Identification of growth factor independent-1 (GFI1) as a repressor of 25-hydroxyvitamin D 1-alpha hydroxylase (CYP27B1) gene expression in human prostate cancer cells

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Abstract

The hormone 1,25-dihydroxyvitamin D (1,25D) may play a protective role in prostate cancer. 25-hydroxyvitamin D 1-α hydroxylase (CYP27B1) is the enzyme responsible for the regulation of cellular 1,25D levels. CYP27B1 is substantially repressed in prostate cancer cells. We have investigated the molecular basis for this inhibition. First, we identify a repressive region between −997 and −1200 in the human CYP27B1 promoter following transient transfection analysis in the prostate cancer cell lines DU145, PC3 and LNCaP. Next, we demonstrate a role for the transcription factor growth factor independent-1 (GFI1) in the repression of CYP27B1. Electrophoretic mobility assays with nuclear extracts from prostate cancer cell lines established binding of GFI1 to the sequence 5′-TGGTACAATCATAACTCACTGCAG-3′ present at −997 to −1200 in the repressive region. Site directed mutagenesis of the core GFI1 binding sequence (5′-AATC-3′) substantially increased while forced expression of GFI1 decreased the expression of the CYP27B1 reporter construct. Importantly, GFI1 repression is dependent on an intact GFI1 binding site in the −997 to −1200 region. GFI1 is an oncoprotein known to form a large protein complex with co-repressors that recruit histone deacetylases. We propose that the formation of such a repressive complex on the inhibitory domain of the CYP27B1 gene in prostate cancer cells could lead to silencing of either the nearby enhancer or proximal promoter domains and lead to cancer progression by reducing local production of 1,25D. These studies provide the basis for a more detailed understanding of CYP27B1 repression in prostate cancer cells and could provide a novel insight in future diagnosis and treatment.

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Introduction

The active form of vitamin D, 1,25-dihydroxyvitamin D (1,25D) plays a central role in calcium and bone metabolism, but more recent studies have revealed broadened properties for the hormone including anti-proliferation, prodifferentiation and immunosuppressive actions (Hewison & O’Riordan 1994, Christakos et al. 1996, Issa et al. 1998, Jones et al. 1998). Parental vitamin D is synthesized from 7-dehydrocholesterol in the basal epidermal layer of the skin by a UV-radiation dependent process. Vitamin D subsequently acquires its biological activity via a series of sequential hydroxylations. The first of these occurs in the liver to generate 25-hydroxyvitamin D (25D), which is transported primarily to the renal proximal tubules, but also to extra-renal sites such as the bone, skin, immune system, small intestine, colon, breast and
prostate (Omdahl et al. 2002). At these tissue sites, 25D is converted to 1,25D by the mitochondrial cytochrome P450 enzyme, 25-hydroxyvitamin D 1α-hydroxylase (CYP27B1) (Howard et al. 1981, Adams & Gacad 1985, Anderson et al. 2003). The molecular actions of 1,25D are mediated through the vitamin D receptor (VDR), which acts as a ligand-dependent transcription factor to regulate the expression of vitamin D responsive genes in a genomic and non-genomic manner (Carlberg & Polly 1998, Dwivedi et al. 2002, Norman et al. 2003).

While the precise mechanisms leading to the development of prostate cancer remain to be elucidated, there is evidence that 1,25D may have a protective role in the development and/or progression of the cancer. Such a role for 1,25D was first proposed by Schwartz & Hulka (1990), based on epidemiological studies that indicated an inverse relationship between UV-radiation exposure and mortality rate for prostate cancer. Furthermore, prostate epithelial cells have been shown to localize a domain that is strongly inhibitory and have identified a transcription factor oncprotein that plays a key role in the suppression mechanism.

Materials and methods

Materials

Restriction enzymes and T4 DNA ligase were purchased from New England Bio-labs (Beverly, MA, USA). Oligonucleotides were synthesized by Geneworks (Adelaide, South Australia). Cell culture media and associated tissue culture products were from Life Technologies (Grand Island, NY, USA). The dual-luciferase assay kit was supplied by Promega (Madison, WI, USA).

