eIF4E Activation Is Commonly Elevated in Advanced Human Prostate Cancers and Significantly Related to Reduced Patient Survival


Abstract

Elevated eukaryotic translation initiation factor 4E (eIF4E) function induces malignancy in experimental models by selectively enhancing translation of key malignancy-related mRNAs (c-myc and BCL-2). eIF4E activation may reflect increased eIF4E expression or phosphorylation of its inhibitory binding proteins (4E-BP). By immunohistochemical analyses of 148 tissues from 89 prostate cancer patients, we now show that both eIF4E expression and 4E-BP1 phosphorylation (p4E-BP1) are increased significantly, particularly in advanced prostate cancer versus benign prostatic hyperplasia tissues. Further, increased eIF4E and p4E-BP1 levels are significantly related to reduced patient survival, whereas uniform 4E-BP1 expression is significantly related to better patient survival. Both immunohistochemistry and Western blotting reveal that elevated eIF4E and p4E-BP1 are evident in the same prostate cancer tissues. In two distinct prostate cancer cell models, the progression to androgen independence also involves increased eIF4E activation. In these prostate cancer cells, reducing eIF4E expression with an eIF4E-specific antisense oligonucleotide currently in phase I clinical trials robustly induces apoptosis, regardless of cell cycle phase, and reduces expression of the eIF4E-regulated proteins BCL-2 and c-myc. Collectively, these data implicate eIF4E activation in prostate cancer and suggest that targeting eIF4E may be attractive for prostate cancer therapy. [Cancer Res 2009; 69(9):3866–73]

Introduction

Eukaryotic translation initiation factor 4E (eIF4E) binds the 5′-terminal, 7-methylguanosine cap of cellular mRNAs, bringing these mRNAs to the eIF4F translation initiation complex, which then scans 5′-3′ from the cap, unwinding RNA secondary structure to reveal the translation initiation codon and enable mRNA translation. Although required for translation of all cap-dependent mRNAs, elevated eIF4E function selectively and preferentially enhances the translation of mRNAs with lengthy, highly structured 5′ untranslated regions, as these mRNAs require increased eIF4F complex activity for ribosome loading (1–3). eIF4E also promotes the nucleocytoplasmic transport of select mRNAs (4). eIF4E-regulated mRNAs generally encode proteins involved in cellular growth and survival (e.g., c-myc, BCL-2, vascular endothelial growth factor, cyclin D1, and survivin; refs. 1–4). By selectively up-regulating translation of these malignancy-related mRNAs, eIF4E overexpression in experimental models drives malignancy (5–8). Conversely, reducing eIF4E expression reverses malignancy in experimental cancer models by selectively diminishing expression of these malignancy-related mRNAs (9–12), inducing apoptosis and suppressing tumor growth, invasion, and metastasis (13–15).

eIF4E availability is regulated by the inhibitory binding proteins, the 4E-BPs. 4E-BPs bind the same residues on eIF4E necessary for the eIF4E-eIF4G interaction, thereby blocking eIF4E complex assembly and cap-dependent translation (16, 17). AKT-mammalian target of rapamycin pathway signaling elicits 4E-BP phosphorylation, which liberates eIF4E from 4E-BP, promoting eIF4E complex assembly (3, 17) and cap-dependent translation (1–3, 18, 19).

Human prostate cancers initially depend on androgens for growth and survival and, accordingly, are treated with androgen deprivation therapy. However, even with androgen deprivation, prostate cancer cells re-emerge often due to the activation of cell survival signals (20), including increased BCL-2 expression (21) and AKT pathway activation (22), both of which have been repeatedly linked to prostate cancer progression in both human prostate cancer tissues and animal prostate cancer models (21–23).

