Progesterone Regulates Transcription of the p21WAF1 Cyclin-dependent Kinase Inhibitor Gene through Sp1 and CBP/p300*

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Progesterone has biphasic effects on proliferation of breast cancer cells; it stimulates growth in the first cell cycle, then arrests cells at G1/S of the second cycle accompanied by up-regulation of the cyclin-dependent kinase inhibitor, p21. We now show that progesterone regulates transcription of the p21 promoter by an unusual mechanism. This promoter lacks a canonical progesterone response element. Instead, progesterone receptors (PRs) interact with the promoter through the transcription factor Sp1 at the third and fourth of six Sp1 binding sites located downstream of nucleotide 154. Mutation of Sp1 site 3 eliminates basal transcription, and mutation of sites 3 and 4 eliminates transcriptional up-regulation by progesterone. Progesterone-mediated transcription is further prevented by overexpression of E1A, suggesting that CBP/p300 is required. Indeed, in HeLa cells, Sp1 and CBP/p300 associate with stably integrated flag-tagged PRs in a multiprotein complex. Since many signals converge on p21, cross-talk between PRs and other factors co-localized on the p21 promoter, may explain how progesterone can be either proliferative or differentiative in different target cells.

Progesterone is a paradoxical hormone having either growth stimulatory effects or growth inhibitory and differentiative effects, depending on the tissue in question and the dose and treatment regimen (1, 2). In the uterus for example, progesterone inhibits epithelial growth and has differentiative effects (3). It is therefore used to counteract the proliferative and carcinogenic effects of unopposed estrogens in women prescribed hormone replacement therapy (4). In the breast, the role of progesterone is more complex. The hormone is required for terminal growth and differentiation of the mammary gland (2). Therefore, mice lacking progesterone receptors (PRs)1 exhibit incomplete mammary gland ductal branching and failure of lobulo-alveolar development (5). In animal models of mammary carcinogenesis, progesterone, depending on the regimen used, can either inhibit or promote tumor formation (2). On the other hand, in animals with established PR-positive mammary tumors, progesterone is usually proliferative, and progesterone antagonists inhibit tumor growth (6). Despite this, in humans, second-line high dose progesterin therapy effectively suppresses the growth of hormone-dependent PR- and estrogen receptor-positive breast cancers that have acquired resistance to the antiestrogen tamoxifen (6).

How can these contradictory effects of progesterone be reconciled? Recent studies have dealt with the effects of progesterone on mitosis and key cell cycle regulatory proteins in cultured human breast cancer cells (1, 7–9). Treatment of such cells with progesterins produces biphasic effects. Studies focusing on the initial growth stimulatory component show that progesterin-induced entry of cells into S-phase is accompanied by transient increases of cyclin D1 and cyclin-dependent kinase 4 activity (1, 7). Indeed, cyclin D1 is a critical component of the mitogenic response to progestins, and its overexpression in transgenic mice produces lobulo-alveolar changes in the mammary gland usually associated with progestational effects in pregnancy (8). Growth stimulation by progesterone is restricted to one cycle, however, and is followed by growth arrest at the G1/S boundary of the second cycle (1, 7, 9). Cells then enter a period of resistance to growth regulatory effects of additional progesterone, accompanied by hypophosphorylation and profound down-regulation of pRb, loss of cyclins D, A, and B, and sequential increases first, in the levels of the cyclin-dependent kinase inhibitor p21 (p21Waf1, Cip1, Kip1, Sdi1) followed by increases in the cyclin-dependent kinase inhibitor p27 (1).

The control of proliferation and differentiation by many hormones and growth factors is linked by events that occur at the G1/S boundary of the cell cycle (10, 11). Recent studies impli- cate growth arrest accompanied by up-regulation of p21 not only in inhibiting proliferation but in promoting differentiation (12). Elevated p21 levels are associated with phorbol ester-, retinoic acid-, and vitamin D-induced differentiation in the myelomonocytic cell line U937, with butyrate-induced differentiation in WiDr cells, MyoD-induced differentiation of myoblasts, and thrombopoietin-induced differentiation of the megakaryoblastic leukemia cell line, CMK (12–18). In each case, the differentiating agents were also shown to induce transcription in a p53-independent manner from the p21 promoter fused to a reporter gene.

We therefore asked whether the up-regulation of p21 protein levels induced by progesterone involves transcriptional regulation of the p21 promoter. We find that this promoter lacks a canonical progesterone response element (PRE). Instead, progesterone activates the gene through a novel mechanism that involves interactions between PRs and CBP/p300, with the transcription factor Sp1, at Sp1 DNA binding sites lying just upstream of the TATA box. Since other agents, such as phorbol esters, butyrate, Ca2+, BRCA-1, and TGF-β also induce p21

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1 The abbreviations used are: PR, progesterone receptor; PRE, progesterone response element; TGFB-β, transcription growth factor-β; MEM, Eagle’s minimum essential medium with Earle’s salts; nt, nucleotides; bp, base pair(s).
from this region of the promoter (13, 16, 19–21), this model may provide a means of analyzing cross-talk between steroid hormones and other signal transduction pathways.

