elevated phospho-ERK levels in both melanoma cell lines. B-Raf<sup>V600E</sup>–expressing cells subjected to immunostaining exhibited high frequency (∼76%) of spindle abnormalities with misaligned chromosomes (see Fig. 1B). Approximately 55% of the abnormal spindles consisted of multipolar structures with amplified centrosomes as confirmed by costaining with anti–γ-tubulin (Fig. 1B; Supplementary Fig. S2A). The remaining abnormal spindles structures were associated with two centrosomes. Similar spindle abnormalities, including multipolar spindle structures, were generated in SK-MEL-5 melanoma cells transfected with a pGST-B-Raf<sup>V600E</sup> construct (Fig. 1C; Supplementary Fig. S2B). In contrast, 90% of parental SBcl2 and SK-MEL-5 melanoma cells had normal metaphase spindles with proper chromosome alignment (Fig. 1B and C). Interestingly, overexpression of wild-type B-Raf in SK-MEL-5 cells had little effect on spindle formation (Fig. 1C).
Supplementary Fig. S2B) and ERK activity (Fig. 1A), suggesting that the induced pleiotropic spindle abnormalities are due to the constitutively active B-RafV600E mutant rather than the higher levels of B-Raf protein being expressed.

Centrosome amplification was further quantitated in interphase cells that were immunostained with an anti-γ-tubulin antibody to assess centrosome numbers. Depending of the phase of the cell cycle, one (unduplicated) or two (duplicated) centrosomes were detected in more than 95% of the parental or vector control interphase cells (Fig. 2). In contrast, abnormal numbers of centrosomes (>2) were detected in ∼30% of interphase cells for both SBcl2 and SK-MEL-5 cell lines transfected with GST vector (control) or GST-B-RafV600E plasmids. Data were collected from 500 interphase cells per condition. Bar, 5 μm or 2 μm (inset).

Selective knockdown of B-RafV600E mutant reduces the incidence of mitotic abnormalities. To determine whether the mitotic abnormalities are dependent on the continued expression of the B-RafV600E mutant, a mutant-specific shRNA (pSUPER-Mut-A) was used to selectively knock down B-RafV600E levels while keeping endogenous wild-type B-Raf levels intact, as previously shown (17). SBcl2 cells selected to contain the B-RafV600E mutant were subsequently infected with pSUPER-Mut-A retrovirus, which, after 48 hours, effectively reduced B-Raf and phospho-ERK to levels comparable to that of parental SBcl2 cells (Fig. 3A). Under these conditions, a substantial reduction in amplified centrosomes (Fig. 3B) and abnormal spindles (Fig. 3C) was detected compared with B-RafV600E-expressing cells. Finally, we showed that the mitotic delay induced by the B-RafV600E mutant (30), as indicated by an increase in prometaphase cells and

Figure 2. B-RafV600E promotes centrosome amplification in melanoma cells. The B-RafV600E mutant or control vectors were introduced into SBcl2 and SK-MEL-5 cells as described in the legend to Fig. 1. Both melanoma cell lines were subjected to γ-tubulin immunostaining (green) to assess centrosome numbers in interphase cells. DNA (blue) of nuclei was visualized by DAPI staining. A, microscopy images of centrosomes detected during interphase in SBcl2 cells infected with pBabe (empty vector) or B-RafV600E-containing retroviruses. B, quantitation of centrosome numbers in SBcl2 cells. C, microscopy images of centrosomes detected during interphase in SK-MEL-5 cells transfected with GST vector (control) or GST-B-RafV600E plasmids. D, quantitation of centrosome numbers detected in SK-MEL-5 cells. Data were collected from 500 interphase cells per condition. Bar, 5 μm or 2 μm (inset).
a decrease in anaphase cells, was relieved in cells treated with the B-Raf-mutant shRNA (Fig. 3D, compare B-Raf<sup>V600E</sup> +/− Mut-A shRNA). Together, we conclude that persistent expression of the B-Raf<sup>V600E</sup> mutant is critical to sustain centrosome amplification, mitotic delay, and spindle abnormalities in Sbcl2 cells.