Although eIF4E activation has been associated with malignant progression in many human cancers (e.g., head and neck, bladder, colon, breast, lung, and lymphoma; ref. 1), a role for eIF4E in human prostate cancer has not been established. eIF4E may be activated by eIF4E overexpression, reduced 4E-BP expression, or 4E-BP phosphorylation elicited by AKT pathway signaling. Herein, we show that eIF4E activation is elevated significantly with progression in human and experimental prostate cancer and is significantly related to reduced patient survival. Moreover, blocking eIF4E expression in prostate cancer cells with an eIF4E-specific antisense oligonucleotide (4EASO) now in clinical trials suppresses expression of eIF4E and the eIF4E-regulated proteins, c-myc and BCL-2, robustly inducing apoptosis regardless of cell cycle phase. Collectively, these data implicate enhanced eIF4E activation in human prostate cancer progression and indicate that eIF4E may be an attractive target for prostate cancer therapy.

Materials and Methods

Cell culture, transfection, and lysate preparation. Prostate cancer cells, LNCaP (androgen-dependent) and CWR22Rv1 (androgen-independent), were purchased from the American Type Culture Collection. Androgen-independent LNAI cells were derived from LNCaP xenografts...
Figure 1. eIF4E expression in primary human prostate cancer tissues. A, representative examples of eIF4E immunohistochemistry in BPH tissue from patients without prostate cancer (CaP), prostate cancer tissue, and adjacent (adj) BPH tissue from patients with Gleason score (G) 5 or 8. An IgG staining control is shown. B, eIF4E immunohistochemistry (IHC) scores are shown for the five tissue groups: BPH without prostate cancer, BPH adjacent to prostate cancer with a Gleason score <7 or ≥7 or prostate cancer <7 or ≥7. C, Western blot analyses for eIF4E, peIF4E5209, and β-actin in fresh-frozen human prostate cancer tissues. Each lane represents an individual patient sample.

selected for tumor growth after castration (22). Cells were transfected with 4EASO (5′-TGTGATATCTCTGATCCT-3′) as described (15). Lysates from cultured cells, mouse xenografts, or frozen human prostate cancer tissues were prepared for Western blotting and 7-methyl-GTP cocapture as described (15, 24). eIF4E and 4E-BP1 cocapture were executed from cell extracts by 7-methyl-GTP-Sepharose chromatography as described (25). For TaqMan quantitative reverse transcription-PCR, cDNA was generated using SuperScript III First Strand (Invitrogen) following RNA isolation with the RNeasy kit (Qiagen) and treated with DNase I (Ambion). TaqMan was done according to the manufacturer’s specifications on a 7900HT Real-time PCR System (Applied Biosystems) with these primer sets (Applied Biosystems): BCL-2 (Hs00608023_m1), myc (Hs00153408_m1), and eIF4E (forward 5′-GGGCGACTGTCGAACCG-3′, reverse 5′-AGATTTCCGCGTTCCTCT-3′, and probe 5′-AAACCCACCTACTCTCAA-3′; ref. 15).

Tissues, histopathology, and clinical information. Immunohistochemistry was done on 148 archived primary prostate tissue samples removed at surgery from 89 patients between 1986 and 1988 at St. Elizabeth Medical Center (Covington/Edgewood, KY) with institutional review board approval. For pathologic diagnosis, Gleason grade of each archived specimen was assessed by a board-certified pathologist (L.E.D.; ref. 26). Tissue consultation reports from the Department of Laboratory Medicine of the Tri-State Tumor Registry and St. Elizabeth Medical Center were used to confirm patient Gleason score. Clinical follow-up was obtained from the Tri-State Tumor Registry and consultation reports from the Department of Laboratory Medicine of St. Elizabeth Medical Center (Covington/Edgewood, KY) with institutional review board approval. For pathologic diagnosis, Gleason grade of each archived specimen was assessed by a board-certified pathologist (L.E.D.; ref. 26). Tissue consultation reports from the Department of Laboratory Medicine of St. Elizabeth Medical Center were used to confirm patient Gleason score. Clinical follow-up was obtained from the Tri-State Tumor Registry and consultation reports from the Department of Laboratory Medicine of St. Elizabeth Medical Center (Covington/Edgewood, KY) with institutional review board approval. Histoscores were generated by multiplying average stain intensity for each tissue by average percent area stained (histoscore = intensity × area). Accordingly, the most intense, uniformly stained specimen would have a histoscore of 2.7 (3 × 0.9; ref. 27).

