An Animal Model of MYC-Driven Medulloblastoma


Summary

Medulloblastoma (MB) is the most common malignant brain tumor in children. Patients whose tumors exhibit overexpression or amplification of the MYC oncogene (c-MYC) usually have an extremely poor prognosis, but there are no animal models of this subtype of the disease. Here, we show that cerebellar stem cells expressing Myc and mutant Trp53 (p53) generate aggressive tumors following orthotopic transplantation. These tumors consist of large, pleiomorphic cells and resemble human MYC-driven MB at a molecular level. Notably, antagonists of PI3K/mTOR signaling, but not Hedgehog signaling, inhibit growth of tumor cells. These findings suggest that cerebellar stem cells can give rise to MYC-driven MB and identify a novel model that can be used to test therapies for this devastating disease.

Introduction

Medulloblastoma (MB) is a highly malignant tumor of the cerebellum that occurs most frequently in children between 5 and 10 years of age (Polkinghorn and Tarbell, 2007). Current treatment for MB includes resection of the tumor followed by radiation and high-dose chemotherapy. Although this has resulted in significant increases in survival, approximately one-third of MB patients still die from their disease. Moreover, survivors often suffer severe side effects, including dramatic losses in cognitive function, endocrine disorders, and increased susceptibility to secondary tumors (Palmer et al., 2007; Stavrou et al., 2001). Thus, more effective and less toxic therapies for MB are desperately needed.

Traditionally, MB has been classified based on histological characteristics. In this context, tumors with large-cell-anaplastic...
and the fact that high MYC levels are associated with poor clinical outcome (Cho et al., 2011; Grotzer et al., 2001) suggest that MYC might play a key role in the biology of MB. But while the association between MYC and poor prognosis is well established, it remains unclear whether the gene is involved in tumor initiation, maintenance, or progression. Likewise, MYC-driven tumors frequently exhibit loss of one allele of the TP53 tumor suppressor (in the context of isochromosome 17q) (Northcott et al., 2011; Pfister et al., 2009), and LCA tumors have been reported to express high levels of p53 protein, an indicator of dysregulation of the TP53 pathway (Eberhart et al., 2005; Frank et al., 2004). However, it is not clear whether alterations in TP53 represent causal events.

Animal models of brain tumors can be generated by targeting expression of oncogenes to neural progenitors or stem cells. Recent studies suggest that different populations of progenitors may be susceptible to transformation by distinct signaling pathways (Gilbertson and Ellison, 2008). For example, mutations in the SHH pathway promote transformation of granule neuron precursors (GNPs) in the external germinal layer of the cerebellum (Schüller et al., 2008; Yang et al., 2008), whereas dysregulation of WNT signaling causes transformation of progenitors in the lower rhombic lip and embryonic dorsal brainstem (Gibson et al., 2010). We recently identified a population of stem cells in the white matter of the postnatal cerebellum (Lee et al., 2005) and hypothesized that they might give rise to some types of MB. To test this hypothesis, and to address the functional importance of MYC and TP53 in MB, we examined the effects of overexpressing MYC and disrupting p53 function in these cells.

RESULTS

Myc Promotes Proliferation of Cerebellar Stem Cells In Vitro
Stem cells can be isolated from the postnatal cerebellum based on expression of Prominin1 (CD133) and lack of neuronal and glial lineage markers (Prom1+Lin−). To investigate the effects of MYC on these cells, we infected them with control retroviruses or viruses encoding a stabilized form of MYC (MycT58A) (Chang et al., 2000) and measured their proliferation. As shown in Figure 1A, Myc-infected cells showed a 2.5-fold increase in proliferation compared to cells infected with control viruses. To examine the effects of MYC on self-renewal, infected Prom1+ Lin− cells were cultured at low density (2000 cells/ml) in the presence of basic fibroblast growth factor (bFGF) and epithelial growth factor (EGF) to promote neurosphere formation. As shown in Figures 1B–1D, the number of neurospheres in Myc-infected cultures was 9-fold higher than that in control cultures. To determine whether the effects of MYC persisted in longer-term cultures, neurospheres were dissociated into single-cell suspensions and replated every 7 days. Over the course of 5 weeks, Myc-infected cultures exhibited a 1000-fold increase in cell number, compared to a 2-fold increase in control cultures (Figure S1 available online). These data indicate that overexpression of MYC in cerebellar stem cells promotes short-term proliferation, as well as long-term self-renewal in vitro.

