GLIPR1 Suppresses Prostate Cancer Development through Targeted Oncoprotein Destruction

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Abstract

Downregulation of the proapoptotic p53 target gene glioma pathogenesis-related protein 1 (GLIPR1) occurs frequently in prostate cancer, but the functional meaning of this event is obscure. Here, we report the discovery of a functional relationship between GLIPR1 and c-Myc in prostate cancer where c-Myc is often upregulated. We found that the expression of GLIPR1 and c-Myc were inversely correlated in human prostate cancer. Restoration of GLIPR1 expression in prostate cancer cells downregulated c-myc levels, inhibiting cell-cycle progression. Downregulation was linked to a reduction in β-catenin/TCF4-mediated transcription of the c-myc gene, which was caused by GLIPR1-mediated redistribution of casein kinase 1α (CK1α) from the Golgi apparatus to the cytoplasm where CK1α could phosphorylate β-catenin and mediate its destruction. In parallel, GLIPR1 also promoted c-Myc protein ubiquitination and degradation by glycogen synthase kinase-3β and/or CK1α-mediated c-Myc phosphorylation. Notably, genetic ablation of the mouse homolog of Glipr1 cooperated with c-myc overexpression to induce prostatic intraepithelial neoplasia and prostate cancer. Together, our findings provide evidence for CK1α-mediated destruction of c-Myc and identify c-Myc S252 as a crucial CK1α phosphorylation site for c-Myc degradation. Furthermore, they reveal parallel mechanisms of c-myc downregulation by GLIPR1 that when ablated in the prostate are sufficient to drive c-Myc expression and malignant development. Cancer Res; 71(24): 7694–704. ©2011 AACR.

Introduction

Human glioma pathogenesis-related protein 1 (GLIPR1) and its mouse counterpart, Glipr1, are downregulated in prostate cancer and other malignant cell lines (1, 2), owing partly to methylation in the gene's regulatory region (3). Loss of Glipr1 function predisposed mice to tumorigenesis (1). Restoration of GLIPR1 expression in prostate cancer cells and other malignant cells led to growth suppression and/or apoptosis (1–4). Furthermore, a novel Glipr1 gene–modified tumor cell vaccine had significant antitumor activity in a mouse model of recurrent prostate cancer (5). These preclinical results led to a clinical trial in which prostate cancer patients received a neoadjuvant adenoviral vector–mediated GLIPR1 injection before undergoing radical prostatectomy. GLIPR1 tumor suppressor activities were also found in 2 other malignancies: deletion of chromosome region 12q13-24, which contains GLIPR1 and GLIPR1-like genes (6), was found in 34 of 47 colorectal cancer tissues (7), and GLIPR1 was deleted in 9% of multiple myeloma patients (8).

In contrast to GLIPR1's tumor suppressor activities in prostate cancer, in glioblastomas, GLIPR1 was upregulated and promoted cell growth, survival, and invasion, suggesting a context-specific role for GLIPR1 in malignant growth (9). c-MYC is one of the most frequently deregulated genes in cancer (reviewed in refs. 10–12). In malignant cells, deregulated c-Myc expression occurs via many mechanisms, including transactivation by certain transcriptional factors, and stabilization of c-Myc mRNA and protein (11–14). Recent studies identified a complex signaling pathway that controls c-Myc protein stability, involving reversible phosphorylation at threonine 58 (T58) and serine 62 (S62) of c-Myc and Fbw7-mediated ubiquitination and proteasome degradation (15–21). Interestingly, casein kinase 1 (CK1) was recently reported to be involved in ubiquitination and proteasome degradation of dMyc in Drosophila (22). Because functional conservation of c-Myc and dMyc was shown in several experimental systems (23), CK1's regulation of dMyc protein stability in Drosophila...
raises the question whether CK1 also has a role in regulating c-Myc protein stability in mammals. GSK3β and CK1α are members of the serine/threonine-specific protein kinase family. In many cases, GSK3β phosphorylation marks target proteins for ubiquitination and proteolysis (24, 25). GSK3β phosphorylation of c-Myc creates a recognition motif for E3 ubiquitin ligase Fbw7, leading to subsequent ubiquitination and proteasome-mediated c-Myc degradation. In the canonical Wnt signaling pathway, GSK3β phosphorylation of β-catenin promotes proteasomal targeting and degradation of β-catenin (24–26). GSK-3β phosphorylation is also implicated in ubiquitination and destruction of several other important signaling molecules, such as HIF-1α, NFκB, cyclins D1 and E, and Cdc25A (reviewed in ref. 24).

