Research article

Akt-mediated phosphorylation of Bmi1 modulates its oncogenic potential, E3 ligase activity, and DNA damage repair activity in mouse prostate cancer

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Prostate cancer (PCa) is a major lethal malignancy in men, but the molecular events and their interplay underlying prostate carcinogenesis remain poorly understood. Epigenetic events and the upregulation of polycomb group silencing proteins including Bmi1 have been described to occur during PCa progression. Here, we found that conditional overexpression of Bmi1 in mice induced prostatic intraepithelial neoplasia, and elicited invasive adenocarcinoma when combined with PTEN haploinsufficiency. In addition, Bmi1 and the PI3K/Akt pathway were coactivated in a substantial fraction of human high-grade tumors. We found that Akt mediated Bmi1 phosphorylation, enhancing its oncogenic potential in an Ink4a/Arf-independent manner. This process also modulated the DNA damage response and affected genomic stability. Together, our findings demonstrate the etiological role of Bmi1 in PCa, unravel an oncogenic collaboration between Bmi1 and the PI3K/Akt pathway, and provide mechanistic insights into the modulation of Bmi1 function by phosphorylation during prostate carcinogenesis.

Introduction
Prostate cancer (PCa) is the most frequently diagnosed noncutaneous malignancy and a leading cause of cancer death among men in the Western world (1). PCa develops in gradual stages that display increasing pathology, ranging from premalignant low- and high-grade prostatic intraepithelial neoplasia (PIN) to capsule-confined and invasive carcinoma, ultimately evolving to lethal hormone-refractory metastatic disease. Despite its clinical impact, the molecular mechanisms underlying prostate carcinogenesis remain poorly understood. Several genetic events have been implicated in PCa development, including alteration of PTEN, CDKN1B (also referred to as p27), RB, androgen receptor, RNaseL, and NKX3.1; amplification of Bcl2 and c-Myc oncogenes; and TMPRSS2-ETS fusion gene rearrangements (2). Among the most frequent, PTEN monoallelic loss is found in 30%–70% of PCa patients at the time of diagnosis, whereas loss of heterozygosity is associated with advanced PCa (3–5). PTEN antagonizes the actions of PI3K by dephosphorylating the lipid second messenger phosphatidylinositol 3,4,5-trisphosphate (PIP3) and thereby exerts its tumor suppressor function mainly by restraining the PI3K/Akt prosurvival pathway (6). There is no evidence of germline PTEN mutations in hereditary prostate cancer (7, 8), which suggests that interactions between PTEN haploinsufficiency and other genetic and/or epigenetic determinants are required for prostate tumorigenesis.

In the past years, epigenetic events such as DNA methylation and histone modification have emerged as important mechanisms in the course of PCa (9). In line with this, upregulation of polycomb group (PcG) epigenetic silencers EZH2, Ring1B, and Bmi1 has been shown to accompany PCa progression and correlate with poor clinical outcome (10–14).

Bmi1 is a core component of the polycomb repressive complex 1 (PRC1). It forms a heterodimer with Ring1B/Rnf2 and stimulates its ubiquitin ligase activity toward lysine 119 of histone 2A (H2A-K119) (15, 16), thereby contributing to a crucial mechanism of PcG-mediated gene silencing (17). Bmi1 was initially identified as an oncogene cooperating with c-Myc in lymphomagenesis (18); later, Bmi1 upregulation was detected in a variety of human malignancies, including PCa (19). Bmi1 protein also undergoes phosphorylation (20, 21) at 3 highly conserved serines (22–30), which suggests that, beyond the cellular level, Bmi1 activity may also be regulated posttranslationally. In addition to its role in cellular transformation, Bmi1 is also a critical regulator of cellular senescence and stem cell self-renewal (31, 32). Mechanistically, Bmi1 functions are largely attributed to its potent transcriptional repression of the CDK2A locus that encodes p16INK4A and p19ARF/ p14ARF cell cycle regulators (31, 33), although Ink4a/Arf-independent functions of Bmi1 have also been demonstrated (34, 35).

Despite correlative evidence, a causal role for Bmi1 in PCa, alone or in the context of additional somatic mutations, has not been demonstrated. In the current study, we generated a
conditional transgenic mouse model in order to address the role of forced prostate-specific expression of Bmi1 in PCa etiology. We showed that the rise of Bmi1 led to PIN formation and acted synergistically with PTEN haploinsufficiency in the transition from PIN to invasive cancer. We provided evidence that this cooperation occurred through Akt-mediated phosphorylation of Bmi1, a posttranslational modification that increased its oncogenic potential, stimulated H2A-K119 ubiquitination in vitro and at sites of DNA double-strand breaks (DSBs) and promoted homologous recombination (HR) and genomic instability in PCa.

**Results**

Overexpression of Bmi1 induces neoplastic transformation of the prostate epithelium. In order to gain more insight into the etiological role of Bmi1 elevation in prostate tumorigenesis, we generated mice with conditional, Cre-mediated Bmi1 overexpression in the prostate epithelium (Figure 1A and Supplemental Methods; supplemental material available online with this article; doi:10.1172/JCI57477DS1). Expression of the ROSA26 Lox-STOP-Lox Bmi1 allele (Bmi1^{1SL}) in the luminal cells of the prostate epithelium was achieved by crossing Bmi1^{1SL} animals to the ARR2Probasin-Cre (PbCre4) transgenic line (ref. 36 and Supplemental Figure 1A).
Mouse cohorts were systematically analyzed at 3, 6, 9, and 12 months. At 6 months, atypical hyperplastic foci were observed in the prostate lobes of PbCre4;Bmi1LSL mice. These early lesions were characterized by enlargement of nuclear diameter, thickening of nuclear membrane, hyperchromasia, and conspicuous presence of nucleoli. From 9 months onward, about 20% of PbCre4;Bmi1LSL animals showed multifocal PIN lesions, a precursor stage of PCa (Figure 1, B and C). PbCre4;Bmi1LSL PINs displayed micropapillary, cribriform, and/or tuft-like structural organizations reminiscent of human low-grade PINs (Figure 1E and Supplemental Figure 1B). However, histopathological analysis of a large cohort of PbCre4;Bmi1LSL males did not show adenocarcinoma lesions over a year of monitoring. These data demonstrated that Bmi1 overexpression in the prostate was sufficient to initiate epithelial neoplastic transformation.