Figure 1. Myc Promotes Proliferation of Cerebellar Stem Cells In Vitro
(A) Prom1+Lin− cells sorted from cerebella of 5- to 7-day-old mice were infected with Myc-IRE-EGFP or control (GFP only) viruses for 48 hr, pulsed with tritiated thymidine (³H-Td), and cultured overnight before being assayed for ³H-Td incorporation. Data represent the mean ± SEM of triplicate samples. (B–D) Prom1+Lin− cells infected with Myc-IRE-EGFP or control viruses were cultured at low density in the presence of EGF and bFGF for 7 days. Representative fields are shown in (C) and (D) (scale bars = 100 μm). The number of GFP+ neurospheres is quantified in (B); data represent the mean ± SEM of triplicate samples. The infection efficiency was 80% with Myc-IRE-GFP and 90% with control retrovirus.

See also Figure S1.
Figure 2. Myc-Infected Stem Cells Give Rise to Transient Hyperplastic Lesions following Transplantation

(A–F) Prom1+Lin− cells were infected with Myc-ires-GFP or control retrovirus for 20 hr and then transplanted into the cerebella of NSG mice. Hosts were sacrificed after 2.5 weeks. Frozen sections from mice that received GFP-infected (A and B) or Myc-infected (C–F) cells were stained with anti-Ki67 antibodies (A–D) or H&E (E and F). Note the large mass of proliferating (Ki67+) cells seen in animals that received Myc-infected cells (C and D). The box in (E) corresponds to the high-power field shown in (F). Scale bars = 50 μm (A–D and F) and 100 μm (E).

(G and H) Prom1+ cells were infected with Myc-IRES-GFP or control-GFP viruses for 20 hr and then transplanted into the cerebella of NSG hosts. Mice were sacrificed after 2 weeks. Frozen sections from mice that received control (G) or Myc-infected cells (H) were stained with antibodies specific for cleaved caspase-3 (CC3) to detect apoptotic cells. Scale bars = 50 μm.

See also Figure S2.

Myc-Expressing Stem Cells Form Transient Hyperplastic Lesions In Vivo

In light of the above results, we investigated whether Myc-expressing cells could give rise to tumors in vivo. We stereotaxically implanted control (GFP virus-infected) or Myc-infected stem cells into the cerebella of immunocompromised (NOD-SCID-IL2Rγnull) or NSG mice and examined cerebella of recipients 2–3 weeks later. As shown in Figures 2A and 2B, in animals that had received control cells, few infected cells (marked by GFP) could be detected, and only a small proportion of these were proliferating (based on Ki67 staining). In contrast, in animals transplanted with Myc-expressing cells, large masses of infected cells could be detected, and the majority of these were proliferating (Figures 2C–2F). These results suggest that Myc-infected cells can undergo persistent proliferation in vivo.

To determine whether Myc-infected cells can continue to grow and give rise to tumors, we sacrificed animals (n = 5) four weeks after transplantation. Surprisingly, at this stage, few transplanted cells could be detected in the cerebella of mice that had received either control or Myc-infected cells. Consistent with this, we followed a cohort of mice (n = 6) transplanted with Myc-infected cells for 6 months, and found that none of them developed symptoms during this period (data not shown). This suggested that Myc can drive proliferation of stem cells, but is not sufficient to promote tumor growth.

The fact that Myc-infected cells formed large masses 2 weeks after transplantation but were undetectable 4 weeks after transplantation raised the question of what happened to these cells. Since Myc can induce apoptosis as well as proliferation (Pelen et al., 2000), we examined cerebella from recipients of control and Myc-infected cells for evidence of apoptosis by staining with anti-cleaved caspase 3 (CC3). Few control virus-infected cells were labeled with anti-CC3 (although some staining was seen around the transplant site), whereas Myc-infected cells exhibited a significant amount of CC3 staining (Figures 2G and 2H), suggesting that they were undergoing apoptosis in situ. These data suggest that Myc promotes proliferation as well as apoptosis of cerebellar stem cells.

Mutant p53 Synergizes with Myc to Promote Tumor Formation

Myc-induced apoptosis is frequently dependent on TP53 (Heremek and Eick, 1994). To test whether inactivation of p53 could inhibit Myc-induced cell death in cerebellar stem cells, we measured apoptosis in cells infected with control (GFP), Myc, dominant-negative p53 (DNp53) (Bowman et al., 1996), or Myc + DNp53 viruses. As shown in Figures S2A–S2D, cells infected with Myc viruses alone exhibited a marked increase in apoptosis compared to cells infected with control viruses (Figures S2A and S2B), but DNp53 completely abolished the proapoptotic effects of Myc (Figures S2C and S2D). These results suggest that Myc-mediated apoptosis of stem cells can be blocked by inhibition of p53 function.