Like GSK3β, CK1 is implicated in ubiquitination and degradation of several important signaling molecules. In the canonical Wnt signaling pathway, CK1α phosphorylates β-catenin at S45, priming for subsequent phosphorylation of β-catenin at T41, S37, and S33 by GSK3β and leading to proteasomal targeting and degradation of β-catenin (27–30). CK1α is also involved in proteasomal degradation of Ci-155 in Hedgehog signaling (28, 31).

To explore the prospect of using GLIPR1 as a potential therapeutic agent for prostate cancer and other cancers in which c-myc is upregulated, we studied the functional relationship between GLIPR1 and c-Myc in prostate cancer, focusing on GLIPR1’s regulation of c-Myc, the synergistic effects of Glipr1 loss and c-Myc overexpression on tumorigenesis in experimental mouse models, and the mechanisms involved in GLIPR1-induced c-Myc downregulation.

Materials and Methods

Cell lines and cell culture

LNCaP, VCaP, DU145, PC-3, and TSU-Pr1 were from American Type Culture Collection. B24 is a GLIPR1-inducible stable clone derived from TSU-Pr1 (1). LAPC4 was a gift from Dr. Charles Sawyer of the University of California at Los Angeles and 293PE was obtained from Dr. Margaret Goodell of Baylor College of Medicine. Cell lines were validated by short tandem repeat (STR) DNA fingerprinting using the AmpFlSTR Identifiler kit in the MDACC Cell Line Core.

Cell synchronization and serum restimulation

After adenovirus-vector-mediated gene transduction or cDNA transfection, cells were grown in complete medium for 24 hours, synchronized by serum starvation for 24 hours, and then restimulated by the addition of 10% FBS for 30 minutes.

Quantitative reverse transcriptase PCR

Quantitative reverse transcriptase PCR (qRT-PCR) was done as described previously (1) using specific Taqman probes and primers (see Supplementary Materials and Methods). In the 34 specimens used for GLIPR1 and c-myc mRNA expression correlation analysis, there were 3 pT1, 27 pT2, and 4 pT3 cancers, with Gleason scores of 6 (n = 17), 7 (n = 16), and 8 (n = 1).

cDNA microarray analysis

Total RNA was isolated from LNCaP, VCaP, and DU145 prostate cancer cell lines. cDNA microarray analysis was done, and the data were normalized and statistical analysis was done as previously described (32). Microarray data were deposited in GEO database (accession number: GSE32367).

Western blotting analysis

Antibodies: GLIPR1 (described previously; ref. 2); c-Myc, CK1α, and CK1β (Santa Cruz); active β-catenin (Millipore); P-β-Myc (T58), P-c-Myc (S62), and fibrillarin (Abcam); GSK-3β, P-GSK-3β (S9), β-catenin (total), P-β-catenin (S45), P-β-catenin (T41/S45), and P-β-catenin (S33/S37/T41; Cell Signaling); β-actin (Sigma). Quantitative analysis was done using computer-assisted densitometry, in which total protein was normalized with β-actin and phosphorylated protein was normalized by its total protein. The fraction of phosphorylated protein in control cells was set as 1.

Generation of PB-c-myc;Glipr1 bigenic mice

We intercrossed founder hemizygous PB-c-myc mice (Supplementary Materials and Methods) with Glipr1+/+/ or Glipr1−/− mice and bred these mice to generate the following 4 genotypes: PB-c-myc(+/+);Glipr1+/+, PB-c-myc(−/−);Glipr1+/−, PB-c-myc(+/−);Glipr1+/+, and PB-c-myc(−/−);Glipr1−/−. The resulting male bigenic mice were euthanized when they were approximately 1 year old or when they displayed signs of distress or became moribund.

Immunohistochemistry

Twenty radical prostatectomy specimens which had a pathologic differentiation pattern of Gleason score 6 and a pathologic stage of TpT2b were used for correlative analysis of c-Myc and GLIPR1. GLIPR-1 immunostaining was scored according to the staining intensity ranging from 0 (negative) to 3 (strong) and the extent of positive staining of the cancerous area (1 ≤ 10%; 2 = 10%–50%; 3 ≥ 50%). c-Myc immunostaining was measured quantitatively by a Nikon Eclipse 90i system with NIS-element AR software (version 3.0); the results were recorded as the c-Myc–nuclear area ratio of cancer cells (33).