Bmi1 cooperates with PTEN haploinsufficiency in prostate cancer progression. The absence of adenocarcinoma in PbCre4;Bmi1LSL mice prompted us to investigate whether additional mutations could collaborate with Bmi1 overexpression to promote tumorigenesis. We addressed this in the context of heterozygous PTEN deletion because (a) PTEN monoallelic mutations are often detected in human primary PCAs, (b) Bmi1 exerts a positive effect on Akt activation in breast cancer cells (37, 38), and (c) Bmi1 represses PTEN expression in nasopharyngeal cancer cells (39).

At 9 months of age, nearly 40% of PbCre4;PtenloxP/ mice developed multifocal PIN lesions that never progressed to carcinoma (Figure 1, B, C, and F, and Supplemental Figure 1B), confirming previous reports (40). Analysis of the compound mutant mice revealed that elevation of Bmi1 and PTEN heterozygous loss displayed striking cooperativity. Aside from a significantly shortened latency of PIN lesions to 6 months of age, from 9 months, PbCre4;Bmi1LSL;PtenloxP/ mice developed prostate adenocarcinomas that reached a penetrance of 55% at 1 year (Figure 1, B, C, and G, and Supplemental Figure 1B).

PbCre4;Bmi1LSL;PtenloxP/ tumors were multifocal, with predominant localization in the dorsolateral lobe, accompanied by frequent bladder outlet obstruction, locally invasive and highly vascularized (Supplemental Figure 2, A and B, and Figure 1G). Stromal reaction as well as lymphocyte and neutrophil infiltrations were frequently observed (data not shown). Histologically, adenocarcinomas were composed of poorly differentiated cells with perturbed polarity, as well as areas of picnotic/necrotic cells (Figure 1G). Lesions were

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**Figure 2**

Secretory luminal epithelial phenotype of PbCre4;Bmi1LSL;PtenloxP/ prostate cancer cells. Immunohistochemical staining of formalin-fixed paraffin-embedded prostate tissue sections. (A–D) Cytokeratin 14 (CK14) and (E–H) p63, marking basal cells. (I–L) Synaptophysin, marking neuroendocrine cells. (M–P) Cytokeratin 8 (CK8), (Q–T) androgen receptor (AR), and (U–X) E-cadherin, marking secretory luminal cells. Insets are enlarged 5-fold; in X, insets show both tumor (T) and normal prostatic duct (N). Scale bar: 100 μm.
highly proliferative, as indicated by the prevalence of mitotic figures and the abundance of Ki-67-labeled nuclei (Figure 1G and Supplemental Figure 2C). Metastases were not detected over the course of monitoring (lymph nodes, testes, kidney, lung, liver, pelvic, and femur were systematically analyzed).

Prostate immunohistological analysis of the entire animal cohort revealed that PbCre4;Bmi1LSL and PbCre4;Bmi1LSL;PtenloxP/loxP prostate consistently expressed high levels of Bmi1, whereas PbCre4;PtenloxP/loxP and PbCre4;Bmi1LSL;PtenloxP/loxP prostate showed upregulation of phosphorylated Akt (pAkt; Figure 1, H–O, and Supplemental Figures 3 and 4), indicative of PI3K/Akt pathway activation. Together, these results demonstrated the oncogenic collaboration between Bmi1 and PTEN haploinsufficiency and identified a Bmi1-PI3K/Akt synergistic axis driving invasive prostate carcinogenesis. PbCre4;Bmi1LSL;PtenloxP/loxP tumors recapitulate features of human PCa. The prostate epithelium consists of 3 differentiated cell types: luminal-secretory, basal, and neuroendocrine. In order to identify the subpopulation of cells present in the PINs and adenocarcinoma, prostates from different mouse genotypes were analyzed for the subpopulation of cells present in the PINs and adenocarcinoma.

Figure 3

Bmi1 expression and activation of PI3K/Akt pathway correlate in high-grade prostate cancer clinical samples. (A) Representative immunohistochemical staining for Bmi1 and pAkt on adjacent sections of formalin-fixed, paraffin-embedded human prostate cancer specimens. Scale bar: 100 μm. (B) Immunohistochemical assessment of Bmi1 and pAkt expression status in 168 human prostate tumors categorized according to histological or clinical grade (see Table 1). Bmi1+pAkt+ tumors were associated with high Gleason scores (P = 0.001) and with advanced pathological stage (P = 0.002). (C) Immunohistochemical assessment of Bmi1 and pAkt expression status in 168 human prostate tumors categorized according to both histological and clinical grade (see Table 1). Bmi1+pAkt+ tumors were associated with worsening of both Gleason score and pathological stage (i.e., Gleason ≥ 8 and pT3; P = 0.001). Clinical tissue specimens were selected from patients subjected to radical prostatectomy at our institution and classified according to their respective histopathological grade (postoperative Gleason score) or clinical stage (TNM system). Histological categories divided tumors with Gleason score of 7 or less from those with Gleason score of 8 or more (Gleason ≤ 7, 89 cases; Gleason ≥ 8, 79 cases), whereas clinical stage groups were defined as prostate-confined disease (pT2, 75 cases) and disease with extraprostatic extension (pT3, 93 cases). The results are summarized in Figure 3, B and C, and detailed in Table 1. The total proportion of Bmi1-expressing tumors (i.e., Bmi1+pAkt and Bmi1+pAkt+) appeared nearly equal between pT2 and pT3 stages (57.3% and 61.3%, respectively) and increased in Gleason ≥ 8 compared with Gleason ≤ 7 tumors (69.6% versus 50.5%; Figure 3B and Table 1).