**Mitotic abnormalities are prevalent in melanoma cells harboring B-Raf<sup>V600E</sup> mutations.** We extended our analysis of mitosis to melanoma cell lines that harbor endogenous B-Raf<sup>V600E</sup> mutations (A375, SK-MEL-28, and WM1205). Interestingly, high frequencies (70–85%) of abnormal spindle morphologies and misaligned chromosomes were observed in all three B-Raf mutant melanoma cell lines but not in parental Sbcl2 and SK-MEL-5 cells (Fig. 4A–C). Of the mitotic figures in the B-Raf mutant melanoma cell lines, 28% to 38% exhibited multipolar spindles associated with extra (>2) centrosome numbers (Fig. 4C). Furthermore, knockdown of mutant B-Raf by shRNA greatly diminished the presence of supernumerary centrosomes and abnormal spindles, especially multipolar spindles, in all three melanoma cell lines (see Fig. 4C and Supplementary Fig. S3), indicating that its expression is important to sustaining these mitotic abnormalities.

To determine whether the mitotic abnormalities induced by the B-Raf<sup>V600E</sup> mutant were exerted through the MEK–MAPK pathway, we treated various melanoma cells with the MEK-specific inhibitor U0126, which led to the inhibition of ERK activity (Supplementary Fig. S4A). After 24 hours, mitotic cells were analyzed for spindle abnormalities and supernumerary centrosomes in the presence or absence of U0126. Treatment of B-Raf<sup>V600E</sup> mutant-expressing cells with U0126 resulted in a marked reduction in supernumerary centrosomes and multipolar spindles while partially restoring normal mitotic spindles (Fig. 4D; Supplementary Fig. S4). However, irregular spindle structures (20–28% range) were only modestly reduced (~50%) in some of the MEK-inhibited melanoma cells (A375, SK-MEL-28, and WM1205) examined, consistent with the role for MAPK activity in regulating proper spindle formation (5). Interestingly, monopolar-like spindle structures were detected in parental and B-Raf<sup>V600E</sup>-expressing cells treated with U0126 (Supplementary Fig. S4B and C). Taken together, our results suggest that persistent expression of the B-Raf<sup>V600E</sup> mutant and its activation of MAPK are critical for promoting and maintaining mitotic spindle abnormalities in melanoma cells.

**B-Raf<sup>V600E</sup> induces chromosome mis-segregation and aneuploidy in human melanoma cells.** To determine whether the spindle abnormalities induced by oncogenic B-Raf give rise to chromosome segregation errors, we examined later stages (anaphase/telophase) of mitosis. In contrast to vector control cells, expression of the B-Raf<sup>V600E</sup> mutant in either Sbcl2 or SK-MEL-5 cells resulted in a high frequency of chromosome segregation anomalies, including lagging chromosomes and chromosome bridges (Supplementary Fig. SS4A–C). Similar observations were made in A375 and SK-MEL-28 melanoma cell lines, both of which carry an activating B-Raf<sup>V600E</sup> mutation (Supplementary Fig. SS4A, D, and E).

It stands to reason that the high incidence of chromosome mis-segregation observed in the B-Raf<sup>V600E</sup> mutant expressing cells would result in aneuploidy. To test for this directly, chromosome counts on metaphase spreads were done from vector control or B-Raf<sup>V600E</sup>-expressing Sbcl2 cells. A mode of 46 chromosomes was observed for vector control Sbcl2 cells (Fig. 5B, top graph), indicating that most of the cells in culture are diploid. In contrast, ectopic expression of B-Raf<sup>V600E</sup> in Sbcl2 cells, confirmed by Western blot analysis (Fig. 5A), resulted in the absence of a chromosome mode and a wider distribution of chromosome counts (15–87 chromosomes) compared with vector control cells (Fig. 5B, bottom graph). A representative chromosome spread from vector control (46 chromosomes) or B-Raf<sup>V600E</sup> mutant (40 chromosomes)
SBcl2 cells is shown alongside of the graphs (Fig. 5B). As a second approach to assess for aneuploidy, interphase FISH analysis was done on nuclei of SBcl2 cells using probes specific to chromosome 2 or 8 (Fig. 5C). A low percent of nuclei (5.5% for chromosome 2 and 9.5% for chromosome 8 probes) in vector control SBcl2 cells scored positive for aneuploidy, which is expected for an established cell line. However, the incidence of aneuploidy was markedly increased for each chromosome probe in the B-Raf V600E mutant–expressing SBcl2 cells (Fig. 5C). Based on low P values from data obtained with either chromosome probe, the increase in aneuploidy for B-RafV600E–SBcl2 cells compared with the background for controls was determined to be statistically highly significant (see Fig. 5 legend). Taken together, we conclude that B-RafV600E induces aneuploidy in SBcl2 cells.