CYP27B1 5′-flanking-luciferase constructs and expression plasmids

5′-deletion constructs of the CYP27B1 1501 bp 5′-flanking region fused to the firefly luciferase reporter gene in the pGL3 vector have been previously described and are designated as pCYP27B1(−1501)-Luc, pCYP27B1(−997)-Luc, pCYP27B1(−884)-Luc, pCYP27B1(−531)-Luc and pCYP27B1(−305)-Luc (Gao et al. 2002). Further 5′-deletions of the 5′-flanking sequence (together with 44 bp of CYP27B1-untranslated region) were generated by the polymerase chain reaction (PCR) during this study and named pCYP27B1(−1306)-Luc, pCYP27B1(−1200)-Luc and pCYP27B1(−1100)-Luc. For the PCR the following oligonucleotide primers were designed with a restriction enzyme site for XhoI (bold letters) so that the PCR products could be cloned into XhoI digested pGL3-basic vector: reverse primer (+24), 5′-CTTAGATCGGAGGCTGCTGTTTTCAGGTTG-3′; forward primer-1 (−1318),...
Mutations in putative transcription factor binding sites were introduced using the Quik-Change Site Directed Mutagenesis protocol (Stratagene, La Jolla, USA). Oligonucleotides for site directed (SD) mutagenesis were designed as follows. The core sequence is underlined in each wild type sequence and altered nucleotides are in bold letters: WT CRE-I, 5'-CCATGGCTGACTCCTGGCC-ACAGAG-3'; forward primer-2 (−1211), 5'-AATTTTCTGGAACAGCCCTCCTCTCTGTCG-C-3' and forward primer-3 (−1117), 5'-GTAATCCACCTGAGCTCTCAAGGCACTACAGGC-3'.

Site-directed mutagenesis

Mutations were maintained in RPMI-1640 supplemented with 5% fetal calf serum (FCS). All transient transfections were performed using Lipofectamine 2000 (Life Technologies) according to the manufacturer’s instructions. Human embryonic kidney cells (293T) were maintained with 10% FCS and transfections were carried out using DOTAP (Roche Diagnostics, USA). For transient transfection analysis, cells were grown in 175 cm² flasks to 60–70% confluency, washed once with phosphate buffered saline and removed by trypsinization. Cells (approximately 1 × 10⁶) were seeded into 24 well trays containing 400 µl RPMI-1640 supplemented with FCS. Within an experiment, transfections were carried out in triplicate and the data averaged; each transfection was performed using 200 ng of each of the CYP27B1 deletion constructs, together with 50 ng of the thymidine kinase (TK) promoter directed Renilla luciferase plasmid (pRLTK-LUC) from (Promega) to normalize transfection efficiency. Cells were cultured overnight and harvested in 50 μl Passive Lysis Buffer (Promega). Luciferase activity in cell lysates was determined as described previously (Gao et al. 2002) using the Dual Luciferase Reporter assay kit (Promega) and measured using a Luminometer model TD 20/20 (Turner Design Instruments, Sunnyvale, CA, USA). All experiments reported here were repeated on at least three separate occasions and the data shown are from one representative experiment.

Electrophoretic mobility assays (EMSA)

Double-stranded oligonucleotides (shown below) were synthesized.

**Electrophoretic mobility assays (EMSA)**

Double-stranded oligonucleotides (shown below) were synthesized. The wild type CYP27B1 GFI1 + AP-1 like oligonucleotide encompassed both the GFI1 core sequence (bold letters) and AP-1 like sequence (underlined). The core binding sequence of GFI1 and the AP-1 like binding sites were mutated (bold and underlined) in the respective oligonucleotides CYP27B1mGFI1 + AP-1 like and CYP27B1mGFI1 + mAP-1 like oligonucleotides. An oligonucleotide that encompassed an authentic GFI1 binding site (located on the reverse strand) was employed as a control (Tong et al. 2000). The GFI1 over-expression clone, pGEM3-Myc-GFI1, has been described previously (Grimes et al. 1996a). The over-expression clone for prostate derived Ets factor (PDEF) was kindly donated by JP Brody, Whitaker Center for Biomedical Engineering, University of California, Irvine, USA. The expression clone for Ets-1 transcription factor (pEFSosEts-1) has been described previously (Dwivedi et al. 2000).
oligonucleotide, 5’-CGAAGTACCGTGATTTCCAGGCATGCACG-3’ and 3’-GGCTTCATGGCACAATTACGTCG-5’.