The above findings raised the possibility that cells overexpressing Myc and DNp53 might be able to give rise to tumors. To test this, we coinfected stem cells with viruses encoding these genes and implanted them into the cerebella of NSG mice. Animals transplanted with cells coexpressing the two genes developed highly aggressive tumors and had to be sacrificed at 6–12 weeks (Figures 3A and 3B). These experiments were performed using the T58A mutant of Myc. Notably, stem cells infected with WT Myc + DNp53 also gave rise to tumors, albeit with reduced penetrance (33%) and longer latency (15–20 weeks). These studies suggest that mutant p53 can cooperate with Myc to promote transformation of cerebellar stem cells.

We characterized tumors arising from stem cells infected with Myc and DNp53 (MP tumors), using tumors from Ptc1 mutant mice (a model for SHH-associated MB) for comparison (Figures 3C–3H). Whereas Ptc1+/− tumor cells were not much bigger...
Previous studies have suggested that SHH-associated MB can be initiated in GNPs or neural stem cells (Schüller et al., 2008; Yang et al., 2008). We therefore determined whether GNPs could also be transformed by Myc and DNp53. To test this, we FACScsort GFP⁺ cells (GNPs) from neonatal Math1-GFP transgenic mice (Lee et al., 2005; Lumpkin et al., 2003) (Figures S4A and S4B), infected these cells with Myc and DNp53 viruses, and then transplanted them into the cerebellum of NSG mice. We found that 7 out of 22 recipients developed tumors, with a latency of 108 days (Figures S4D–S4F). Interestingly, although the cells were GFP⁺ prior to transplantation (Figure S4B), the tumors that developed from them were no longer GFP⁺ when analyzed by microscopy or flow cytometry (Figures S4C and S4E), suggesting that they had lost a key marker of the granule lineage during the course of transformation. These studies demonstrate that both stem cells and GNPs can give rise to MYC-driven tumors.

**Myc Is Required to Maintain MP Tumor Growth**

In many tumors driven by MYC, shutting off the expression of MYC results in tumor regression (Jain et al., 2002; Soucek et al., 2008). To determine whether MP tumors continue to depend on Myc once they are established, we infected stem cells with viruses encoding a tetracycline-inducible form of Myc (Lee et al., 2008). Animals were fed doxycycline (DOX)-containing food until they developed tumors (3–4 weeks after transplantation). Tumors were removed, dissociated, and retransplanted into cerebella of naive NSG mice. Secondary recipients were separated into three groups: Group 1 (n = 14) was maintained on DOX-containing food; Group 2 (n = 14) was fed DOX-containing food for 1 week, then switched to normal food; and Group 3 (n = 12) was fed food without DOX (Figure 5A). Animals in all groups developed bioluminescent signals from the luciferase encoded by the DNp53 virus, indicating the presence of transplanted tumor cells. Group 1 animals...
showed a rapid and dramatic increase in bioluminescence (Figure 5B, top graph), and by 3-4 weeks after transplantation, all mice had developed symptoms and had to be sacrificed (Figure 5F). Analysis of brains from these mice revealed large tumors in every animal (Figure 5C). In contrast, bioluminescence in Group 2 and Group 3 mice decayed in the absence of DOX (Figure 5B, bottom two graphs). Moreover, no tumors could be detected in these animals 3 weeks after transplantation (Figures 5D and 5E), and animals remained asymptomatic at 6 weeks (Figure 5F). Together these data suggest that Myc is not only necessary for tumor initiation but is also required to maintain growth of MP tumors.

MP Tumors Resemble Human MYC-Driven MB

Our histological analysis indicated that MP tumors resemble human LCA MB. Since LCA histology is more common in MYC-driven tumors (Cho et al., 2011; Northcott et al., 2011), this supported the notion that MP tumors might represent a model for human MYC-driven MB. To test whether MP tumors resembled human MYC-driven MB at a molecular level, we performed gene expression analysis of MP tumors and compared the resulting gene expression profiles with profiles of the four subtypes of human MB (WNT, SHH, Group C, and Group D) defined by Northcott et al. (2011). In this classification scheme, Group C tumors, which are associated with the poorest prognosis, frequently exhibit amplification or overexpression of MYC (Northcott et al., 2011). Using genes differentially expressed in each subgroup and previously published methods (Bild et al., 2006), we identified four sets of genes (“subgroup signatures”) whose expression accurately predicted the subgroup of the human MB samples (see Human Tumor Analysis in the Supplemental Information).