Immunofluorescence

Immunofluorescence was evaluated by using a Nikon Eclipse 90i system with NIS-Elements AR software (version 3.0). To evaluate the cellular distribution of CK1α, a Z series of optical sections (0.10-μm steps) was digitally imaged and deconvoluted by using AutoQuant deconvolution software (Media Cybernetics) to generate high-resolution images.

Chromatin immunoprecipitation assay

Chromatin immunoprecipitation (ChIP) assays were done by using a Millipore ChIP kit. The input and immunoprecipitated DNAs were subjected to PCR using primers corresponding to the −718 to −460 base pairs upstream of the c-myc transcription start site (upper primer: 5′CTCAGTCTGG-TGGAGGTA3′; lower primer: 5′CAGGGAAGTGGAGGA-AAGA3′). Antibodies: TCF4 (Santa Cruz), trimethyl-histone H3K4 (Ab8580, Abcam), trimethyl-histone H3K27 (Millipore),
acetyl-histone H3K27 (Millipore) RNA polymerase II (Sigma), and normal rabbit IgG (Santa Cruz).

Promoter construction and luciferase assay
The c-myc promoter (1,316 bp) was amplified by PCR using genomic DNA from normal prostate tissue (see Supplementary Materials and Methods). The purified PCR product was phosphorylated and then cloned to pGL3-Basic vector (Promega) using the SmaI site to generate c-myc-luc. Luciferase assay was done as described previously (1).

c-Myc ubiquitination analysis
The 293 cells were transfected with HA-ubiquitin (Addgene), c-myc, and GLIPR1 or control vector pcDNA. Cells were grown in complete medium for 24 hours and synchronized by incubation in serum-free medium (SFM) for 24 hours; GM132 was added in the last 4 hours of incubation in SFM. Immunoprecipitation was done with an ubiquitin monoclonal antibody (Sigma).

c-Myc phosphorylation mutants
c-Myc T58A, S67A, and S252A point mutations were each introduced by 2-round PCR (Phusion High-Fidelity PCR kit, New England BioLabs). See Supplementary Materials and Methods for details.

Protein stability analysis
DU145 cells were transfected with wild-type (wt) or mutant c-myc. Cells were grown in complete medium for 48 hours and then treated with cycloheximide (100 μg/mL) in SFM for the indicated time. After Western blotting, c-Myc protein band was measured by computer-assisted densitometry, and the half-life was determined by linear fitting the densitometry data.

Statistical analysis
Paired t testing was used for statistical comparisons of GLIPR1 and c-myc mRNA expression in normal and malignant human prostate tissues, and unpaired t testing was used in other experiments in which probability was determined. Spearman's rank-order correlation coefficient test was applied to GLIPR1 and c-myc mRNA levels, to GLIPR1 methylation and c-myc mRNA expression and to GLIPR1 and c-Myc nuclear immunostaining scores on human prostate cancer specimens.

Results
GLIPR1 and c-Myc expression are inversely correlated in human prostate cancer tissue
To identify a possible functional relationship between GLIPR1 and c-Myc in human prostate cancer, we conducted qRT-PCR comparing 34 human prostate cancer tissue samples and their paired adjacent normal prostate tissue samples. GLIPR1 was downregulated in 27 of the 34 prostate cancer samples relative to the corresponding adjacent normal prostate tissue. In contrast, c-Myc was upregulated in 29 of the 34 prostate cancer tissue samples (Fig. 1A and B). Overall, GLIPR1 mRNA expression was significantly lower and c-myc mRNA expression, significantly higher in the prostate cancer tissue samples than in the normal prostate tissue samples (inserts in Fig. 1A and B). Spearman's rank-order correlation analysis revealed an inverse correlation between GLIPR1 mRNA expression and c-myc mRNA expression (Fig. 1C). Using our previous GLIPR1 methylation data (3) from 11 pairs of human prostate cancer patient tissue samples that overlapped with 34 pairs of human prostate cancer patient tissue samples used in this study, we found that GLIPR1 methylation is significantly positively correlated to c-myc mRNA expression (Fig. 1D).