For EMSA experiments, nuclear extracts were prepared from 2 x 10⁶ DU145 cells (Andrews & Faller 1991). Each double-stranded oligonucleotide was labeled by end-filling with [α-32P]dCTP using Klenow enzyme and purified by ethanol precipitation. Binding reactions for the detection of bound GF1 were carried out using 2 μg nuclear protein and 1 μg Poly (dl-dC) in a final volume of 12 μl in Dignam Buffer C (20 mM HEPES buffer, (pH 7.6), 420 mM NaCl, 0.5 mM dithiothreitol, 5 mM MgCl₂, 0.5 mM EDTA and 20% glycerol) and were incubated on ice for 15 min. Radiolabeled probe (100 000 c.p.m.) was added and binding reactions were further incubated on ice for 30 min. EMSA competition binding assays were performed with unlabeled competitor oligonucleotide at fold molar excess concentrations (10- and 50-fold) by inclusion in the binding reactions. Binding reactions for the inhibition assays were carried out at 4 °C for 45 min using 8 μl polycytoplasmic goat antibody to GF1 protein N20 (sc-8558X Lot 1702; Santa Cruz Biotechnology Inc.) and a polyclonal goat antibody for C/EBPα included as a control (sc-9315X; Santa Cruz Biotechnology Inc.). Retarded DNA nuclear protein complexes were resolved on a 4% non-denaturing polyacrylamide gel using pre-cooled low ionic strength gel running buffer (0.5 x TBE) at 4 °C. The gel was dried and exposed to Kodak X-Omat AR film with an intensifying screen at -80 °C.

Western blot analysis

Total cell lysates were prepared from DU145 cells as described previously (Dwivedi et al. 2002). Proteins were separated by 10% SDS polyacrylamide gel electrophoresis and transferred to nitrocellulose membranes. The membranes were probed with a polyclonal goat antibody to GF1 protein N20 (sc-8558X Lot 1702; Santa Cruz Biotechnology Inc.) using standard procedures and immune complexes were detected by enhanced chemiluminescence as reported previously (Dwivedi et al. 2002).

Results

Deletion analysis of the CYP27B1 gene 5'-flanking region

An analysis of human CYP27B1 genomic clones showed that sequence upstream from −1501 corresponded to the 3'-untranslated region of an unrelated gene, methyltransferase-like protein METTL1 (Bahr et al. 1999, Omdahl et al. 2001). On this basis, it seemed likely that most if not all CYP27B1 gene regulatory sites would lie within the first −1501 bp and this region has been studied in the present work. Different lengths of the 5'-flanking region, together with 44 bp of the CYP27B1 gene 5'-untranslated region, were fused to the fire-fly luciferase gene as reporter. These deletion constructs designated as pCYP27B1(−1501)-Luc, pCYP27B1(−997)-Luc, pCYP27B1(−884)-Luc, pCYP27B1(−531)-Luc and pCYP27B1(−305)-Luc were introduced into human prostate carcinoma DU145 cells which have been shown to contain low levels of CYP27B1 (Hsu et al. 2001). Cells were cultured in RPMI-1640 media containing 5% FCS. Next day cells were harvested and luciferase activity was determined. The construct pCYP27B1(−305)-Luc directed significant expression that was not altered when the 5'-flanking length was increased to −531 but was almost doubled with the pCYP27B1(−884)-Luc plasmid (Fig. 1A). Further increasing the length to −997 led to the maximal expression level observed that represented an increase of nearly four-fold compared with pCYP27B1(−305)-Luc.