Human MB subgroup signatures were then applied to gene expression data from murine MP and Ptc1 mutant tumors, with each tumor receiving a subgroup signature score representing its similarity to each subgroup of human MB. As shown in Figure 6A and Table S1, murine Ptc1 tumors most closely resembled human SHH-associated tumors, with one exception, which possessed a profile consistent with both the WNT and SHH groups. In contrast, MP tumors were most similar to Group C/D tumors, with the exception of a tumor that resembled both the WNT and Group C/D signatures. To validate these findings, we compared data from murine tumors to expression profiles from a distinct set of human MB samples (Cho et al., 2011). Utilizing a subclass mapping algorithm (Hoshida et al., 2007), we generated a similarity metric between MP tumors and the MB subgroups defined in Cho et al. (2011). As shown in Figure S5, this analysis revealed a high degree of similarity between MP tumors and the ‘c1’ subtype of human MB, which is characterized by copy number gains of c-MYC and gene expression signatures indicative of robust MYC transcriptional activity (Cho et al., 2011).

Finally, we stained an independent set of MP and Ptc1 tumors with antibodies that have been found to mark each of the four human MB subgroups (Northcott et al., 2011). Murine Ptc1 mutant tumors expressed high levels of the SHH-subgroup marker SFRP1 (Figure 6B) and lacked expression of the WNT-subgroup marker nuclear CTNNB1 (not shown), the Group C marker NPR3 (Figure 6C), and the Group D marker KCNA1 (Figure 6D). In contrast, MP tumors exhibited high levels of NPR3 (Figure 6F) and lacked expression of the other markers (Figures 6E and 6G and data not shown). Together, these data suggested that MP tumors resemble human Group C (MYC-driven) MB.

Gene Expression Profile of MP Tumors

We compared the gene-expression profiles of MP tumors to those of freshly isolated cerebellar stem cells and tumors from Ptc1 mutant mice. Using principal component analysis, an unsupervised approach designed to group samples based on their similarity in gene expression, we determined that MP tumors generated by infection of Prom1-Line stem cells and those generated by infection of Prom1-L1 cells were indistinguishable based upon global RNA expression (Figure 7A). Both of these tumor types were distinct from normal (uninfected)

Figure 4. MP Tumors Exhibit Characteristics of Human MB
Cryosections from MP tumors were stained with H&E (A) or with antibodies specific for Ki67 (B), Nestin (C), Tuj1 (D), GFAP (E), or BAF47/Ini1 (F). Images in (A)–(E) represent adjacent sections. Scale bars = 50 μm. See also Figure S4.
To learn about the functional significance of these genes, we analyzed them using gene set enrichment analysis (GSEA) (Subramanian et al., 2005) and NextBio software (Kupershmidt et al., 2010) (see Figure 7 and Table S4 and Table S5). Several important correlations emerged from this analysis. First, we noted that genes expressed at high levels in MP tumors were similar to those found to be targets of MYC in other studies (Figure 7C, Table S4 and Table S5). Another set of differentially expressed genes, which exhibited decreased expression in MP tumors, were targets of forkhead transcription factors (e.g., Foxo1) (Figure 7D). This is notable, because FOXO proteins often inhibit expression of MYC targets, induce expression of MYC antagonists, and suppress MYC-induced transformation (Bouchard et al., 2004, 2007; Delpuech et al., 2007). We also noted a marked similarity between genes expressed in MP tumors and those from cerebellar stem cells and from Ptch1 mutant tumors. Hierarchical clustering (Figure 7B) confirmed the similarity between MP tumors generated from Prom1+Lin− and Prom1+ cells, as well as the differences between these tumors, Ptch1 tumors, and normal stem cells. Focusing on changes in gene expression of 3-fold and higher (p-value with FDR correction < 0.0001), we identified 1228 genes (1465 probe sets) that were differentially expressed between MP tumors and Ptch1 tumors (Comparison A, Table S2), and 812 genes (955 probe sets) differentially expressed between MP tumors and normal stem cells (Comparison B, Table S3).