This is consistent with a previous report suggesting that Bmi1 is overexpressed from early stages of the disease onward (13). pAkt-positive specimens (i.e., Bmi1+pAkt and Bmi1+pAkt+) were predominantly found in the Gleason ≥ 8 group (31.6%, versus 9% in Gleason ≤ 7) and within the pT3 grade tumors (28% versus 9.4% in pT2; Figure 3B and Table 1).

Remarkably, we found a significant correlation between Bmi1 and pAkt coexpression (i.e., Bmi1+pAkt+) and worsened pathological grade (Gleason ≥ 8, 24%; Gleason ≤ 7, 4.5%; P < 0.001). Similarly, Bmi1 and pAkt expression is overexpressed from early stages of the disease onward (13).
Bmi1 and pAkt coexpression was associated with advanced clinical stage (pT3, 22.6%; pT2, 2.7%; \( P = 0.002 \); Figure 3B and Table 1). In addition, when specimens were sorted according to both pathological grade and clinical stage, Bmi1 and pAkt were found to be preferentially coexpressed in the highest tumor grade category, with 30% incidence in Gleason ≥ 8 and pT3 specimens (compared with 9.1% in Gleason ≤ 7 and pT3, 5.3% in Gleason ≥ 8 and pT2, and 1.8% in Gleason ≤ 7 and pT2; \( P = 0.001 \); Figure 3C and Table 1).

Given the heterogeneity and the focality of PCa, it is common to observe the presence of tumor areas, PIN lesions, and normal prostate glands within the same histology slide. When this was the case, we scored PINs and normal glands for Bmi1 and pAkt expression. This revealed that Bmi1 was more frequently expressed in PINs than in normal glands. pAkt, which was rare but present in PINs, was virtually absent in nondiseased tissue, and always associated with Bmi1 (Supplemental Figure 5). This shows that expression of Bmi1 and pAkt and their association are unlikely to reflect variations between individuals, but rather represent a trait of increasing severity of neoplastic lesions. Together, these results indicate that upregulation of Bmi1 and activation of the PI3K/pAkt pathway are associated with adverse tumor characteristics, such as increasing pathological grade (poor cell differentiation) and worsening of clinical stage (extraprostatic extension).

Interestingly, we noticed that PIN lesions arising in 
\( \text{PbC}^{\text{cre}4\text{Pten}^{\text{loxP/lox}}/\text{loxP}} \) prostata ctis exhibited a slight elevation of Bmi1 expression compared with intact prostate ducts (Figure 1, H and J), which further highlights the parallels of the \( \text{PbC}^{\text{cre}4\text{Pten}^{\text{loxP/lox}}/\text{loxP}} \) mouse model with the human disease. We also observed that doxycycline-induced suppression of Bmi1 sensitized the human prostate adenocarcinoma cell line LNCaP (LNCaP-tet-off Bmi1 cell system) to growth inhibition induced by chemical inhibition of pAkt (Supplemental Figure 6), which suggests that Bmi1 and the PI3K pathway might be functionally linked in prostate cancer progression.

\text{Akt phosphor} ylates Bmi1. Next, we investigated the molecular mechanisms underlying the interaction between Bmi1 and the PI3K pathway. Our initial observations in MEFs and in the PNT1a immortalized human prostate epithelial cell line revealed that modulation of Bmi1 did not significantly affect mRNA or protein levels of Pten, and vice versa (data not shown). This prompted us to test other possible mechanisms of interaction.

\text{Bmi1 is a phosphorylated protein (20, 21), yet the biological functions of its phosphorylation remain to be determined. To test whether Bmi1 and the PI3K/Akt pathway interact via phosphorylation of Bmi1, we first quantified the proportion of phosphorylated Bmi1 (pBmi1) relative to total Bmi1 in \text{PTEN}-deficient, pAkt-high cells (Jurkat cells as well as PCa cell lines PC3 and LNCaP) and \text{PTEN}-proficient, pAkt-low cells (MCF7 and U2OS cells as well as PCa cell line DU145). We observed that the pBmi1/Bmi1 ratio was higher in \text{PTEN}-deficient, pAkt-high cells than in \text{PTEN}-proficient cells with lower pAkt levels (Figure 4A). This suggested that phosphorylation of Bmi1 might be directly influenced by PI3K/pAkt activity. To further test that hypothesis in prostate cells, we reconstituted PTEN in LNCaP cells. Expression of PTEN resulted in a dramatic decrease in pAkt levels, which was accompanied by a reduction in the levels of phosphorylated Bmi1 in favor of faster migrating, unphosphorylated Bmi1 species (Figure 4B). These data indicate that the PI3K/Akt pathway stimulates phosphorylation of Bmi1. Consistently, treatment of U2OS cells with PI3K inhibitors reduced the levels of phosphorylated Bmi1 (Supplemental Figure 7A).}