In 20 human prostate cancer radical prostatectomy specimens with a pathologic differentiation pattern of Gleason score 6 and a pathologic stage of pT2b, immunostaining of GLIPR1 and c-Myc showed generally decreased GLIPR1 and increased c-Myc protein expression in the human prostate cancer cells relative to that in the normal prostate epithelial cells (Fig. 1E), a result consistent with previous reports (2, 34). Correlation analysis of the immunostaining results revealed inversely correlated GLIPR1 and c-Myc protein levels (Fig. 1F).

Restoring GLIPR1 expression in prostate cancer cells leads to downregulation of c-Myc and cell-cycle inhibition
To assess the global functions of GLIPR1 and the functional relationship between GLIPR1 and c-myc in prostate cancer, we conducted comparative cDNA microarray analysis on samples from GLIPR1-transduced LNCaP, VCaP, and DU145 prostate cancer cell lines that express low or undetectable GLIPR1. In addition to changes in the genes involved in cell survival, apoptosis, and redox balance (Supplementary Fig. S1A), we found that restoring GLIPR1 expression in prostate cancer cells led to changes in expression of c-myc and multiple c-myc downstream target genes, including downregulation of several cell-cycle–promoting molecules, such as cyclins A2, B1, B2, D1 and CDC25C, and upregulation of the cell-cycle suppressor p21 (Fig. 2A). We confirmed these microarray results by qRT-PCR (Supplementary Fig. S1B) and at the protein level by Western blotting (Fig. 2B).

To assess the biological effects of downregulation of c-myc and cell-cycle–related c-myc target genes, we conducted cell-cycle analysis with propidium iodide staining and flow cytometry. Restoration of GLIPR1 expression in LNCaP and DU145 prostate cancer cells reduced the cells in the S phase and substantially increased those in G2 (Fig. 2C and D). Results in VCaP and PC-3 cells were similar (Supplementary Fig. S1C). Interestingly, in LAPC4 cells, instead of cell increase in G2, a markedly increased cell population was found in post-G2/M (Supplementary Fig. S1C). A substantial increase in sub-G1 phase cells was also induced after GLIPR1 expression in LNCaP, VCaP, and LAPC4 cells (Fig. 2C and D and Supplementary Fig. S1C), which may indicate GLIPR1-induced cell death as we reported previously (1, 2).

Loss of Glipr1 and overexpression of c-myc have synergistic effects
To gain insight into the possible synergism between GLIPR1 loss and c-myc overexpression in prostatic neoplasia in vivo, we bred PB-c-myc+ mice with Glipr1+/− or Glipr1−/− mice (see Supplementary Materials and Methods) and analyzed prostate...
tissues of the bigenic mice. As summarized in Table 1 and shown in Fig. 3A–L, no malignant phenotype was found in wt mice. Loss of Glipr1 alone or overexpression of PB-c-myc alone induced epithelial hyperplasia with atypia and mouse prostatic intraepithelial neoplasia (mPIN), but not prostate cancer. However, Glipr1 loss plus PB-c-myc overexpression significantly increased mPIN lesions and induced locally invasive carcinomas. These carcinomas developed in dorsolateral (n = 3) and ventral (n = 1) prostates of the bigenic mice (Fig. 3). Three of them had a size more than 1 mm and extended into the periprostatic loose connective tissues. Another carcinoma protruded into the desmoplastic periglandular stroma. The nuclei of both the mPIN cells and the cancer cells were strongly labeled by androgen receptor antibody (Supplementary Fig. S2A–D), but not by IgG (Supplementary Fig. S2E) or synaptophysin antibody (Supplementary Fig. S3A and B), a biomarker for neuroendocrine cells (Supplementary Fig. S3C). Proliferating cell nuclear antigen (PCNA)- and terminal deoxynucleotidyl transferase-mediated dUTP nick end labeling (TUNEL)-positive cells were found both in epithelial atypia of PB-c-myc+/Glipr1+/− (Fig. 3D and G) and in mPIN lesions of PB-c-myc+/Glipr1− mice (Fig. 3E and H). Interestingly, the proliferative activity in prostate cancer of PB-c-myc−Glipr1+/− was remarkably increased and its apoptotic activity was relatively low (Fig. 3F and I). In addition, c-Myc immunostaining was stronger in mPIN of PB-c-myc−Glipr1+/− (Fig. 3L) than that in the mPIN of PB-c-myc−Glipr1+/− mice (Fig. 3K). These in vivo data strongly show the synergistic effects of Glipr1 function loss and PB-c-myc overexpression.