Figure 5. Myc Is Required for Continued Growth of MP Tumors
(A) Strategy for generating Tet-regulatable MP tumors.
(B–F) Bioluminescent imaging of animals at 1, 2, and 3 weeks after tumor cell transplantation. (B) Representative images of four animals from each group at each time point (X’s denote animals that died before they could be imaged). Graphs at right show the mean percent increase in bioluminescence for all animals in the group (with the 1-week signal for each animal set at 100%). In the top graph, the 1- and 2-week time points represent the average signal intensity for all 14 animals; the 3-week time point (marked by an asterisk) represents the average for the three animals that remained alive at the time of imaging. (C–E) H&E-stained cerebellar sections from representative animals in Groups 1 (C), 2 (D), and 3 (E) 3 weeks after transplantation. Arrows in (D) and (E) point to the injection site. Scale bars = 250 μm. (F) Survival curve (Groups 1 and 2, n = 14; Group 3, n = 12).
enriched in embryonic stem (ES) cells and induced pluripotent stem (iPS) cells, including those induced by Oct4 and Klf4 (i.e., in the absence of exogenous Myc) (Figure 7F). These genes were enriched in MP tumors compared to Ptc1 tumors, consistent with the fact that the former are derived from stem cells and the latter originate from lineage-restricted neuronal progenitors. However, they were also enriched in MP tumors compared to cerebellar stem cells, suggesting that MP tumors have adopted a more primitive differentiation state than the cells from which they were derived. In support of this notion, MP tumors showed decreased expression of genes associated with neuronal lineage commitment and differentiation (Figure 7E). Finally, our analysis revealed significant enrichment of a PI3K signaling gene set, as well as a set of genes downregulated by rapamycin in another cancer cell line (Table S4 and Table S5). Notably, analysis of human MYC-driven (Group c1) tumors using Connectivity Map (CMAP), an algorithm that screens a given gene expression signature against a compendium of drug-induced gene expression signatures (Lamb et al., 2006), suggested that genes regulated by PI3K and mTOR inhibitors are also enriched in these tumors (Table S6). These observations, and the fact that MP tumors have decreased expression of Foxo targets, which are negatively regulated by the PI3K pathway, suggested that this pathway might play an important role in tumor growth.

**MP Tumors Are Sensitive to Inhibitors of PI3 Kinase and mTOR**

To determine whether MP tumors were dependent on PI3K/mTOR signaling, we first tested the effects of PI3K/mTOR inhibitors on tumor cell growth in vitro (Figure 8A). MP tumors showed complete growth inhibition in the presence of 1–5 μM BEZ-235 (an antagonist of both PI3K and mTOR) and 5 μM BKM-120 (an antagonist of PI3K), and partial inhibition in the presence of lower concentrations of these compounds. The mTOR antagonist RAD-001 also inhibited growth, albeit incompletely, at concentrations of 0.2–5 μM. Consistent with their continued dependency on Myc, tumor cells were dramatically inhibited by 10058-F4, a small molecule that interferes with Myc-Max dimerization (Huang et al., 2006). In contrast, we found that MP tumor cells showed no growth inhibition in response to the SHH antagonist cyclopamine.

To determine whether BEZ-235 and BKM-120 could also affect long-term tumor cell growth, we cultured MP tumor cells for 3, 7, or 14 days in the presence of these inhibitors, and counted cell number at each time point. We found that all three doses of BEZ-235 inhibited cell growth, whereas only the highest concentration of BKM-120 (5 μM) was able to cause growth inhibition (Figure 7B). Similar results were observed when we used neurosphere assays to measure tumor cell clonogenicity (Figure S6).

To confirm that these compounds were acting on the PI3K/mTOR pathway, we performed western blotting to analyze phosphorylation of critical proteins in the pathway. As shown in Figure 8C, MP tumor cells showed substantial amounts of phospho-AKT and phospho-S6 in the absence of inhibitors (DMSO lanes). Treatment with BEZ-235 or BKM-120 inhibited phosphorylation of both AKT and S6. In contrast, RAD-001 inhibited S6 phosphorylation but did not affect phospho-AKT. The fact that BEZ-235 and BKM-120 were more potent inhibitors of tumor cell proliferation than RAD-001 (Figures 8A and 8B) suggested that blocking activity of PI3K, or both PI3K and mTOR, might be required for effective tumor inhibition.

To determine whether inhibition of PI3K/mTOR signaling could also inhibit growth of MP tumors in vivo, we isolated MP tumor cells and transplanted them into naive NSG mice. After 7 days, we began treating animals with BKM-120 once daily until clinical signs of tumor formation were observed. Animals treated with BKM-120 survived significantly longer than controls (median...
survival = 35 versus 25 days) (Figure 8D). These results suggest that inhibitors of PI3K/mTOR signaling might be useful for treatment of MYC-driven MB.

DISCUSSION

MYC-driven MB is a highly malignant pediatric brain tumor that is often resistant to conventional radiation and chemotherapy. More effective approaches to treat this disease are critical, and these can be facilitated by the development of robust animal models. The fact that a subset of human MBs exhibit amplification or overexpression of MYC prompted us to develop a mouse model that can be used to investigate the biology of, and test therapies for, MYC-driven MB.

Cooperation between Myc and Mutant p53

Our observation that Myc induces proliferation of cerebellar stem cells is consistent with previous reports showing mitogenic

Figure 7. MP Tumors Are Molecularly Distinct from Stem Cells and from 
Ptch1 Tumors

(A) Principal component analysis (PCA). Three PCA coordinates describe 55.2% of the total data variation (PC1, 27.2%; PC2, 19.8%; and PC3, 8.23%). Green, MP tumors derived from Prom1+Lin- cells; purple, MP tumors derived from Prom1+ cells; blue, Ptch1 tumors; red, normal stem cells (NSCs).