Besides Akt, PI3K activates other proteins that may influence Bmi1 phosphorylation. Therefore, we sought to determine whether Akt itself is able to phosphorylate Bmi1. First, we treated PC3 and LNCaP cells with inhibitor VIII, which is specific for Akt. This resulted in a diminished pBmi1/Bmi1 ratio from approximately 70% to approximately 55%, down to the level observed in pAkt-low DU145 and PNT1a cells, whereas no effect of pAkt inhibition was observed in these later cells (Figure 4C). Similarly, siRNA-mediated knockdown of Akt1 and Akt2 isomers in LNCaP cells also decreased the pBmi1/Bmi1 ratio (Supplemental Figure 7B). We conclude that Akt activity stimulates phosphorylation of Bmi1 in human PCa cells. Notably, in some instances, the reduced levels of pAkt were accompanied with an apparent increase in total amount of Bmi1, without affecting the global decrease of the pBmi1/Bmi1 ratio. This is likely due to a selection effect of pAkt inhibition, in which cells with higher Bmi1 levels survive/proliferate more during Akt inhibitor treatment than do those with low Bmi1 levels (see Supplemental Figure 6).

Next, we addressed whether Bmi1 is a direct substrate for Akt. We performed an in vitro Akt kinase assay in the presence of [γ-32P]ATP. To ensure stability and proper folding of Bmi1 protein, and because the Bmi1 homolog Mel-18 was shown to be phosphorylated only when complexed with Ring1B (41), we used a recombinant Bmi1/Ring1B complex. As shown in Figure 5A, Akt specifically phosphorylated Bmi1 and its downstream direct substrate, GSK3. The negative control GST was not phosphorylated; neither was Ring1B, which migrates at a lower molecular weight. Bmi1 phosphorylation was not observed in the presence of an inactive Akt protein (data not shown).

In vivo, 9 independent phosphoproteomics studies, using different settings and biological systems, have identified 3 highly conserved phosphorylated serine residues (S251, S253, and S255) of Bmi1. These sites can be phosphorylated by Akt, as indicated by a decrease in their dephosphorylation rate when treated with SR142801, a specific Akt inhibitor (Figure 5B). This indicates that Akt can directly phosphorylate Bmi1 on these serine residues. Together, these results support the notion that Akt regulates Bmi1 phosphorylation, which can contribute to Bmi1-mediated processes in prostate cancer.

Table 1

<table>
<thead>
<tr>
<th>Group</th>
<th>No. of specimens</th>
<th>Bmi1-pAkt−</th>
<th>Bmi1-pAkt+</th>
<th>Immunoactivity</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gleason ≤ 7 and pT2</td>
<td>( n = 56 )</td>
<td>23 (41%)</td>
<td>29 (51.8%)</td>
<td>1 (1.8%)</td>
</tr>
<tr>
<td>Gleason ≤ 7 and pT3</td>
<td>( n = 33 )</td>
<td>17 (51.5%)</td>
<td>12 (36.4%)</td>
<td>1 (3%)</td>
</tr>
<tr>
<td>Gleason ≥ 8 and pT2</td>
<td>( n = 19 )</td>
<td>4 (21%)</td>
<td>12 (63.2%)</td>
<td>2 (10.5%)</td>
</tr>
<tr>
<td>Gleason ≥ 8 and pT3</td>
<td>( n = 60 )</td>
<td>14 (23.3%)</td>
<td>24 (40%)</td>
<td>4 (6.7%)</td>
</tr>
<tr>
<td>All Gleason ≤ 7</td>
<td>( n = 89 )</td>
<td>40 (45%)</td>
<td>41 (46%)</td>
<td>4 (4.5%)</td>
</tr>
<tr>
<td>All Gleason ≥ 8</td>
<td>( n = 79 )</td>
<td>18 (22.8%)</td>
<td>36 (45.6%)</td>
<td>6 (7.6%)</td>
</tr>
<tr>
<td>All pT2</td>
<td>( n = 75 )</td>
<td>27 (36%)</td>
<td>41 (54.6%)</td>
<td>5 (6.7%)</td>
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<tr>
<td>All pT3</td>
<td>( n = 93 )</td>
<td>31 (33.3%)</td>
<td>36 (38.7%)</td>
<td>5 (5.4%)</td>
</tr>
<tr>
<td>Total</td>
<td>( N = 168 )</td>
<td>58 (34.5%)</td>
<td>77 (45.8%)</td>
<td>23 (13.7%)</td>
</tr>
</tbody>
</table>

Expression of Bmi1 and pAkt was evaluated by immunohistochemistry (IHC) on 168 human prostate cancers. Specimens were categorized in groups according to Gleason ≤ 7 and Gleason ≥ 8 and pathological stage pT2 and pT3.

http://www.jci.org/Volumes/122/Number 5/
Bmi1 greatly in vitro, Bmi1 greatly phosphorylates the endogenous protein, HA-tagged Bmi1-WT migrated as 2 distinct species; in contrast, HA-tagged Bmi1-3A migrated as a single band (Figure 5C), which indicates that phosphorylation of the Bmi1-3A mutant, mutation of cognate serines 251, 253, and 255 are critically involved in vitro and in vivo and that the triad serine residues 251, 253, and 255 are critically involved in this process.