**GLIPR1 negatively regulates c-myc promoter activities**

To elucidate the mechanisms by which GLIPR1 regulates c-myc expression, we assessed the changes in c-myc mRNA in response to changes in GLIPR1 expression in prostate cancer cells. Restoring GLIPR1 in prostate cancer cells in which GLIPR1 was downregulated led to reduced c-myc mRNA levels in all 5 prostate cancer cell lines tested (Fig. 4A). Conversely, knockdown of endogenous GLIPR1 expression with GLIPR1-specific siRNA led to increased c-myc mRNA expression in PC-3 and R24 (a GLIPR1-inducible clone generated from TSU-Pr1

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**Figure 1.** GLIPR1 expression and c-Myc expression are inversely correlated in human prostate cancer tissue samples. A and B, graphs show results of qRT-PCR analysis of GLIPR1 and c-myc mRNA levels in 34 pairs of prostate cancer tissues and adjacent normal prostate tissues. Inserts summarize the paired t test results for the comparison of GLIPR1 and c-myc mRNA expression between prostate cancer tissues and adjacent normal prostate tissues. C, correlation analysis of GLIPR1 and c-myc mRNA expression. D, correlation analysis of the methylation of GLIPR1 promoter and c-myc mRNA expression. E, representative immunohistochemically stained slides show GLIPR1 and c-Myc protein levels in normal prostate (NL) and prostate cancer tissues. Bars, 100 μm. F, box plots of c-Myc nuclear immunostaining versus GLIPR1 staining score in human prostate cancer tissue specimens. Error bars indicate SD.
bladder cancer cells), both of which express moderate GLIPR1 levels (Fig. 4B).

Because c-myc mRNA levels are inversely related to GLIPR1 expression, we next asked whether GLIPR1 regulates c-MYC transcription. As c-MYC is an important downstream target of Wnt-β-catenin signaling (13, 35), we speculated that GLIPR1 facilitates c-MYC downregulation by disrupting β-catenin signaling. Western blotting revealed downregulation of β-catenin after enforced GLIPR1 expression in prostate cancer cells (Fig. 4C). Subcellular fractionation analysis further showed that GLIPR1 expression substantially decreases active β-catenin in both cytoplasmic and nuclear cellular fractions (Fig. 4D).

To obtain direct evidence of GLIPR1’s regulation of c-MYC transcription, we conducted both ChIP analysis and luciferase promoter assays in GLIPR1-expressing or control lacZ-expressing prostate cancer cells. ChIP results showed that enforced GLIPR1 expression in prostate cancer cells leads to c-Myc downregulation and cell-cycle inhibition. A, cDNA microarray heat map summarizes the downregulation of c-myc; cyclins B1, D1, B2, and A2; and CDC25C and the upregulation of the cell-cycle inhibitor p21 in the prostate cancer cell lines. B, Western blot analysis. nd, not detectable. C and D, cell-cycle distribution in GLIPR1-transduced LNCaP and DU145 prostate cancer cells.

Table 1. Synergistic effects of c-Myc overexpression and loss of Glipr1 function results in significantly increased mPIN and leads to prostate cancer

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<tr>
<th>Animal group</th>
<th>Type and frequency of lesions*</th>
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<tr>
<td></td>
<td>Epithelial hyperplasia</td>
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<tr>
<td>c-myc transgene status</td>
<td>Glipr1 status</td>
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<tr>
<td>PB-c-myc</td>
<td>Glipr1&lt;sup&gt;++&lt;/sup&gt;</td>
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<td>PB-c-myc&lt;sup&gt;+&lt;/sup&gt;</td>
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<sup>*</sup>P = 0.023 versus PB-c-myc<sup>-</sup>; Glipr1<sup>++</sup> mice and P = 0.0011 versus PB-c-myc<sup>-</sup>; Glipr1<sup>-/-</sup> mice; Fisher’s exact test.
expression of GLIPR1 in DU145 cells led to increased H3K27 trimethylase mark and reduced the pol II, H3K4 trimethylase and H3 acetylation marks on the c-MYC promoter indicating diminished transactivation activities (Fig. 4E). Importantly, GLIPR1 expression led to reduced c-myc promoter binding to TCF4, the DNA-binding protein that mediates β-catenin transcriptional regulation, by more than 3-fold (Fig. 4E). The reduced TCF4 binding to c-MYC promoter together with reduced nuclear active β-catenin (Fig. 4D) indicate diminished c-MYC transcription. We also confirmed that GLIPR1 suppresses c-MYC transcriptional activity by using c-myc-luciferase promoter assays in PC-3M prostate cancer cells (Fig. 4F).