(B) Unsupervised hierarchical clustering analysis. Each column represents a distinct sample and each row represents an individual gene. The normalized (log2) and standardized (each sample to mean signal = 0 and standard deviation = 1) level of gene expression is denoted by color (green, low; dark, intermediate; red, high), as indicated in the gradient at the bottom.

(C–F) Genes differentially expressed between MP tumors and Ptch1 tumors (Comp A) were subjected to NextBio analysis, to identify biogroups and studies (biosets) that contain similar genes. Representative biogroups (C–E) and studies (F) are shown. Venn diagrams show the number of common and unique genes in both sets. Bars at right show the significance of overlap between gene subsets (the scale of the bar is measured in −log(p-value), so the taller the bar, the higher the significance of the gene overlap). Whereas each biogroup is represented by a single list of genes, signature genes from studies have two lists, one for upregulated and one for downregulated genes. Thus, biogroup comparisons consist of just two graphs, whereas comparisons of studies consist of four graphs. See also Tables S2–S6.
effects of Myc in normal and malignant stem cells (Nagao et al., 2008; Wang et al., 2008). However, while Myc can promote proliferation of cerebellar stem cells in vitro, it cannot, on its own, sustain long-term growth in vivo. Our studies suggest that this is due to Myc-induced apoptosis, but this raises the question: why are these cells more sensitive to apoptosis in vivo? One reason may be that in vitro they are maintained under conditions that favor neurosphere formation, including high levels of EGF and bFGF. In the presence of such growth factors, the proliferative response to Myc often dominates over the apoptotic response (Harrington et al., 1994). It is also possible that the in vivo microenvironment contains factors that actively inhibit growth or survival of transplanted stem cells. In either case, it is clear that the potent mitogenic effects of Myc are insufficient to drive transformation.

Whereas stem cells expressing Myc alone do not form tumors, cells expressing Myc and mutant p53 are highly tumorigenic. Dysregulation of the TP53 pathway, as evidenced by elevated expression of p53 protein, is a common feature of human LCA MB (Eberhart et al., 2005; Frank et al., 2004; Tabori et al., 2010). Moreover, human MYC-driven MBs often exhibit isochromosome 17q, which is associated with monoallelic loss of TP53 (Cho et al., 2011; Northcott et al., 2010). Thus, loss of p53 function could synergize with MYC overexpression in human MB as well. The ability of mutant TP53 to cooperate with MYC has been observed in many other cancers (Elson et al., 1995; Hermann et al., 2005), but the mechanisms underlying this cooperation are not fully understood. In our system, Myc-induced apoptosis is dependent on endogenous p53, and DNp53 acts, at least in part, by blocking this function. (Hermeking and Eick,
have recently described animal models of LCA MB. Deletion of human LCA and MYC-driven MB. Interestingly, two other groups described that in many types of cancer, tumors become addicted to expression of the oncogene and undergo regression when expression is shut off (Jain et al., 2002; Soucek et al., 2008). However, there have been reports of tumors that continue to grow even when Myc is silenced (Boxer et al., 2004). Our results suggest that continued expression of Myc is required for maintenance of MP tumor growth. If similar findings hold true for human MYC-driven MB, it would suggest that targeting MYC itself might be an effective approach to therapy.

**MP Tumors as a Model for Human MB**

The tumors that are induced by Myc and DNp53 resemble human LCA and MYC-driven MB. Interestingly, two other groups have recently described animal models of LCA MB. Deletion of Rb and p53 in neural progenitors results in tumors that exhibit amplification of MycN and resemble LCA MB (Shakhova et al., 2006). Likewise, mice in which MycN is overexpressed in Glt1+ progenitors develop either classic or LCA MB (Swartling et al., 2010). While each of these tumors exhibits large cell-anaplastic histology, it is important to note that they may not all represent the same subtype of MB. We have previously reported that LCA histology can occur in all molecular subgroups of MB, including WNT, SHH, Group C and Group D tumors (Northcott et al., 2010). However, MBs that overexpress MYCN are largely distinct from those that overexpress MYC. Thus, the models described by these groups may correspond to human MYCN-associated MB, whereas MP tumors may represent human MYC-driven (Group C) MB. Interestingly, tumors from a recently developed MB model in which Rb and p53 were deleted in postnatal cerebellar stem cells did not overexpress MycN and, like our tumors, expressed high levels of NSC markers (Sutter et al., 2010). It will be interesting to compare these models at a molecular level to determine the similarities and differences between them.