Expression of the 5'-flanking deletion constructs was also examined in PC3 and LNCaP human prostate cancer cell lines that also contain low levels of CYP27B1 (Hsu et al. 2001). In these two cell lines the profiles of expression were similar to that seen with DU145 cells (see Figs 1B and 1C). The level of repression in PC3 cells was about the same as that seen in DU145 cells although the repression was not as great in LNCaP cells. With the latter cells, the levels of luciferase activity expressed by the different constructs were low compared with the other two cell lines and this finding is consistent with the relative low enzyme activity of CYP27B1 exhibited by this cell line (Hsu et al. 2001). For comparison, the deletion constructs were also investigated in human embryonic kidney cells (293T). With these cells, most of the basal activity is achieved with the construct pCYP27B1(−305)-Luc (Fig. 1D) and there is almost no enhancer activity with pCYP27B1(−997)-Luc or repression with pCYP27B1(−1501)-Luc. This favours our hypothesis that the observed repression of the CYP27B1 gene may be specific to prostate cancer cells. In further studies with the prostate cancer cell lines we determined expression of the deletion constructs in serum-free medium. DU145, PC3 and LNCaP cells were initially
cultured in media containing 5% fetal calf serum and then immediately transferred to serum-free RPMI-1640 medium when transfections were carried out. Interestingly, the absence of serum had no effect on the pattern or levels of expression of any of the CYP27B1 5'-flanking deletion constructs in these cell lines. Hence expression of the 5'-flanking region in these cells is unaffected by growth factors and hormones present in serum.

The data in Figures 1A, B and C show that when the 5'-flanking sequence is extended from -997 to -1501 repression of CYP27B1 gene activity is observed. Further localization of the repressive region was carried out using DU145 cells and these cells were
employed for the remainder of the work reported here. Additional 5′-flanking deletion constructs were synthesized of length –1306, –1200, –1100 and –997 of the 5′-flanking sequence. The transient transfection analysis of these constructs was performed as described in Figure 1A–D. The relative luciferase activity shown represents the mean ± S.D. firefly luciferase: Renilla luciferase ratios of triplicate samples from a representative experiment. The experiment was repeated three times.

Figure 2 Further delineation of the repressive region. Three additional deletion constructs were generated using the PCR and CYP27B1(−1501)-Luc as a template and encompassed –1306, –1200, –1100 and –997 of the 5′-flanking sequence. The transient transfection analysis of these constructs was performed as described in Figure 1A–D. The relative luciferase activity shown represents the mean ± S.D. firefly luciferase: Renilla luciferase ratios of triplicate samples from a representative experiment. The experiment was repeated three times.

Characterization of the proximal promoter

Control elements present in the −305 bp proximal promoter have been previously identified by Gao et al. (2002) and are shown in Figure 3. A CCAAT box (5′-ATTGAGCT-3′) at –75 to –70 and a GC rich sequence that is an Sp1 binding site (5′-CCAGCCCCG-3′) at –133 to –125, underlie basal expression in transfected kidney cells (Gao et al. 2002), with no significant contribution from a putative Ets protein binding site (5′-CTGTTCCTGG-3′), designated as EBS at –120 to -111 on the antisense strand and located between the CCAAT box and GC rich sequence. An analysis of promoter mutant constructs in DU145 cells established that the CCAAT box binding site and the GC box are critically important for expression driven by the pCYP27B1(−305)-Luc construct in DU145 cells (Fig. 4A); inactivation of each site lowered expression by approximately 80%. However the Ets protein binding site did not contribute to expression (Fig. 4A). On the basis of earlier studies in which we showed that overexpressed Sp1 acted on the promoter through the GC box in an insect cell line (Gao et al. 2002), it seems reasonable to assume that Sp1 present in prostate cancer cells will bind the GC rich sequence. There is no information as to the identity of the functional protein that binds the CCAAT box.