Because GSK3β and CK1α are involved in the destruction of β-catenin, we examined GSK3β and CK1α expression and distribution in GLIPR1-expressing prostate cancer cells. GSK3β levels were slightly increased in GLIPR1-transduced DU145 cells (Fig. 4G and Supplementary Fig. S4A), whereas CK1α protein levels were remarkably higher in GLIPR1-transduced prostate cancer cells (Fig. 4G and Supplementary Fig. S4B) and inversely correlated with β-catenin and c-Myc protein levels (Figs. 4C and D and Supplementary Fig. S4A). These results are consistent with the results of our cDNA microarray experiments (Supplementary Fig. S5). Interestingly, restoring GLIPR1 expression in prostate cancer cells also led to marked redistribution of CK1α. In control lacZ-expressing cells, CK1α is predominantly localized in the perinuclear region within or near the Golgi complex, but in GLIPR1-expressing cells, CK1α spreads out from the Golgi to the cytoplasm (Fig. 4H), where it can potentially be recruited to the β-catenin destruction complex and contribute to β-catenin’s phosphorylation. Indeed, the fraction of phosphorylated β-catenin at S45 in total β-catenin was approximately 3.8-fold higher in GLIPR1-expressing cells compared with lacZ control cells (Fig. 4I). This crucial serine priming phosphorylation led to remarkably increased subsequent phosphorylation of β-catenin at T41, S37, and S33 (Fig. 4I). These results show that GLIPR1 promotes β-catenin destruction, which in turn leads to suppressed c-myc transcription.

**CK1α is crucial in GLIPR1-induced c-Myc protein ubiquitination and proteasome degradation in prostate cancer cells**

Although our results showed that GLIPR1 downregulates both c-myc mRNA and protein, the GLIPR1-stimulated reductions in c-myc mRNA levels were limited to approximately 50% (Fig. 4A), whereas the reductions in c-Myc protein ranged from 3- to 10-fold (Figs. 2B and 4C and G). We thus asked whether GLIPR1 regulates c-Myc protein stability in addition to its regulation of c-myc transcription. To answer this question, we cotransfected 293 cells with GLIPR1 or control vector pcDNA together with c-myc and ubiquitin and conducted immunoprecipitation and Western blotting analysis for ubiquitinated c-Myc. We found that GLIPR1 expression led to a definitive increase in ubiquitinated c-Myc (Fig. 5A). Three different proteasome inhibitors maintained c-Myc levels in the presence of GLIPR1 levels that effectively suppressed c-Myc in all 4 cell lines tested (Fig. 5B and Supplementary Fig. S6). Thus, our results showed that GLIPR1-induced c-Myc downregulation involves c-Myc protein ubiquitination and proteasome-mediated degradation.

We next addressed the mechanisms by which GLIPR1 facilitates these actions. We examined c-Myc phosphorylation at T58 and the priming phosphorylation at S62. In DU145 cells, GLIPR1 expression led to decreased c-Myc total protein by approximately 3-fold compared with lacZ control. The fraction of phosphorylated c-Myc at T58 in total c-Myc increased approximately 6.6-fold and that at S62 increased
approximately 3.2-fold in GLIPR1 overexpressed cells compared with lacZ control cells (Fig. 5D). We speculate that the higher ratio of c-Myc phosphorylation at T58 to that at S62 may be attributed to higher activity of GSK3β and may contribute to GLIPR1-induced c-Myc downregulation. A different pattern was observed in LNCaP cells, in which the fraction of c-Myc phosphorylation at T58 in total c-Myc was increased approximately 3.1-fold, whereas c-Myc phosphorylation at S62 was increased approximately 4.6-fold in GLIPR1-expressing cells compared with lacZ-expressing cells (Fig. 5D). Thus, GLIPR1-stimulated c-Myc protein degradation may be related to GSK3β phosphorylation at T58 in DU145 cells, but not in LNCaP cells.