Phosphorylation of Bmi1 modulates H2A ubiquitination and DNA repair. In vitro, Bmi1 greatly stimulates Ring1B E3 ligase activity, and both proteins form an active core that is sufficient for the efficient ubiquitination of H2A-K119 (15, 16). To characterize how phosphorylation modulates Bmi1 function, we assayed the H2A ubiquitin ligase activity of the Bmi1/Ring1B complex pretreated with alkaline phosphatase (AP). Whereas Bmi1/Ring1B treated with inactivated AP efficiently ubiquitinated H2A, this was greatly diminished by active AP treatment (Figure 6A). The Mel18/Ring1B complex (41) was used as a positive control. Interestingly, AP treatment did not affect the autopolyubiquitination of the complexes (Figure 6A).

Next, we assessed whether Akt-mediated phosphorylation of Bmi1 could stimulate Bmi1/Ring1B ligase activity. As shown in Figure 6B, addition of active Akt kinase into the ubiquitination assay led to an increase in ubiquitinated H2A (Ub-H2A), whereas addition of inactive Akt had no effect. This indicates that phosphorylation of Bmi1 by Akt contributes to its stimulatory effect on Ring1B ubiquitin ligase activity in vitro. Since increased Ub-H2A levels influence global gene expression, we asked whether phosphorylation of Bmi1 affects global Ub-H2A levels in LNCaP cells. We used LNCaP-tet-shBmi1 cells expressing Bmi1-WT or Bmi1-3A retroviruses. In these cells, we observed that the global Ub-H2A level was not altered (Figure 6C). Similarly, chemical inhibition of Akt did not affect global Ub-H2A levels (Figure 6C). Consistently, we did not observe major changes in gene expression profiles of LNCaP-tet-shBmi1 cells expressing Bmi1-WT or Bmi1-3A (data not shown).

In addition, expression of Bmi1-3A mutant efficiently rescued shBmi1 cells expressing Bmi1-WT or Bmi1-3A retroviruses in the Pten/PI3K/pAkt axis modulates Bmi1 phosphorylation. (A) Western blot analysis and relative quantification of pBmi1/Bmi1 ratio in Jurkat, PC3, and LNCaP Pten-deficient pAkt-high cells and in MCF7, DU145, and U2OS Pten-proficient pAkt-low cells. (B) Western blot showed that retrovirus-induced expression of PTEN in LNCaP cells inhibited pAkt and Bmi1. (C) Bmi1 phosphorylation was positively modulated by pAkt level. Bmi1 phosphorylation and pAkt and PTEN status in DU145, PC3, LNCaP, and PNT1a prostate cell lines either left untreated or treated with 5 μM Akt inhibitor VIII (isozyme selective, Akt-1/2; Calbiochem) for 12 hours and refreshed 2 hours prior to lysis. pBmi1/Bmi1 ratios, quantified using ImageJ, are indicated within blots (2 separate experiments shown). The 3 lower panels corresponded to experiment 2. Phosphorylation status of the Akt substrate GSK-3β (pSer9) is shown as a control for Akt activity. Tubulin was used as a loading control.

![Figure 4](http://www.jci.org)
phosphorylation of Bmi1 is required for DNA damage-induced H2A monoubiquitination, Bmi1−/−;Ink4a/Arf−/− MEFs were reconstituted with vectors encoding either Bmi1-WT or Bmi-3A, and DNA DSBs were induced by UV laser scissor. As shown in Figure 7A, whereas both Bmi1-WT and Bmi1-3A were recruited to sites of DSBs, only Bmi1-WT was able to induce H2A ubiquitination. We also observed that in UV-irradiated cells, hyperphosphorylation of both Bmi1 and Akt was greatly induced (Figure 7B). Interestingly, Fraser et al. recently showed that Akt is phosphorylated in direct response to DNA DSBs, accumulates in the vicinity of IR-induced DSBs, colocalizes with DNA repair factors, and promotes DSBs repair (46). To determine whether UV-induced Bmi1-mediated H2A ubiquitination depends on Akt phosphorylation, we repeated the UV laser scissor treatment in the presence of Akt inhibitor (Figure 7A). Strikingly, this experiment revealed that under Akt inhibition, while still recruited to the damaged sites, Bmi1 behaved like the Bmi1-3A phosphomutant and lost its E3 ligase activity toward H2A.

To examine whether lack of Bmi1 phosphorylation affects HR repair of DSBs in cells, we used an I-Sce1 meganuclease homology-directed DNA repair assay that allows reporting of HR repair events by flow cytometry analysis of cellular GFP (47). Reconstitution of Bmi1-WT expression in Bmi1-depleted U2OS cells led to 3.3% of cells being GFP+, a 2.4-fold induction over empty vector- and Bmi1-3A-transfected cells (Figure 8A), which indicates that impairment of Bmi1 phosphorylation leads to defects in DSB-promoted HR repair.

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**Figure 5**
Bmi1 is phosphorylated by Akt. (A) In vitro Akt kinase assay with recombinant active Akt and Bmi1-WT/Ring1B or Bmi1-3A/Ring1B complex. Reactions were carried out for 40 minutes at 30°C in the presence of [γ-32P]ATP. GST and GST-GSK3α/β crosstide were used as negative and positive controls, respectively; phosphorylated proteins were visualized by autoradiography. A Coomassie-stained gel demonstrating equal loading is also shown. (B) Time course Akt kinase assay with recombinant active Akt and Bmi1-WT/Ring1B or Bmi1-3A/Ring1B complex. Equal amounts of substrate proteins and Akt were used in each assay. (C) Western blot analysis showing that HA-tagged Bmi1-3A was not phosphorylated in LNCaP cells.