B-RafV600E drives aneuploidy in human melanocytes and mammary epithelial cells. To determine whether B-RafV600E is sufficient to induce aneuploidy in a nontransformed
background, we extended these studies to primary human melanocytes and hTERT-immortalized human mammary epithelial 1 (HME1s) cells. B-RafV600E was introduced into hTERT-HME1s or human melanocytes and, 96 hours later (the equivalent of two population doublings), subjected to interphase FISH analysis. A low background (4–10%) of aneuploidy was scored in nontransfected and vector (control) cells, with the majority of these cells showing the expected two signals for each chromosome probe. Strikingly, a high frequency of aneuploidy was scored in nuclei of either hTERT-HME1s or human melanocytes transfected with B-RafV600E (Fig. 6A and B). In addition, many of the nuclei of cells transfected with B-RafV600E exhibited abnormal morphology, consistent with aneuploidy, whereas control cells contained normal round-shaped nuclei. Hence, we conclude that oncogenic B-RafV600E is sufficient to induce aneuploidy in both primary human melanocytes and immortalized epithelial cells.

**Discussion**

Previous work from our laboratory showed normal mitotic functions for B-Raf in human somatic cells (4) as well as a causal role for oncogenic B-RafV600E in promoting hyperactivation of the SAC (30). In this study, we showed that constitutive B-RafV600E signaling abrogates mitosis in human melanoma cells. In particular, B-RafV600E induced pleiotropic spindle abnormalities, supernumerary centrosomes, and chromosome mis-segregation resulting in aneuploidy. The

**Figure 5.** Exogenous B-RafV600E expression drives aneuploidy in SBcl2 melanoma cells. SBcl2 cells infected with pBabe puro (empty vector) or B-RafV600E retroviruses were selected under puromycin (1 μg/mL) for 10 to 12 d. Chromosome counts on metaphase spreads and interphase FISH analysis were done at 2 wk after infection. A, Western blot analysis of cell lysates prepared from control (empty vector) or B-RafV600E–expressing SBcl2 cells. B, percent distribution of chromosome numbers obtained from at least 50 metaphase spreads. Representative photos of metaphase spreads from vector control and B-RafV600E–expressing SBcl2 cells. Chromosomes were stained with DAPI and imaged at ×60 magnification. C, percent nuclei that scored positive for aneuploidy by FISH analysis with probes to chromosome 2 or 8. Two hundred nuclei were analyzed from empty vector or B-RafV600E SBcl2 cells. P < 0.001 and P < 0.005 for chromosomes 2 and 8, respectively, suggesting that the increase in aneuploidy in B-RafV600E–expressing SBcl2 is statistically highly significant. Photos show signals produced from FISH analysis using probes specific to chromosome 2 (red) and chromosome 8 (green). Yellow arrows in V600E mutant cells point to nuclei positive for aneuploidy.
persistence of these mitotic abnormalities was found to be dependent on continued expression of the B-RafV600E mutant and its constitutive activation of the MEK/MAPK pathway. Consistent with our findings, human melanoma cells carrying endogenous B-RafV600E mutations were also found to contain similar mitotic abnormalities, implying that our results from ectopic expression of the B-RafV600E mutant are physiologically relevant.

Centrosome amplification was generally not observed in parental SBcl2 and SK-MEL-5 cells but was readily observed in melanoma cells containing endogenous activating B-Raf mutations or on introducing the B-RafV600E mutant into SBcl2 or SK-MEL-5 cells (Figs. 1, 2, and 4). Although the mechanism through which the B-RafV600E mutant induces centrosome amplification is not understood, one possibility involves p53 because abnormal centrosome amplification is often associated with impaired p53 function in human cancer (27). Therefore, we examined the p53 DNA damage response in SBcl2 and SK-MEL-5 cells. Induction of p53 and its target p21 following irradiation treatment appeared to be normal (Supplementary Fig. S6), indicating that the effects of oncogenic B-RafV600E signaling on centrosome amplification are not dependent on the concomitant loss of function of the p53 tumor suppressor. In addition, ectopic expression of B-RafV600E had little to no effect on p53 protein or phosphorylation (Ser15 and Ser20 residues) levels (Supplementary Fig. S7). This would suggest that other factor(s) acting in concert with or downstream of oncogenic B-Raf signaling are responsible for bringing about abnormal centrosome amplification in melanoma cells.