**Cellular Origins of Myc-Associated Tumors**

Previous studies have shown that activation of the SHH pathway in GNPs results in MB with 100% penetrance (Schüller et al., 2008; Yang et al., 2008). Moreover, activation of the SHH pathway in stem cells within the cerebellar ventricular zone (VZ) results in expansion of the VZ, but cells do not become transformed until they commit to the granule lineage (Schüller et al., 2008; Yang et al., 2008). These studies suggest that lineage restriction is a critical determinant of susceptibility to transformation by SHH signaling. The current studies suggest that Myc + DNp53 can also cause transformation of both stem cells and GNPs. However, once transformed, the stem cells do not appear to undergo lineage commitment; indeed, their gene expression profile suggests that Myc/DNp53-transformed cells are even more immature or undifferentiated than normal neural stem cells. Moreover, when GNPs are infected with Myc and DNp53 viruses, they lose expression of GNP lineage markers during the course of transformation. These results demonstrate that stem cells and GNPs can both serve as cells of origin for MYC-driven MB, and suggest that lineage commitment is not required for (and in fact, may be incompatible with) transformation.

**Molecular Phenotype of MP Tumors**

In addition to highlighting the similarities between MP tumors and human MYC-driven MB, our gene expression analysis also revealed that genes overexpressed in MP tumors are similar to those expressed by embryonic and pluripotent stem cells. The association between pluripotency and cancer has been noted in a number of other systems. For example, in breast cancer, glioblastoma and bladder carcinoma, an ES-like signature is associated with aggressive, poorly differentiated tumors and is a predictor of poor prognosis (Ben-Porath et al., 2008). Likewise, a pluripotency signature is associated with transformation of follicular lymphoma to diffuse large B cell lymphoma (Gentles et al., 2009). There has been some debate about whether this signature reflects true acquisition of pluripotent characteristics or simply activation of a MYC-driven gene expression profile (Kim et al., 2010). In the case of MP tumors, there is no question that a MYC-driven transcriptional program is active and plays a significant role in driving tumor growth. However, it is worth noting that the genes identified as differentially expressed in MP tumors also resemble those associated with pluripotency induced by Oct4 and Klf4, suggesting that the pluripotency program in our cells is not purely a consequence of Myc overexpression. It is also notable that MP tumors express lower levels of neural differentiation markers compared to not only GNP but also normal neural stem cells, from which they were derived. These findings suggest that transformation of NSCs may involve dedifferentiation to a more pluripotent state.

Among the most important results of our analysis was the observation that MP tumors have increased expression of genes associated with PI3K/AKT/mTOR signaling and decreased expression of Foxo target genes. FOXO proteins have been shown to inhibit expression of MYC targets (Bouchard et al., 2004), and MYC-induced transformation requires inactivation of FOXO proteins (Bouchard et al., 2007). Importantly, AKT has been shown to phosphorylate FOXO proteins and thereby prevent them from entering the nucleus (Bouchard et al., 2004). Although the cause of PI3K pathway activation in MP tumors is unclear, it seems likely that this activation interferes with Foxo activity and thereby synergizes with Myc overexpression to promote transformation. PI3K signaling has also been shown to increase Myc protein stability (Kumar et al., 2006) and to enhance Myc function by promoting degradation of its antagonist Mad1 (Zhu et al., 2008). Thus, the PI3K pathway may be a critical regulator of transformation in MP tumors.

In light of the above findings, we hypothesized that inhibition of PI3K signaling might block growth of MP tumors. Whereas
inhibition of the SHH pathway had little effect on growth of these cells, treatment with the PI3K/mTOR inhibitors BEZ-235 and BKM-120 had a potent inhibitory effect on tumor growth both in vitro and in vivo. Several studies have documented activation of PI3K signaling in human MB (Castellino et al., 2010; Hartmann et al., 2006). In particular, genomic analysis suggests that MYC-driven MBs frequently exhibit loss of chromosome 10q (where PTEN is located) (Northcott et al., 2011). Consistent with this, our CMAP analysis (Table S6) suggests that MYC-driven tumors have elevated expression of genes that are regulated by PI3K and mTOR inhibitors. Together, these findings suggest that targeting the PI3K/mTOR pathway may be useful for treatment of human MB. Further studies using this model of MYC-driven MB will shed light on the biology of this disease and open up new targets for therapy.

**EXPERIMENTAL PROCEDURES**

**Animals**

C57BL/6J mice used as a source of stem cells and immunocompromised (WOD-oid IL2Rγmat-/- or NSG) mice used for transplantation were purchased from Jackson Labs (Bar Harbor, ME). Mice were maintained in the Cancer Center Isolation Facility at Duke University and in the Animal Facility at Sanford-Burnham. All experiments were performed in accordance with national guidelines and regulations, and with the approval of the animal care and use committees at each institution.