We thus hypothesized that CK1 participates in c-Myc protein degradation on the basis of the evidence of CK1 phosphorylation and destruction of dMyc in Drosophila (22) and the results from our cDNA microarray analysis (Supplementary Fig. S5), Western blot analyses (Fig. 4G), and immunofluorescence staining (Fig. 4H) that showed increased CK1α levels and marked redistribution of CK1α from Golgi complex into the cytoplasm in GLIPR1-induced prostate cancer cells. According to the consensus sequences of CK1 phosphorylation sites (T/S/XXT/SCX; refs. 27, 28) and reported phosphorylation sites on c-Myc protein (36), we identified 2 potential sites on human c-Myc: S67 and S252 (Fig. 5C). To verify CK1α’s involvement in GLIPR1-induced c-Myc protein degradation, we knocked down endogenous CK1α using specific siRNA and conducted Western blotting for c-Myc. Inhibition of CK1α largely restored c-Myc protein levels in both DU145 and LNCaP cells (Fig. 5E and F), indicating that CK1α participates in GLIPR1-induced c-Myc protein degradation. To further confirm that we cotransfected LNCaP cells with c-myc and GLIPR1, GSK3β, or CK1α and analyzed their effects on c-Myc. We found that GLIPR1 expression and CK1α expression led to similarly reduced c-Myc protein, but GSK3β expression reduced c-Myc levels to a lesser extent (Fig. 5G).
To evaluate the significance of the GSK3β phosphorylation site at c-Myc T58 and the 2 potential CK1α phosphorylation sites at c-Myc S67 and S252 in GLIPR1-induced c-Myc degradation, we constructed 3-single point–mutation mutants by replacing GSK3β- or CK1α-targeted threonine or serine with alanine, and then cotransfected 293 cells with wt c-myc or mutant c-myc and GLIPR1 or control pcDNA empty vector. Figure 6A shows that the T58A and S67A mutants had only a small effect on c-Myc protein levels relative to the wt c-myc, whereas the S252A mutant effectively prevented GLIPR1-induced c-Myc protein degradation.

To verify the role of these phosphorylation sites in maintaining c-Myc protein stability, we expressed wt c-myc and mutant c-myc in DU145 cells and compared their protein stability after cycloheximide treatment. The wt c-Myc protein’s half-life was 25 minutes, fairly close to the previously reported 30 minutes (37). The half-lives of the 3 phosphorylation mutants relative to that of wt c-Myc protein were as follows: T58A, 2-fold increase; S67A, slightly increased; and S252A, greater than 2-fold increase (70 minutes; Fig. 6B).

Overall, our results reveal that a dual mechanism underlies GLIPR1’s downregulation of c-Myc in prostate cancer. In our proposed model (Fig. 6C), the initial step is GLIPR1’s induction of CK1α expression and subcellular redistribution from the Golgi to the cytoplasm, where CK1α together with GSK3β phosphorylate β-catenin, leading to destruction of β-catenin. This primary mechanism leads to reduced active β-catenin and c-myc mRNA levels. In the second step, GLIPR1 promotes c-Myc protein degradation via GSK3β- and/or CK1α-mediated phosphorylation of c-Myc. This secondary mechanism generates recognition motif(s) for subsequent E3 ligase targeting and proteasome degradation of c-Myc. The resulting decrease in c-Myc activities leads to cell-cycle arrest and inhibition of tumor growth. Importantly, the loss of Glipr1 function and c-myc overexpression leads to premalignant phenotypic changes in vivo in mouse models.

Figure 5. GLIPR1-induced c-Myc downregulation involves ubiquitination, proteasome degradation, and CK1α. A, immunoprecipitation (IP) analysis of ubiquitinated c-Myc in GLIPR1-expressing cells. B, blots depict that proteasome inhibitor MG132 (MG) abrogates GLIPR1-induced c-Myc protein degradation in prostate cancer cells. C, diagram illustrates the reported phosphorylated serine (S)/threonine (T) and potential CK1 phosphorylation sites on the ubiquitinated c-Myc in GLIPR1-expressing cells. B, blots depict that proteasome inhibitor MG132 (MG) abrogates GLIPR1-induced c-Myc protein degradation.