Characterisation of the enhancer region

A computer analysis of the enhancer region from −305 to −997 using the transcription factor binding site database (TFSEARCH 2001–2002) revealed three
possible Ets protein binding sites (EBSs) that were similar in sequence and contained a 5'-GGAT-3' core. Two of these sites designated EBS-I (5'-CCACAG-GATTCTGA-3') and EBS-III (5'-TGTGGAATTACAGT-3') were located on the sense strand, while the third site, EBS-II (5'-ATGCCATCTCTCTG-3') was present on the non-coding strand (Fig. 3). Each of these sites was inactivated by site-directed mutagenesis within the pCYP27B1(-997)-Luc construct. It can be seen from Figure 4B that while each site contributed to
characterized by a core binding sequence (5'-AACTCA-3' to 5'-AACTTG-3') located upstream the sequence 5'-GGAT-3' rather than a 5'-GGAA-3' core and has been shown to activate an upstream enhancer in the prostate specific antigen (PSA) gene (Oettgen et al. 2000). This raised the possibility that PDEF may be important for regulation of the CYP27B1 5'-flanking region. However, over expressed PDEF at plasmid concentrations of 200, 500 and 1000 ng had no effect on expression of the −997 construct in DU145 cells (data not shown). Similarly, over expression of another Ets family member, Ets-1, at these concentrations had no effect. Hence PDEF overexpression of another Ets family member, Ets-1, may be important for regulation of the CYP27B1 5'-flanking region. However, over expressed PDEF at plasmid concentrations of 200, 500 and 1000 ng had no effect on expression of the −997 construct in DU145 cells (data not shown). Similarly, over expression of another Ets family member, Ets-1, at these concentrations had no effect. Hence PDEF and Ets-1 are apparently not involved in enhancer activity in these cells.

Characterization of the repressor region

Possible transcription factor binding sites were noted within the repressor region from −997 to −1200 (Fig. 3). Two putative cAMP responsive elements (CREs), CRE-I (5'-CTGGCTAA-3') and CRE-II (5'-TGA-CCTCC-3') were identified at −1069 to −1062 and −1134 to −1127, respectively, together with a putative AP-1 like sequence at −1150 to −1144 (5'-TAACCTCA-3', underlined in Fig. 3). Each of these sites was inactivated within the context of the −1200 deletion construct. It can be seen that inactivation of the AP-1 like site (5'-TAACCTCA-3' to 5'-TAACCTTG-3') in construct pCYP27B1mAP-1 like (−1200)-Luc significantly reversed the inhibitory level of expression observed with the wild type −1200 construct while inactivation of CRE-I also led to increased expression (Fig. 4C). Alteration of the remaining putative site, CRE-II, did not affect expression. It is concluded that the CRE-I and the AP-1 like sites are important for mediating repression of the −1200 construct. We have focused on the AP-1 like site.

Initially, EMSA experiments were carried out using a double stranded oligonucleotide containing the AP-1 like sequence (5'-TAACCTCAGTGCAG-3') and binding was compared with a known AP-1 binding sequence (5'-CGCTTGATCTAGCCGGAA-3') from the SV40 promoter (Santa Cruz Biotechnology Inc). A strong band was retarded on the authentic SV40 AP-1 probe but the AP-1 like probe from CYP27B1 did not significantly retard any nuclear protein complex in repeated experiments (data not shown). The lack of protein binding by the AP-1 like probe was surprising since mutagenesis of the sequence (5'-TAACCTCA-3' to 5'-TAACCTTG-3') within the pCYP27B1(−1200)-Luc construct had been shown to reverse the inhibitory response (see Fig. 4C). This led us to examine nearby sequences that could be critical for binding of proteins to the AP-1 like sequence. We located upstream the sequence 5'-AATC-3' (see Fig. 3, bold and underlined) which can act as the core binding sequence for the zinc-finger transcription factor oncoprotein growth factor independent–1 (GFI1) (Zweidler-Mckay et al. 1996) and this sequence was further investigated.

Mutational analysis of the putative GFI1 core binding sequence

Mutagenesis of the putative GFI1 core sequence (5'-AATC-3' to 5'-GGTC-3') was carried out within the context of the −1200 deletion construct (pCYP27B1mGFI1(−1200)-Luc) and also in combination with the AP-1 like sequence (pCYP27B1mGFI1 + mAP-1 like (−1200)-Luc). Transfection analysis of these constructs, together with pCYP27B1mAP-1 like (−200)-Luc, was carried out in DU145 cells (Fig. 5A). The data showed that inactivation of the putative GFI1 core sequence substantially reversed repression of the wild type construct pCYP27B1 WT (−1200) to a level even greater than that seen with the mutation in the AP-1 like sequence. However, mutations in both the GFI1 core and the AP-1 like sequence did not further increase expression of the construct compared with the mutation alone in the GFI1 core sequence. This favours the proposal that the AP-1 like sequence does not bind any protein on its own but serves as a flanking sequence for the nearby GFI1 core. To support the presence of endogenous GFI-1 in DU145 cells, a Western blot analysis was carried out using the GFI1 antibody (Fig. 5B). A major cross reacting band was observed with an approximate molecular size of 55–60 kDa that corresponds with that reported for GFI1 (Duan & Horwitz 2003), together with two lower molecular weight bands.