High-content imaging for apoptosis, cell cycle, and eIF4E expression. Cell cycle, apoptosis, and eIF4E protein expression were measured simultaneously by multiplexing activated caspase-3, TUNEL, and eIF4E immunostaining with cell-level nuclear parameters including DNA content, nuclear area, average DNA content, and DNA variation as described (28). Cells were fixed with 3.7% formaldehyde solution (Sigma-Aldrich), washed in Dulbecco’s PBS (D-PBS), permeabilized with 0.1% Triton X-100/D-PBS, washed with D-PBS, and blocked 1 h in D-PBS/1% bovine serum albumin (Invitrogen). Cells were then incubated for 1 h with anti-activated caspase-3 (BD Biosciences; 1:250) and anti-eIF4E antibody (BD Biosciences; 1:150) in Permount (Fisher Scientific).
D-PBS/1% bovine serum albumin. Cells were washed twice with D-PBS and incubated 1 h with Alexa Fluor 488 goat anti-rabbit IgG (Invitrogen; 1:250), Alexa Fluor 647 goat anti-mouse IgG (Invitrogen; 1:250), and 200 ng/mL Hoechst 33342 (Invitrogen) diluted in D-PBS/1% bovine serum albumin. Cells were washed twice in D-PBS, and TUNEL staining was done (in situ Cell Death Detection kit, TMR Red; Roche Biochemicals) as per the manufacturer. Stained plates were scanned using ArrayScan Vti (Cellomics) and the Target Activation Bioapplication was used for four-channel quantification of signal as described (28).

**Statistical analyses.** All statistical analyses were done with the SAS program (SAS). Tissues were divided into five groups: (a) benign prostatic hyperplasia (BPH) from patients without prostate cancer, (b) BPH adjacent to moderately differentiated and well-differentiated prostate cancer (Gleason score <7), (c) BPH adjacent to poorly differentiated, high-grade prostate cancer (Gleason score ≥7), (d) low-grade prostate cancer (Gleason score <7), and (e) high-grade prostate cancer (Gleason score ≥7). Repeated-measures ANOVAs were done to evaluate relationships between staining patterns and tissue groups 1 to 5. Tukey's adjustment method was used to obtain P values when comparing tissue groups. Trend analyses were used to compare staining patterns across all tissue groups. Kaplan-Meier analyses (log-rank tests) and Cox proportional hazards regression were run to assess whether the staining patterns were related to patient survival.

**Results**

**eIF4E expression in human prostate tissues.** Increased eIF4E expression has been shown in a variety of human cancers (e.g., head and neck and breast; ref. 1). However, eIF4E expression in human prostate cancer tissues has not been established. We therefore evaluated eIF4E protein expression by immunohistochemistry in 148 human primary prostate tissues from 89 prostate cancer patients. We scored eIF4E immunostaining for percent area stained and immunostaining intensity. All prostate tissues, benign or malignant, showed similar percent area stained for cytoplasmic eIF4E but varied in staining intensity (Fig. 1A). In BPH tissues, eIF4E cytoplasmic staining intensity is low (mean intensity score, 1.1-1.3). In low-grade prostate cancer tissues (Gleason score <7), the cytoplasmic stain intensity is increased (mean intensity score, 1.7) and further elevated in high-grade prostate cancer (Gleason score ≥7; mean intensity score, 2.3; Fig. 1A and B). eIF4E cytoplasmic stain intensity is significantly increased across all tissue types (P < 0.0001, Pearson’s and Spearman’s correlation coefficients), low-grade prostate cancer versus adjacent BPH (P < 0.0001), high-grade prostate cancer versus adjacent BPH (P < 0.0001), and high-grade versus low-grade prostate cancer (P = 0.0016; Supplementary Table S1).