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Discussion

This study showed that (i) c-myc expression is inversely correlated with GLIPR1 expression and is positively correlated with GLIPR1 gene methylation in human prostate cancer; (ii) Glipr1 loss and c-myc overexpression have synergistic effects on induction of mPIN and prostate cancer in mice; (iii) GLIPR1 suppresses c-MYC transcription by increasing CK1α expression and inducing CK1α redistribution in prostate cancer cells, leading to cytoplasmic destruction of β-catenin and reduced β-catenin/TCF4-mediated c-MYC transcription; (iv) GSK3β and CK1α mediate GLIPR1-induced c-Myc protein degradation via c-Myc phosphorylation; and (v) mutation of c-Myc S252, a consensus CK1 phosphorylation site point-mutation mutants (left) were generated by replacing GSK3β- and CK1α-targeted threonine (T) and serine (S) with alanine (A) at the indicated positions (in red). Western blots (right) show the resulting c-Myc protein levels after cotransfection of 293 cells with wt or mutant c-myc and GLIPR1 or pcDNA. B, DU145 prostate cancer cells were transfected with wt or mutant c-Myc and then treated with cycloheximide (CHX) for the indicated times, followed by (top) Western blot analysis and (bottom) quantitative analysis for c-Myc protein stability. t1/2, half-life. C, diagram illustrates our proposed model of GLIPR1-induced molecular signaling.

Regulation of c-Myc protein degradation is an important mechanism underlying the precise control of this oncoprotein’s cellular concentration. In this study, we identified a role for CK1α in regulating c-Myc protein’s stability in experiments using CK1α siRNA and CK1α overexpression, validating the results of the point-mutation experiments. In the 293 cell line, a point mutation at c-Myc S252 effectively abolished GLIPR1-induced c-Myc degradation; in DU145 cells, this point mutation markedly increased c-Myc protein destruction of β-catenin and c-Myc proteins. Together, these lead to dramatically reduced c-Myc protein levels.

Our ChIP assay results showing that GLIPR1 expression reduced TCF4 binding to the c-myc promoter, together with our results showing that GLIPR1 induced CK1α-mediated destruction of β-catenin, establish a mechanistic link between GLIPR1 and suppression of c-myc transcription. Over the last 2 decades, aberrant β-catenin signaling was documented in many types of cancers, including prostate cancer, and was associated with several important oncogenic signaling pathways, including Wnt (38–40). Phosphorylation of β-catenin S45 by CK1α is a well-documented crucial step leading to β-catenin destruction. We found that GLIPR1 can not only increase CK1α expression but also induce its dramatic redistribution from the Golgi to the cytoplasm where it phosphorylates and thus promotes the destruction of β-catenin, thereby reducing c-myc transcription. To our knowledge, this is the first report of CK1α redistribution from the Golgi to the cytoplasm. In our opinion, this redistribution is critical to targeted destruction of both β-catenin and c-Myc.
stability. In contrast to GSK3β’s well-documented role in c-Myc ubiquitination and degradation (15, 17–21), the role of CK1 in these functions was previously reported only in Drosophila. Therefore, our results are the first evidence of CK1-mediated c-Myc ubiquitination and degradation in a mammalian system. This is also the first identification of c-Myc S252 as a key CK1 phosphorylation site that mediates c-Myc protein degradation. The finding of a role for CK1 in the regulation of c-Myc protein stability has special significance for prostate cancer, given that Akt, which is deregulated in most prostate cancers, suppresses GSK3β and its inhibitory effect on c-Myc protein stability.

GLIPR1’s capacity for stimulating targeted destruction of oncogenic β-catenin and c-Myc holds promise for its use (in gene or protein applications) as a therapeutic agent for prostate cancer and other malignancies in which β-catenin and c-myc expression is deregulated.

Disclosures of Potential Conflicts of Interest
No potential conflicts of interest were disclosed.

Acknowledgments

We thank Karen F. Phillips, ELS, for editing the manuscript.

Grant Support

This work was supported by grant R01CA09588 from the National Cancer Institute; by National Cancer Institute grant P50CA09898, the Prostate Cancer Specialized Program of Research Excellence at The University of Texas MD Anderson Cancer Center; and in part by the NIH through MD Anderson’s Cancer Center Support Grant, CA016672.

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Received May 24, 2011; revised September 28, 2011; accepted October 11, 2011; published OnlineFirst October 24, 2011.
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doi:10.1158/0008-5472.CAN-11-1714

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