Binding of endogenous nuclear proteins to the GFI1 binding site

Nuclear protein binding to the possible GFI1 site in the CYP27B1 5'-flanking region was analysed by EMSA using nuclear extracts from DU145 cells and the probe designated CYP27B1 GFI1/AP-1 like oligonucleotide, which encompassed the AP-1 like sequence and core for GFI1 binding (5'-TGGTA-CAATCAACTCAGGCAG-3'). For comparison,
a p21 GFI1 probe was also examined (5'-CGAAGTACCGTGATTTCAGGCATGCACG-3') that has been shown to strongly bind GFI1 (Tong et al. 1998). The CYP27B1 GFI1/AP-1 like probe retarded a major complex (C-I) and a minor complex (C-II) (Fig. 6A, lane 2) and the profile of binding was identical to that of the p21 GFI1 probe (Fig. 6A, lane 1). When the SV40 probe (5'-CGCTTGATGACTCAGCCGGAA-3') was employed, a major band was observed but was of considerably lower mobility compared with complexes C-I and C-II (data not shown). Moreover, in other experiments C-I and C-II did not react with the following antibodies to AP-1 family members c-fos, c-jun, fra-1 and fra-2. Hence the protein complexes binding to the CYP27B1 GFI1/AP-1 like sequence are unlikely to be members of the AP-1 family.

To further investigate this possibility, self-competition experiments were undertaken with the unlabeled CYP27B1 GFI1/AP-1 like probe. At a 10-fold molar excess of probe, the binding of both complexes was markedly reduced with binding of C-II being completely inhibited (Fig. 6A, lane 3) while at 50-fold molar excess, both C-I and C-II were totally abolished (Fig. 6A, lane 4). Hence C-I and C-II are specifically bound complexes. This result was further supported by competition experiments employing an unlabeled CYP27B1mGFI1/AP-1 like oligonucleotide probe where the core sequence of GFI1 (5 '-AATC-3' to 5 '-GGTC-3') was inactivated. This mutated oligonucleotide probe (CYP27B1mGFI1/AP-1 like) at 10- or 50-fold molar excess did not affect binding of C-I or C-II (Fig. 6A, lanes 7 and 8), confirming the specificity of binding of these complexes to the GFI1 binding sequence. Cross competition experiments were also carried out using 10- and 50-fold molar excess of the unlabeled p21 GFI1 oligonucleotide probe and this competitor was found to completely abolish both the C-I and C-II complexes even at 10-fold molar excess (Fig. 6A, lanes 5 and 6). These results provide evidence that C-I and C-II retarded on the CYP27B1mGFI1/AP-1 like probe are GFI1 proteins.

To confirm the presence of GFI1 in C-I and C-II complexes, EMSA experiments were performed using a
polyclonal antibody for GFI1. This antibody totally reduced the formation of both complexes C-I and C-II on the p21 GFI1 probe (Fig. 6B, lane 2) and the CYP27B1GFI1/AP-1 like probe (Fig. 6B, lane 5). However, in a control experiment using the same amount of antibody for the unrelated transcription factor C/EBP alpha, the formation of these complexes was unaffected (Fig. 6B, lanes 3 and 6). These results confirm that C-I and C-II contain GFI1 protein.

We next examined the contribution to GFI1 binding of the AP-1 like sequence and the GFI1 core. EMSA was carried out using the wild type (CYP27B1GFI1/AP-1 like) probe and mutated GFI1 and AP-1 like probes (CYP27B1mGFI1/AP-1 like and CYP27-B1GF11/mAP-1 like; Fig. 6C). The mutation in the GFI1 core sequence completely abolished binding (Fig. 6C, lane 3), however binding was only partially affected when the AP-1 like site was mutated (Fig. 6C, lane 2). These results support the notion that the AP-1 like sequence constitutes flanking sequence for optimal binding of GFI1.