Nuclear eIF4E localization has been reported previously and may mediate the nucleocytoplasmic transport of select mRNAs (e.g., cyclin D1; ref. 4). Unlike cytoplasmic staining, nuclear eIF4E staining varied in intensity and percent area stained and is therefore presented by histoscore (percent area stained × intensity; Fig. 1A and B). The highest nuclear eIF4E histoscores were evident in prostate cancer tissues relative to BPH tissues (Fig. 1B). Indeed, nuclear eIF4E histoscores were significantly increased across all tissue groups (P = 0.0004 and 0.0002, Pearson’s and Spearman’s correlation coefficients, respectively). Individual group comparisons showed significantly increased staining only in high-grade prostate cancer versus BPH from patients without prostate cancer (P = 0.0473; Supplementary Table S1).

These data show that eIF4E expression is elevated in prostate cancer tissues, particularly high-grade prostate cancer (Fig. 1). To...
support these immunohistochemical data, we evaluated eIF4E expression in fresh-frozen human prostate cancer tissues by Western blotting. eIF4E protein levels were markedly increased in the prostate cancer relative to benign prostate tissue samples (Fig. 1C) as were levels of eIF4E phosphorylation at Ser209 (Fig. 1C), a site phosphorylated by MNK kinase only when eIF4E is bound to eIF4G (with eIF4F complex assembly; refs. 1–3). These data collectively show that eIF4E expression is significantly elevated in human prostate cancer tissues.

**4E-BP and p4E-BP1Ser65 levels in human prostate cancer samples.** eIF4E may also be activated by liberation from its inhibitory binding proteins, the 4E-BPs, via 4E-BP phosphorylation at Thr37, Thr46, Thr70, and, finally, Ser65 (16, 17). 4E-BP phosphorylation results from AKT-mammalian target of rapamycin pathway signaling, which is activated particularly in high-grade prostate cancer (23). We therefore examined these primary human prostate cancer tissues for 4E-BP expression and Ser65 phosphorylation (p4E-BP1Ser65), the final residue phosphorylated before release from eIF4E (17).

4E-BP1 and p4E-BP1Ser65 were evident in both the cytoplasm and the nucleus of prostate tissues (Fig. 2A). Group-by-group comparisons revealed that total cytoplasmic and nuclear 4E-BP1 expression was similar in all groups, although by trend analyses there was a significant increase in expression across all tissue types (Supplementary Table S1). p4E-BP1Ser65 cytoplasmic intensity was significantly increased in prostate cancer tissues across tissue types, with the highest stain in high-grade prostate cancer (trend analyses, groups 1-5, $P < 0.0001$ and $P = 0.0018$, Pearson’s and Spearman’s correlation coefficients, respectively; Fig. 2A and B). Cytoplasmic p4E-BP1Ser65 intensity was significantly increased in high-grade prostate cancer versus adjacent BPH ($P < 0.0001$), low-grade prostate cancer versus adjacent BPH ($P = 0.0223$), and high-grade prostate cancer versus BPH from patients without prostate cancer ($P = 0.0357$; Supplementary Table S1).

Breast and ovarian cancers show nuclear p4E-BP1 stain (29, 30). Our analyses also show nuclear p4E-BP1Ser65 (Fig. 2). Because this stain varied in percent area stained and intensity, the data are represented as histoscores (percent area stained $\times$ intensity). Trend analyses revealed that nuclear p4E-BP1Ser65 histoscores were significantly increased across all tissue types ($P = 0.0028$ and 0.005, Pearson’s and Spearman’s correlation coefficients, respectively), with the highest nuclear histoscores evident in prostate cancer tissues (Fig. 2B; Supplementary Table S1). Group-by-group comparisons revealed increased nuclear p4E-BP1Ser65 only in high-grade prostate cancer versus BPH from patients without prostate cancer ($P = 0.0475$; Supplementary Table S1). These immunohistochemical analyses indicated that p4E-BP1Ser65 levels are increased in human prostate cancer versus BPH tissues. Western blotting of fresh-frozen prostate tissues also showed increased p4E-BP1Ser65 levels in prostate cancer, whereas total 4E-BP1 protein expression was similar, although variable, in both prostate cancer and BPH samples (Fig. 2C). Collectively, these data show elevated p4E-BP1Ser65 levels in prostate cancer tissues (Fig. 2).