**Orthotopic Transplantation and Tumor Formation**

Before transplantation, cerebellar stem cells (Prom1+Lin- cells) or GNPs (GFP+ cells FACs-sorted from Matri1-GFP transgenic mice) were injected with Myc and Dnps3 retroviruses for 20 hr. Either 1 x 10^5 stem cells in Neurocult medium or 1 x 10^6 GNPs suspended in Neurobasal medium were injected into the cerebella of NSG mice (6–8 weeks old) using a stereotaxic frame with a mouse adaptor (David Kopf Instruments), as described previously (Yang et al., 2008). Animals were monitored weekly, and sacrificed when they showed symptoms of MB.

To generate tetracycline (Tet)-regulatable tumors, stem cells were infected with Tet-inducible Myc lentivirus and Dnps3 retrovirus. The Tet-inducible vector (pcUVE-mycT10tet) consisted of a Tet-response element (TRE2) controlling expression of tet red fluorescent protein (tetRFP) and Myc-T58A and a constitutive promoter controlling expression of the reverse tetracycline transactivator (tT3A) and eGFP (Meerbrey et al., 2011). Infected cells were implanted into cerebella of NSG mice, and mice were maintained on DOX-containing food. When mice became symptomatic, they were sacrificed and tumor cells were retransplanted into secondary NSG mice. These mice were separated into three groups. Group 1 (n = 14) was continually fed DOX-containing food, Group 2 (n = 14) was fed DOX-food for one week and normal food thereafter, and Group 3 (n = 12) was not fed DOX-food at all. Mice were subjected to bioluminescent imaging at 1, 2, and 3 weeks and were sacrificed at the onset of symptoms. At the time of sacrifice, brains were removed, paraffin-embedded, sectioned, and stained with H&E.

**In Vivo Bioluminescent Imaging**

Mice were given intraperitoneal injections of 150 ng/g D-Luciferin (Caliper Life Sciences, cat#12279) and anesthetized with 2.5% isoflurane. At 7–8 min after injection, animals were imaged using the Xenogen Spectrum (IVIS-200) imaging system.

**In Vivo Inhibitor Treatment**

To study effects of the PI3-kinase antagonist BKM-120 on tumor growth in vivo, we retransplanted 500 MP tumor cells into the cerebella of secondary NSG mice. Seven days after transplantation, mice were randomly separated into two groups: Group 1 was given vehicle (0.5% methylcellulose) and Group 2 was given 30 mg/kg BKM-120 by oral gavage once daily until symptom onset. BKM-120 was dissolved in 0.5% methylcellulose and sonicated using an ultrasonicator (Misonix) at an amplitude of 20 for 12 min. Survival was defined as the time from transplantation until symptom onset.

**ACCESSION NUMBERS**

Microarray data have been deposited in the GEO public database (http://www.ncbi.nlm.nih.gov/geo/), with accession number GSE34126.

**SUPPLEMENTAL INFORMATION**

Supplemental Information includes six figures, six tables, and Supplemental Experimental Procedures and can be found with this article online at doi:10.1016/j.ccr.2011.12.021.

**ACKNOWLEDGMENTS**

We dedicate this paper to the memory of Cameron Jackson. In addition, we would like to thank Jack Dutton and Adriana Charbono for assistance with animal colony maintenance and screening; Beth Harvat, Lynn Martinek, Mike Cook, Amy Cortez, and Yoav Altman for help with flow cytometry; Zhengzheng Wei for processing and analysis of microarrays; Irina Leis for performing immunohistochemistry; and Daisuke Kawauchi and Martine Roussei for helpful discussions. This work was supported by funds from the Alexander and Margaret Stewart Trust and the Duke Comprehensive Cancer Center (R.W.R.), the Southeastern Brain Tumor Foundation (R.W.R.), Alex’s Lemonade Stand Foundation (R.W.R.), Pediatric Brain Tumor Foundation (R.E.M. and R.W.R.), NIgrant CA122759 (R.W.R.) and CA159859 (M.D.T. and R.W.R.), C.R.M. is a Damon Runyon-Genentech Clinical Investigator supported in part by a grant (CI-45-09) from the Damon Runyon Cancer Research Foundation. R.W.R. is supported by a Leadership Award (LA1-01747) from the California Institute of Regenerative Medicine.

Received: July 7, 2011
Revised: November 21, 2011
Accepted: December 22, 2011
Published: February 13, 2012

**REFERENCES**