Repressive action of GFI1

To examine directly whether GFI1 can reduce expression of the CYP27B1 5’-flanking region, the effect of
Discussion

The observation that 1,25D prevents proliferation of prostate cancer cells (Peehl & Feldman 2003) has attracted considerable interest because of the possibility of using vitamin D based therapies for prostate cancer (Chen et al. 2000, Chen & Holick 2003). A deficiency of CYP27B1 enzyme activity levels was noted in prostate cancer cells compared with normal cells (Chen et al. 2003) and this correlated with the inability of exogenous 25D to inhibit cellular proliferation presumably because of insufficient local 1,25D production by CYP27B1 (Chen et al. 2003). In support of this proposal, when prostate cancer cells were transfected with a cDNA clone for human CYP27B1, exogenously added 25D regained the ability to inhibit cellular proliferation (Whitlatch et al. 2002, Chen et al. 2003). The data support the current contention that the reduced ability of prostate cancer cells to synthesize 1,25D contributes to their uncontrolled growth rate (Peehl et al. 1994, Schwartz et al. 1994).

The molecular basis for the lowered production of CYP27B1 enzyme in prostate cancer cell lines is currently of great interest. Chen et al. (2003) provided evidence that reduced CYP27B1 promoter activity was responsible but no repressive site was reported. In the current work, we have shown by transient expression analysis of deletion constructs in three different human prostate cancer cell lines cultured in serum free conditions that the 5'-flanking region of the human CYP27B1 gene comprises three regulatory domains. There is a proximal promoter region located within the first 305 bp, an enhancer region from −305 to −997 and a strong upstream inhibitory region from −997 to −1200. We report here for the first time a sequence within the inhibitory region at −1161 to −1138 that plays a substantial role in the repression of the 5'-flanking region of the CYP27B1 gene in prostate cancer cells. We provide evidence from EMSA experiments and over expression studies that the zinc finger transcription factor GFI1 represses gene expression through binding to this sequence.

In initial studies, we investigated the role of an apparent binding site for AP-1 (Tong et al. 1998) that was located in the inhibitory domain. While mutagenesis of this AP-1 like sequence (5'-TAACTCAGTGCAG-3' to 5'-TAACTTGCTGCAG-3') allowed significant reversal of gene inhibition in transient transfection studies, we were unable to detect binding of any protein to this sequence using EMSA experiments and DU145 cell nuclear extracts. The situation was clarified by the identification of a nearby core sequence for GFI1 (5'-AATC-3') that was not included in the oligonucleotide used in the EMSA experiments. With an extended oligonucleotide (5'-TGTTGACATACAACTCAG-3') we showed using a specific antibody that GFI1 protein binds to this sequence in EMSA experiments employing DU145 nuclear extracts. A major and a minor protein complex were detected; the minor band may represent a degradation product. Competition studies using an unlabeled self...
oligonucleotide confirmed that the binding of these proteins was specific, while an authentic GFI1 probe (p21 GFI1) competed with binding of the two complexes. We also showed that mutagenesis of the core within the context of the 5′-flanking region led to a marked reversal of CYP27B1 gene expression with this reversal being greater than that observed when the AP-1 like sequence was mutated. The AP-1 like sequence was therefore considered an important flanking sequence for functioning of the GFI1 core. In support of this concept, mutagenesis of the core sequence strongly prevented binding of GFI1 in EMSA experiments, while inactivation of the flanking AP-1 sequence inhibited binding, but to a lesser extent. In fact, DMS methylation interference experiments have previously indicated that GFI1 zinc fingers contact nucleotides at these positions flanking the core AATC sequence (Zweidler-McKay et al. 1996). Thus, both core and flanking regions are critical for GFI1 action on CYP27B1.

Both the major and minor protein complexes were also observed to bind to the p21 probe and to about the same extent as to the CYP27B1 probe (see Fig. 6A). A study of many potential GFI1 sites has reported that the GFI1 site in the p21 promoter has the highest affinity in EMSA studies (Duan & Horwitz 2003). There is almost no similarity in the flanking sequences surrounding the core in the p21 and CYP27B1 GFI1 sites and this is also interesting since we have identified flanking sequences as being particularly important for the binding and functional activity of the CYP27B1 GFI1 site. However, both sites contain nucleotides that were preferred in a random nucleotide selection with GFI1 zinc fingers (Zweidler-McKay et al. 1996).