**Elevated eIF4E and p4E-BP1Ser65 levels and reduced patient survival.** We next determined whether increased eIF4E and p4E-BP1Ser65 levels might be related to patient survival. Patients who died with prostate cancer but from other causes were excluded from these analyses. Patients were segregated into high and low eIF4E expression groups (cytoplasmic intensity score $\geq 2$ or $<2$, respectively). High eIF4E expression was significantly related to
death from prostate cancer (Kaplan-Meier analyses χ²-log rank test, P = 0.03; Fig. 3A). Patients in the high eIF4E expression group were ~2.7 times likelier to die of prostate cancer than patients with low eIF4E levels (hazard ratio, 2.66; P = 0.037; Fig. 3A).

Similarly, elevated p4E-BP1Ser65 levels (cytoplasmic intensity score >1) were also related to death from prostate cancer (Kaplan-Meier analyses χ²-log rank test, P = 0.026). Patients with high cytoplasmic p4E-BP1Ser65 levels were ~2.5 times likelier to die of prostate cancer (hazard ratio, 2.495; P = 0.031; Fig. 3B).

Our immunohistochemical analyses revealed that total 4E-BP1 levels were similar between individual groups. However, a fraction of patients showed reduced 4E-BP1 expression (Fig. 3C and D). These patients showed substantially reduced survival when compared with prostate cancer patients showing uniform 4E-BP1 expression (Kaplan-Meier analyses, log-rank test, P = 0.001). Patients whose prostate cancer tissues showed uniform 4E-BP1 expression were only ~25% as likely to die of prostate cancer as patients whose tumors showed reduced 4E-BP1 immunostaining (hazard ratio, 0.264; P = 0.002; Fig. 3C and D).

Elevated eIF4E in experimental prostate cancer. The immunohistochemical analyses revealed that eIF4E and p4E-BP1 levels are elevated and related to reduced prostate cancer patient survival. We therefore evaluated whether eIF4E activation may also be enhanced in experimental models of prostate cancer progression to androgen independence, the CWR22-CWR22R (31) and LNCaP-LNAI (22) models. Western blotting showed that eIF4E expression was substantially elevated in four separate hormone-refractory CWR22R xenograft samples versus three separate CWR22 hormone-dependent xenografts (Fig. 4A). To account for the variable tissue content of xenograft tumors (murine endothelial and stromal tissues plus healthy and necrotic human prostate cancer tissues), multiple tumors are depicted for each line and the expression of eIF4E normalized to β-actin is shown for each xenograft. CWR22 prostate cancer tumors are PTEN-positive. There were no substantial differences between CWR22 and CWR22R in levels of total or phosphorylated 4E-BP1 (data not shown).

In the LNCaP-LNAI model, eIF4E levels were largely unchanged, but 4E-BP1 protein expression was substantially reduced, particularly in the aggressive, androgen-independent LNAI16 cells (Fig. 4B). These LNAI cells show AKT hyperactivation relative to the hormone-dependent LNCaP cells (22). Accordingly, LNAI16 show ~2-fold increase in p4E-BP1Ser65 levels versus LNCaP (data not shown). We therefore assessed the amount of eIF4E bound to 4E-BP1 using the 7-methyl-GTP (mRNA cap-analogue) bead capture assay (25). Consistent with reduced 4E-BP1 expression and increased 4E-BP1 phosphorylation, LNA16 cells show decreased levels of 4E-BP1 bound to eIF4E versus LNCaP (Fig. 4B), indicating increased eIF4E function in LNAI cells. Indeed, expression of the eIF4E-regulated protein BCL-2 is increased 2.4-fold in LNAI versus LNCaP, whereas BCL-2 RNA levels are virtually unchanged (Fig. 4C). Together, these data provide evidence that androgen-independent prostate cancer cells up-regulate eIF4E, either directly by overexpression (CWR22R) or indirectly, via increased AKT pathway signaling (22) and reduced 4E-BP1 expression (LNAI).