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**Figure 6**
Effect of Bmi1 phosphorylation on H2A ubiquitination and cellular senescence. (A) Bmi1/Ring1B recombinant complex was first treated with AP or Na3VO4-inactivated AP, then assayed for ubiquitin ligase activity on purified nucleosomes. Dephosphorylation of Bmi1 reduced Bmi1/Ring1B E3 ligase activity on H2A (Ub-H2A); Mel18/Ring1B is shown as a positive control. Autopolyubiquitination of Bmi1/Ring1B and Mel18/Ring1B complexes is also shown. (B) Bmi1/Ring1B complex was first incubated with Akt or inactive Akt (inAkt), then assayed for ubiquitin ligase activity as in A. (C) Global Ub-H2A levels were not affected in doxycycline-treated (Dox) LNCaP-tet-shBmi1 cells expressing Bmi1-3A, nor in the presence of Akt inhibitor. (D) Phosphorylation of Bmi1 was not required for repression of cellular senescence. Bmi1−/− MEFs were infected with a control retrovirus (EV; empty vector) or with retroviruses encoding Bmi1-WT or Bmi1-3A. 3T3 assay was performed over a period of 32 days; Western blot against Bmi1, p16INK4A, and tubulin (loading control) is also shown.
To extend our results, we examined HR in our LNCaP-tet-shBmi1 cell system by measuring the frequency of spontaneous sister chromatid exchanges (SCEs), a commonly used index of chromosomal stability. In doxycycline-treated LNCaP-tet-shBmi1 cells, expression of Bmi1-WT, but not Bmi1-3A, led to a statistically significant, 2.3-fold increase of spontaneous SCEs (Figure 8B). Importantly, this effect was dependent on Akt activity, since Akt inhibition completely abolished the effect of Bmi1-WT, reducing the number of SCEs to basal levels (Figure 8B). These results prompted us to assess the level of DNA damage in our mouse and human prostate tumor sets using γ-H2AX immunohistochemistry. Tumor areas of PbCre4;Bmi1LSL;PtenloxP/+ mice and Bmi1/pAkt positive human samples exhibited high levels of DNA damage, which was absent — or present to a much lesser extent — in control mouse prostates and Bmi1/pAkt single-positive and double-negative human samples (Figure 8C). Together, these data showed that Akt-dependent phosphorylation of Bmi1 was required for DNA damage-induced H2A ubiquitination and efficient DNA repair and that sustained phosphorylation of Bmi1 by Akt led to genomic instability, as assessed by high HR rates.

Figure 8B
Phosphorylation of Bmi1 increases its oncogenic potential in vitro and in vivo. To determine whether Bmi1 phosphorylation influences its oncogenic function, we assessed the transformation potential of Bmi1-3A in a soft agar colony formation assay using Ink4a/Arf–/– MEFs overexpressing c-Myc. As expected, Bmi1-WT readily conferred anchorage-independent cell growth, whereas Bmi1-3A was severely impaired in this process (Figure 9A), which indicates that Bmi1 phosphorylation is a requisite for its transformation ability.

To address the relevance of these findings in the context of PCa, we assessed the ability of Bmi1-WT or Bmi1-3A to rescue the growth defect observed in doxycycline-treated LNCaP-tet-shBmi1 cells. LNCaP-tet-shBmi1 cells were then superinfected with retroviruses encoding shRNA-insensitive mouse Bmi1-WT or Bmi1-3A. Ectopically expressed Bmi1-WT significantly rescued the growth defect of LNCaP-tet-shBmi1, whereas expression of Bmi1-3A remained ineffective (Figure 9B). This effect
was partly dependent on the expression of the cell cycle regulator p21CDKN1A (Supplemental Figure 9A). Consistently, when injected subcutaneously in Balb/c nude mice, LNCaPs expressing Bmi1-WT generated significantly larger tumors than parental and Bmi1-3A–expressing LNCaPs (Figure 9C and Supplemental Figure 9B). In addition, we performed orthotopic transplant experiments using immortalized human prostate epithelial cells (hPrECs). hPrECs expressing SV40 LT, hTERT, c-Myc, and PI3K (LHMK) were previously shown to have limited tumor-forming capability (48). In our study, we used hPrECs that express SV40 LT, hTERT, c-Myc, and shPTEN (LHMshP) (Supplemental Figure 9C). LHMshP hPrECs also displayed limited tumor-forming ability (Figure 9D). However, overexpression of Bmi1-WT in these cells increased their tumorigenicity 2.5-fold relative to empty vector–expressing LHMshP hPrECs (Figure 9D). Expression of Bmi1-3A in LHMshP hPrECs only had a moderate effect on tumorigenicity, which indicates that Bmi1 phosphorylation is required for efficient stimulation of PCA cell growth. Finally, we investigated whether these findings could be extended to other tumor types. It is well established that Bmi1 cooperates with c-Myc to induce lymphoma in mice (18, 33). We therefore tested the ability of Bmi1-3A to accelerate lymphomagenesis in a transduction/reconstitution assay using the Eμ-Myc lymphoma model (49). Eμ-Myc–derived hematopoietic stem and progenitor cells (HSPCs) transduced with a retrovirus encoding Bmi1-WT or Bmi1-3A were engrafted into lethally irradiated syngeneic mice. Animals reconstituted with Eμ-Myc control cells developed lymphoma with a median survival of 88 days (Figure 9E and Supplemental Figure 9D). As expected, overexpression of Bmi1-WT resulted in significant acceleration of lymphomagenesis compared with control (median survival, 61 days; \( P = 0.0064 \)). In contrast, overexpression of Bmi1-3A had no significant effect on lymphoma
onset compared with control (median survival, 73 days; \( P = 0.061 \); Figure 9E), which indicates that phosphorylation of Bmi1 constitutes an important signal for its in vivo lymphomagenic potential as well. Together, these results show that Bmi1 phosphorylation, by Akt and possibly other kinases, plays a major role in the modulation of Bmi1 oncogenic potential in vitro and in vivo.