There is evidence that GFI1 forms a large protein complex with its co-repressors ETO, mSin3A and N-CoR and this acts as a scaffold for recruitment of histone deacetylases that can shut down gene expression through chromatin condensation (McGhee et al. 2003). Other corepressors may affect GFI1 repression, and such corepressors may lead to the formation of different sized GFI1 transcriptional multi-protein complexes. A key question then relates to the mechanism by which GFI1 represses the activity of the 5′-flanking region in prostate cancer cells. Perhaps a histone deacetylase containing multi-protein complex assembles on the far upstream GFI1 site leading to condensation of chromatin and silencing of the proximal promoter and/or the enhancer.

We have identified several important regulatory elements involved in positive and negative expression of the CYP27B1 5′-flanking region. The proximal promoter region from +1 to −305 drives basal expression of the CYP27B1 gene through the action of a GC box (that likely binds Sp1) and a CCAAT box. Further upstream within the enhancer region there are three putative Ets protein binding sites with the core sequence 5′-GGAT-3′. One of these sites referred to here as EBS-I (at −807 to −895; Fig. 3), is particularly important since inactivation markedly lowered expression of the pCYP27B1(−997)-Luc construct. The identification of the protein that binds to this site is not known, but apparently is not the prostate specific protein, PDEF (Oettgen et al. 2000). We have also noted the presence of a CRE at −1069 to −1062 (see Fig. 3) that partially contributes to the repression of the CYP27B1 5′-flanking region, although maximum repression is only observed when the GFI1 site is included. Further studies are required to identify the CRE binding protein and its role in repression. There is recent evidence that NFkB can down regulate the CYP27B1 promoter in human embryonic 293 cells through a site in the CYP27B1 proximal promoter at −92 to −83 (Ebert et al. 2004). While this site clearly plays no role in the upstream repression phenomenon reported in the current work, it is possible that an NFkB site located in the far upstream region may be involved in repression, although such a site would be expected to contribute in only a minor way.

Our finding that GFI1 is important for repression of CYP27B1 gene expression in prostate cancer cell lines is novel. While GFI1 has been recognised as a transcriptional repressor from early studies (Grimes et al. 1996a, b), its functional role appeared to be confined to hemopoietic cells (Gilks et al. 1993) and its expression restricted to the bone marrow, thymus, spleen and testis and neurons (Gilks et al. 1993, Wallis et al. 2003). Recently, GFI1 expression was identified in primary human lung cancers, in association with neuroendocrine transcription factors and the neuroendocrine phenotype (Kazanjian et al. 2004). Our work extends the pattern of expression of GFI1 to include epithelial tumors of the prostate. Many putative GFI1 target genes have been suggested (Zweidler-McKay et al. 1996, Duan & Horwitz 2003) but the first and only report which thoroughly established a target for GFI1 (Doan et al. 2004), and which has been validated by others (Yucel et al. 2004), identified the GFI1 gene itself as a target of autoregulation in lymphocytes, but not myeloid lineage cells. Our work identifies CYP27B1 as a new target of the GFI1 oncprotein. More work is needed to determine if GFI1 is oncogenic in prostate epithelial malignancies. If so, the repression of CYP27B1, and thus inactivation of the local tumor
suppressive effects of 1,25D, could be a mechanism for such oncogenic action.

In a recent report, Ma et al. (2004) confirmed that endogenous mRNA levels for CYP27B1 are reduced in DU145, PC3 and LNCaP cells correlating with reduced enzyme activity measured in these cells in earlier studies (Hsu et al. 2001). The finding of lowered CYP27B1 mRNA levels in these cell lines is in keeping with the present work where we have established reduced CYP27B1 promoter activity. However, it has been reported that in primary prostate cell cultures derived from normal and cancer tissues, there are equivalent amounts of CYP27B1 mRNA and protein. It is suggested that an unknown post-translational mechanism is responsible for the associated reduced CYP27B1 enzyme activity in the cultures from cancer tissue (Ma et al. 2004). Our studies reported here indicate that it would be of great interest to identify whether GFII is expressed in human prostate cancer as a first step toward clarifying its postulated role in the disease.

Dedication

This paper is dedicated to the memory of John Omdahl.

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