Reducing eIF4E in prostate cancer cells induces apoptosis regardless of cell cycle phase. Immunohistochemistry and
Western blot analyses of prostate cancer tissues and cells implicate elevated eIF4E function in prostate cancer, particularly in advanced disease. Increased eIF4E function would selectively enhance the translation of mRNAs with lengthy, G+C-rich 5′ untranslated regions (e.g., c-myc and BCL-2), enabling prostate cancer tumor growth and survival (1). Reducing eIF4E function may therefore be an effective therapeutic strategy for prostate cancer (32). Indeed, we recently showed that a 4EASO effectively reduced eIF4E expression in a wide array of cancer cells, repressing expression of eIF4E-regulated proteins (e.g., c-myc and BCL-2) and inducing apoptosis. Intravenous administration of this 4EASO effectively suppressed growth of breast and prostate cancer xenografts, reducing eIF4E protein expression, inducing apoptosis, and reducing cellular proliferation in the treated xenograft tissues (15). We sought to extend these data to additional prostate cancer cells to explore further the potential of the 4EASO for prostate cancer treatment.

Transfection with the 4EASO reduced eIF4E protein expression in CWR22Rv1 cells. Consistent with its mechanism of action, the 4EASO specifically targets eIF4E mRNA for degradation (15), subsequently decreasing eIF4E protein expression. Reduced eIF4E protein would then suppress expression of eIF4E-regulated proteins. Accordingly, 4EASO transfection resulted in reduced expression of the eIF4E-regulated proteins c-myc and BCL-2 (Fig. 5A), both of which have been linked to the emergence of advanced, hormone-independent disease (33, 34). 4EASO transfection did not markedly reduce c-myc or BCL-2 RNA levels (Fig. 5B). These data support the notion that blocking eIF4E function would primarily suppress expression of eIF4E-regulated proteins without substantially affecting mRNA levels for these proteins (1, 15, 32).

We next evaluated the biological consequences of reducing eIF4E expression in prostate cancer cells. In both LNCaP and CWR22Rv1, 4EASO transfection robustly induced apoptosis as evidenced by increased TUNEL staining and an overall reduction in cell number (Hoechst-stained nuclei; Fig. 6A and B). To assess whether apoptosis elicited by eIF4E reduction may be induced in one or more phases of the cell cycle, we used high-content cellular imaging (28) to evaluate simultaneously cell cycle phase, apoptosis (TUNEL and activated caspase-3 staining), and eIF4E expression. Cell cycle was determined by simultaneously monitoring nuclear DNA content, nuclear area, average DNA content, and DNA variation as described (28). For each cell line and treatment, >1,000 cells were evaluated. The data are displayed as a heat map (lowest levels in blue and highest in red) with the cell cycle phase shown to the right. Each horizontal line represents a single cell. In both LNCaP and CWR22Rv1 cells, eIF4E reduction was evident in cells treated with 4EASO versus mismatch in all phases of the cell cycle (represented by the preponderance of blue lines after 4EASO transfection). In these same 4EASO-treated cells, activated caspase-3 and TUNEL staining were increased versus mismatch ASO-transfected cells and evident in cells in all phases of the cell cycle (horizontal lines show increased yellow-to-red intensity). The greatest positivity for both markers of apoptosis is evident in cells in late S to M phase of the cell cycle (Fig. 6A and B). These data indicate that reducing eIF4E in prostate cancer cells elicits apoptosis in a cell cycle phase-independent manner.