**Discussion**

Bmi1 overexpression cooperates with PTEN haploinsufficiency in invasive prostate cancer. Although previous studies suggested a positive correlation between Bmi1 expression and PCA progression (11, 13), a causal role was not demonstrated experimentally. By targeting Bmi1 overexpression to the murine prostate, we showed that it was sufficient to initiate the first steps of prostate carcinogenesis. Hence, this established a direct role for the PcG epigenetic silencer Bmi1 in the etiology of prostate cancer.

We found that Bmi1 and PI3K/Akt were coactivated in high-grade human PCAs. Consistently, \( PbCre4;Bmi1^{L58S};Pten^{lox/lox} \) animals developed invasive prostate adenocarcinoma that recapitulated features of human disease: medium/late onset, exhibition of neoplastic precursor stages, and multifocality. Moreover, the cancerous lesions developed for the most part in the dorsolateral lobe of the mouse prostate, which is considered homologous to the human peripheral zone from which most cancers arise (50). In \( PbCre4;Bmi1^{L58S};Pten^{lox/lox} \), mouse progression to metastatic disease was not observed, suggestive of the requirement of additional genetic and/or epigenetic events. In this regard, another PcG member, EZH2, which is expressed in high-grade and metastatic PCAs (10), promotes metastasis in an orthotopic transplantation PCA model (51). It will be of interest to address whether prostate-targeted EZH2 expression can induce metastatic conversion of \( PbCre4;Bmi1^{L58S};Pten^{lox/lox} \) tumors.

Both Bmi1 and PI3K/Akt signaling pathways are activated in PCA stem-like cell populations (52). Recently, Lukacs and colleagues reported that Bmi1 inhibition attenuates the growth of Pten-null prostate cancer cells and that Bmi1 expression is required for the maintenance of normal stem-like cells (53). Our studies support and extend these findings by describing underlying molecular mechanisms and prompt new investigations using \( PbCre4;Bmi1^{L58S} \) and \( PbCre4;Bmi1^{L58S};Pten^{lox/lox} \) models to further characterize the cancer cell of origin and pathways involved in normal and cancer stem cell maintenance in the prostate epithelium.

**Regulation of Bmi1 oncogenic potential by phosphorylation**

Besides their increased levels in a variety of cancers, including in the prostate, PcG proteins also undergo posttranslational modifications (54), the consequences of which remain largely unknown. Recent studies have uncovered a function for Bmi1 in DNA damage response and demonstrated its role in H2A\(\gamma\)-H2AX ubiquitination at DSBs and for efficient DNA damage repair (42–45, 55). Here, we revealed an important role for Bmi1 phosphorylation in mediating HR repair through the stimulation of H2A ubiquitination.
tion at damaged sites. Consistent with Akt activation in response to DNA damage and its accumulation at DSBs (46), we demonstrated that Akt plays an important role in the local stimulation of Bmi1 ubiquitin ligase activity on H2A. Although our in vitro experiments showed direct phosphorylation of Bmi1 by Akt, we cannot exclude that Akt-mediated phosphorylation of Bmi1 in vivo may be indirect. Nevertheless, our findings suggest a great degree of complexity in the regulation of Bmi1 and validate the existence of cross-talk between Bmi1/PI3K/Akt and DNA damage repair pathways. It is critical to understand the mechanisms underlying this cross-talk for the design of rational therapeutic strategies that could disrupt these connections for the radiosensitization of tumors with hyperactivated Bmi1 and PI3K/Akt signaling. From its earliest stages, cancer development of various tumor types is associated with DNA replication stress, which leads to DNA strand breaks. Both deficient and exacerbated HR activity determine genome instability (56, 57), which is directly implicated in tumor progression (58). Although DNA damage repair per se would not cause cancer, it is likely that over time, constitutively increased DNA damage repair activity in combination with pro-survival signals can enable cancerous and/or precancerous cells to survive disastrous DNA damage and, in an insidious loop, allow accumulation of mutation events, increasing overall genomic instability and cancer progression.

Elevated DNA repair capacity in cancer cells is also known to limit the efficacy of radiation therapy. In line with this, Bmi1 confers radioresistance to normal and cancerous cells (43, 44). The PI3K/Akt pathway is also involved in increased radioresistance (59–62). This raises the possibility that patients with advanced prostate cancer showing elevated Bmi1 and pAkt may benefit from pharmacological inhibition of Bmi1 and/or Akt combined with radiation therapy.

Loss of PTEN leads to genomic instability, and physiological activation of Akt (as a result of genetic inactivation of PTEN) was previously shown to suppress DNA damage processing and checkpoint activation in late G2 (63). Ginjala et al. reported that loss of Bmi1 leads to accumulation of cells in G2/M associated with DNA damage checkpoint activation (45). Therefore, increase of Bmi1 level and its phosphorylation, together with Akt activation, may synergize to increase their potential to bypass G2/M checkpoint arrest in the face of genotoxic damage and increase genomic instability, which is a hallmark of neoplastic progression.

Phosphorylation of Bmi1 is likely to be involved in the fine-tuning of its activity in a gene- or context-specific manner, rather than in the global regulation of PRC1 function. Indeed, mutation of Bmi1 phosphorylated sites or Akt inhibition did not affect the global levels of Ub-H2A or the ability to repress the Ink4a/Arf locus, and we did not observe major differences in global gene expression profiles of Bmi1-3A– versus Bmi1-WT–expressing LNCaP cells, although some changes in potentially important cell cycle regulators were observed (such as p21; Supplemental Figure 8A).