MAPK activity was found to be important for maintenance of centrosome amplification in melanoma cells (Fig. 4D; Supplementary Fig. S4). Impressively, the incidence of supernumerary centrosomes in B-RafV600E-expressing melanoma was rapidly reduced within 24 hours following treatment with the MEK inhibitor U0126. Yun and colleagues (32) showed similar effects on reducing amplified centrosomes in cells treated with the MEK inhibitor PD98059. We speculate that a rapid reduction in amplified centrosomes by MEK inhibition could be a consequence of centrosome duplication being suppressed in the absence of MAPK activity. Indeed, monopolar spindles containing a single centrosome were observed specifically in U0126-treated melanoma cells (see Supplementary Fig. S4), implying a possible role for MAPK activity in centrosome duplication in melanoma cells. Alternatively, cells containing supernumerary centrosomes may exhibit a higher

Figure 6. B-RafV600E induces aneuploidy in hTERT-HME1s and primary human melanocytes. B-RafV600E or empty vector plasmids were transfected into early-passage hTERT-HME1s or primary human melanocytes with a transfection efficiency of ∼90% (see Materials and Methods). Interphase FISH analysis was done using probes to chromosome 3 (red) and chromosome 10 (green). A, percent aneuploidy detected for individual chromosome probes in nontransfected (no TF), vector alone (Empty), and B-RafV600E (V600E) hTERT-HME1 cells. Note that ∼40% of nuclei scored positive for aneuploidy with either probe. B, percent aneuploidy detected for individual chromosome probes in nontransfected, vector alone–transfected, and B-RafV600E–transfected human melanocytes. Note that 44% of nuclei scored positive for aneuploidy with either probe. Representative photos from FISH analysis for hTERT-HME1 cells and human melanocytes are shown below each graph. FISH analysis was calculated from at least 200 nuclei. All results are representative of three independent experiments.
Consistent with overexpression of B-RafV600E causing aneuploidy in SMC12 cells, melanoma cells with endogenous activating B-Raf mutations (A375 and SK-MEL-28 cells) also scored positive for aneuploidy (Supplementary Fig. S8). Thus, our studies suggest a novel link between oncogenic B-RafV600E and aneuploidy in melanoma. Although activating B-Raf mutations are found in 60% to 70% of cutaneous melanomas, alterations in chromosomal numbers are typically detected in 95% of primary and metastatic melanomas (33–35), suggesting that other genetic mutations (independent of B-Raf mutations) can contribute to aneuploidy in melanoma. For instance, activating N-Ras mutations are detected in 18% to 22% of human melanomas (36, 37) and may also have a causal role in promoting aneuploidy. Indeed, it has been known for some time that activated Ras is associated with chromosome instability in human cancer (38, 39). Interestingly, acute expression of H-RasV12 in thyroid PCCL3 cells was shown to promote centrosome amplification and defects in spindle checkpoint regulation (40, 41). However, in contrast to the spindle checkpoint effects mediated by oncogenic B-Raf in melanoma cells (30), H-RasV12 was shown to accelerate mitotic progression by overriding the SAC in a MAPK-independent manner (40). Finally, it has been shown that gene copies of cyclin-dependent kinase 4 or cyclin D (CCND1), downstream effectors of the MAPK pathway, are amplified in melanomas (42, 43) and may contribute to cell cycle defects that feed into mitotic dysfunction.

A large proportion (~82%) of benign nev Harboractivating B-Raf mutations (44), lending to the idea that B-Raf activation is an early and critical step in the development of melanocytic neoplasia. Whereas genetic evidence supports an early role for B-RafV600E in nevus formation (45), sustained B-RafV600E activity is also associated with oncogene-induced senescence (46, 47), explaining why most nevi never develop into invasive melanomas and remain dormant over long periods of time. Then, how do melanocytes harboring activated B-RafV600E mutations progress to neoplasia? The results from our study show that oncogenic B-RafV600E is sufficient to rapidly induce aneuploidy in primary human melanocytes (Fig. 6A) and raise the possibility that random mitotic errors may occur during early nevus formation. Although mitotic errors in most cells would lead to mitotic catastrophe or cell death, we speculate that induction of aneuploidy in proliferating melanocytes could allow for additional genetic changes to occur, which, if tolerated, might contribute to melanoma initiation. This would be in line with several reports showing that additional mutations in melanoma susceptibility genes (i.e., p16INK4a, ARF, and PTEN) cooperate with oncogenic B-Raf (or Ras) to allow for melanoma initiation (see review in ref. 46).

In summary, our work shows for the first time a link between the B-Raf oncogene and chromosome instability in melanoma that is explained, in part, by the ability of B-RafV600E to induce spindle abnormalities and supernumerary centrosomes. These findings have important implications for understanding the mechanisms that drive the development and progression of melanoma and may aid in developing effective therapeutic interventions that target Raf signaling and mitosis.

Disclosure of Potential Conflicts of Interest

No potential conflicts of interest were disclosed.

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