**Discussion**

The emergence of hormone-refractory, castration-independent prostate cancer is driven by activation of survival pathways (e.g., increased expression of the antiapoptotic oncoprotein BCL-2 and AKT pathway activation; refs. 20–22). AKT pathway activation, in particular, has been repeatedly linked to prostate cancer progression in both human prostate cancer tissues and animal models of prostate cancer (22, 23). eIF4E is activated downstream of AKT and may be a critical effector molecule of the AKT pathway (8).

Data presented herein show that eIF4E activation is commonly elevated with advanced disease in both human primary prostate cancer tissues and prostate cancer cells. Both eIF4E expression and 4E-BP phosphorylation are elevated in high-grade primary human prostate cancer tissues, particularly advanced disease, and
significantly related to reduced patient survival. In a minority of patients who die very quickly of disease, 4E-BP1 protein expression is significantly reduced. In two separate experimental prostate cancer models, progression to androgen independence involves increased eIF4E activation either by eIF4E overexpression or by reduced 4E-BP1 expression and binding to eIF4E. In these same models, blocking eIF4E expression with a 4EASO robustly induces apoptosis and suppresses expression of the eIF4E-regulated proteins c-myc and BCL-2, both of which have been linked to prostate cancer progression (33, 34). Taken together, these data implicate enhanced eIF4E function in malignant prostate cancer progression and suggest that targeting eIF4E may be an attractive strategy for prostate cancer therapy.

Enhanced eIF4E activation has been reported in a variety of human and experimental cancers as a result of either elevated eIF4E expression or decreased 4E-BP1 function (1, 35). Like recent reports in breast and ovarian cancers, our data in prostate cancer now also show p-E4E and 4E-BP1 staining in the nucleus, with cytoplasmic p-E4E staining restricted to tumor tissue (29, 30). Our data now also reveal that elevated eIF4E and p-E4P1 levels are evident in the same samples, suggesting that prostate cancer progression may involve both eIF4E up-regulation and increased AKT pathway signaling.

Previous reports in gastric carcinoma (36), prostate (37), and breast (38) carcinomas have shown increased 4E-BP1 expression in advanced malignancies. In this study, there were no significant differences in 4E-BP1 expression between individual tissue groups, but there was a trend for increased expression in the highest-grade prostate cancer samples. The selection for such increased 4E-BP1 expression is unclear, although it may reflect a reliance on both cap-independent and cap-dependent protein translation as suggested recently for inflammatory breast cancers (38).

Although there was a trend for increased 4E-BP1 expression in this study, a minority of prostate cancer tissues showed markedly reduced 4E-BP1 expression and this reduction was significantly associated with dramatically shortened survival (Fig. 3C and D). Consistent with a previous report relating reduced 4E-BP1 levels with pathologic stage ≥T3 (37), these data suggest that loss of 4E-BP1 may portend a particularly poor prognosis in a minority of prostate cancer patients.

Prostate cancer has a notoriously low rate of proliferation (<5% Ki-67-positive), even in high-grade, recurrent, and metastatic prostate cancer (39), indicating that prostate cancer progression is characterized by relentless prostate cancer cell survival. As such, therapies targeting survival pathways, particularly in a cell cycle-independent manner, may be particularly attractive for prostate cancer treatment (20, 39). eIF4E suppresses the apoptotic response to many proapoptotic insults including thapsigargin (40–42), which has been repeatedly proposed as a putative prostate cancer therapeutic (20). Our data now extend these observations, showing that reduction of eIF4E robustly induces apoptosis in either LNCaP or CWR22Rv1 cells and that apoptosis is evident in all phases of the cell cycle. As suggested for thapsigargin (20), the induction of apoptosis in a cell cycle phase-independent manner may be particularly important for prostate cancer therapy where the proportion of cycling cells is low.

With our earlier reports showing that 4EASO treatment induces apoptosis in, and suppresses growth of, PC-3 human prostate xenografts (15), the data in this report further substantiate the notion that eIF4E might be an attractive target for prostate cancer therapy and have prompted the advance of the 4EASO into cancer clinical trials (32).

**Disclosure of Potential Conflicts of Interest**


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