This phosphoregulation may serve to separate Bmi1-repressive and repair functions and to rapidly modulate its enzymatic activity in a local, specific context, while leaving global H2A ubiquitination and PRC1-mediated gene repression intact. Such a “local” mode of regulation benefits from its reversibility, as dephosphorylation of Bmi1 may occur readily after repair along with H2A deubiquitination at repaired DSBs, while global Ub-H2A levels must remain stable.

Acute loss of Pten in MEFs and in the prostate triggers oncogene-induced senescence via upregulation of the Ink4a/Arf locus and the p53 pathway (64). Overexpression of Bmi1 in MEFs bypasses Pten loss-induced senescence and is accompanied by Ink4a/Arf downregulation (Supplemental Figure 10), which suggests that part of Bmi1’s oncogenic activity involves its repression function, notably toward Ink4a/Arf. However, the involvement of Ink4a/Arf in prostate carcinogenesis is still debated, since Arf deficiency partially inhibits the prostate cancer phenotype of Pten-deficient mice (65) and prostates lacking Ink4a/Arf do not develop cancerous/precancerous lesions over a long period of time (66), in line with a notable rarity of INK4a/ARF inactivation in human PCa. It was suggested that Bmi1 may stimulate human PCa cell growth in part via repression of the INK4a/ARF locus (67). As far as we have observed, the expression of that locus was low to absent in most PCa cells tested, and Bmi1 expression (either WT or 3A) did not further repress it (data not shown).

Our study revealed that Bmi1 induced PIN lesions, which suggests that the role of Bmi1 in PCa is more complex and goes beyond Ink4a/Arf repression and is, at least in part, uncoupled from its antisenescence activity and modulated by its phosphor-

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Methods

Mice. Bmi1+/id mice (see Supplemental Methods) were crossed with P6Crend (36) and Pten1/2 (68) FVB mice to generate the cohort used in the present study.

For the LNCAP xenograft assay, 7-week-old male Balb/c nude mice were subcutaneously injected with 2 x 10^6 cells in PBS with 50% Matrigel (BD) in a volume of 500 μl. Tumor growth was monitored daily, and mice were sacrificed after 4 weeks. Tumor size was determined by direct measurement after dissection, and samples were fixed in formalin for histopathological analysis.

Parental lprEC cells were a gift from W.C. Hahn (Dana-Farber Cancer Institute, Boston, Massachusetts, USA). For orthotopic transplantation of LHMShp lprECs, 10^6 cells (10 μl) were mixed with Matrigel (10 μl) and injected into the anterior prostate lobe of 8-week-old nude mature males. Injected cells expressed luciferase, and tumor outgrowths were monitored weekly by IVIS bioluminescence Imaging System.

The lymphoma assay was performed essentially as described previously (69). Hematoxytopic Eμ-Myc fetal liver cells were infected with retroviruses encoding Bmi1-WT or Bmi1-3A and intravenously injected into lethally irradiated mice. Reconstituted animals (5 per group) were monitored for illness by lymph node palpation and overall morbidity. Overall survival was defined as the time from stem cell reconstitution until the animal reached morbidity, and statistical analysis was performed using the Mantel-Cox test.

Histopathology and immunohistochemistry. Prostate lobes were individu-ally evaluated for pathology according to the guidelines of the Bar Har- bor Mouse Models of Human Cancer Consortium Prostate Pathology committee. IHC was done according to the manufacturers’ recommenda-tions. The following primary antibodies were used: Bmi1 mAb (clone F6; Upstate); pAkt (Ser473) (D9E; Cell Signaling); Cytokeratin14 (PRB-155P; Babco/Covance); p63 (4A4; Santa Cruz); synaptophysin (A00100; Dako); cytokeratin 8 (Troma-1; Developmental Study Hybridoma Bank, University of Iowa); androgen receptor (sc-816; Santa Cruz); E-cadherin (36/EC; BD Transduction Laboratories); Ki-67 (TEC-3; Dako). Secondary antibodies were coupled to Strep-AB complex, and immunodetection was performed using Liquid DAB Substrate Chromogen System (Dako) and counterstained with hematoxylin.

Human tissue specimens. 168 formalin-fixed paraffin-embedded primary PCa specimens were provided from the Nederlands Kanker Instituut-Antoni van Leeuwenhoek (NKI-AVL). Pathohistological characterization and grading of the 168 PCa cases was assessed by the Division of Human Pathology, NKI-AVL, as part of routine clinical management. The tissue cohort was divided by both Gleason score (≥ 7 and ≥ 8) and TNM tumor staging (pT2 and pT3). Scoring of immunostained slides was done accord-ing to the percentage of tumor cells exhibiting nuclear (Bmi1) or nuclear/ cytoplasmic (S473-pAkt) staining. To define positive and negative expres-sors, we used a cutoff of 30% or more positive tumor cells. Tumors were scored as double positive if they fulfilled above criteria in the same glandular area of 2 consecutive sections.

Statistics. Data are expressed as mean ± SD. Statistical significance was determined by 2-tailed Student’s t test, except for human tissue specimen analysis, for which χ^2 test was used. A P value less than 0.05 was considered statistically significant.

Study approval. All experiments involving the use of animals, including for the generation of MEFs, were reviewed and approved by the local Ani-mal Experiment Committee (DEC NKI, Amsterdam) and were conducted in compliance with the animal welfare regulations of The Netherlands. Paraffin-embedded human PCa tissue samples were provided by the tissue bank of the NKI in accordance with the regulations of the tissue bank and with the approval of the ethics committee of the NKI. Patients provided informed consent for the use of tissue.

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