MATERIALS AND METHODS

Cell Lines and Reagents—Wild-type PR-positive T47D CO breast cancer cells were previously described (22). HeLa cells stably expressing flag-tagged PR A or B will be described elsewhere. Cells are routinely cultured in 75-cm² plastic flasks and incubated in 5% CO₂ at 37 °C in a humidified environment. The stock medium consists of Eagle’s minimum essential medium with Earle’s salts (MEM), containing l-glutamine (2 mM) buffered with sodium bicarbonate (4 mg/ml) and HEPES (4.8 mg/liter), insulin (6 ng/ml), and 5% fetal calf serum (HyClone, Logan, UT) without antibiotics. For routine subculturing, cells are diluted 1:10 into new flasks once per week, and the medium is replaced every 2–3 days. Cells are harvested by incubation in Hank’s solution-EDTA for 15 min at 37 °C.

Antibodies were obtained from the following sources. Anti-mouse polyclonal CBP-CT and anti-human monoclonal p300 were from Upstate Biotechnology, Lake Placid, NY; anti-p21 and anti-Sp1 were from Santa Cruz Biotechnology, Santa Cruz, CA; anti-PR AB-52 and B-30 were produced in our laboratories (23); and secondary antibodies were from Bio-Rad.

Various p21 promoter and expression vectors were obtained as follows: the wild-type −2320 promoter and serial 5′-truncated derivatives (13) were a gift of Andrew Kraft and Joseph Biggs (Div. of Oncology, University of Colorado Health Sciences Center, Denver). They were cloned by blunt-end ligation into the Spe I site of the luciferase reporter vector, PA3-LUC (24), a gift of William Wood (Div. of Endocrinology, UCHSC, Denver). The −93 to −33 p21PGS-S wild-type construct and its mutants (21) were generously provided by Xiao-Fan Wang (Dept. of Pharmacology, Duke University Medical Center, NC). The wild-type E1A expression vector, and the 2–36 deletion mutant were also a gift from Andrew Kraft and Joseph Biggs. hPR1 and hPR2, the PR B and A expression vectors were gifts from Pierre Chambon (Strasbourg, France).

Transfection and Transcription—T47D breast cancer cells (1 million) were plated and grown in 100-mm cell culture plates in MEM supplemented with 5% fetal calf serum. Transfection of plasmid DNA by calcium phosphate coprecipitation was usually performed 24 h after plating using 3 μg of the luciferase-fused reporter construct (23), 3 μg of the β-galactosidase expression plasmid PCH110 (Amersham Phamacia Biotech) to correct for transfection efficiency, and Bluescript™ carrier plasmid (Stratagene, La Jolla, CA) for a total of 20 μg of DNA as described previously (23). 16 h later, transfection was completed when the medium was aspirated, and the cells shocked at room temperature for 2 min with 2 ml of phosphate-buffered saline containing 20% glycerol, then 10 ml of MEM containing 5% fetal calf serum were added per dish either with 30 nM progesterone or ethanol vehicle. Cells in duplicate plates were harvested 48 h later in 250 μl of lysis solution (Analytical Luminescence Laboratories, Ann Arbor, MI), and 100 μl of lysis was analyzed for luciferase activity using the Enhanced Luciferase Assay Kit and a Monolight 2010 Luminometer (Analytical Luminescence Laboratories, Ann Arbor, MI) as described by the manufacturer. A further 100 μl of lysis was assayed for β-galactosidase activity as described previously (25) to normalize for transfection efficiency. In Fig. 1, T47D cells were treated with progesterone or ethanol for 48 h prior to transfection, then re-treated with progesterone or ethanol for a second 48-h period as shown. HeLa cell transfection was carried out as above with the exception that 90,000 cells were plated in 60-mm dishes in 5% charcoal-stripped phenol red-free MEM. HeLa cells were not glycerol shocked and were harvested for analysis 24 h after hormone treatment.

In Vivo Association among PRs, Sp1, and CBP/p300—HeLa cells were stably transfected with flag epitope-tagged PR B (f(PR)B) or A (f(PR)A) by electroporation. If the presence of transiently transfected PRE-TATAa–chlamaphenomin acetyltransferase reporter and the synthetic progesterin R5020, the flag-tagged and wild-type receptors produce equal chloramphenicol acetyltransferase activity (not shown). For co-immunoprecipitation assays, nuclear extracts were prepared from HeLa f(PR) cells or PR-negative HeLa cells treated with or without 100 nM R5020 for 1 h. The PRs were immunoprecipitated using an anti-Flag M2 affinity gel (Eastman Kodak Co.), washed twice with TEDG (10 mM Tris, pH 7.4, 1 mM EDTA, 1 mM dithiothreitol, 10% glycerol), twice with 0.3 M KCl in TEDG, twice with 0.1% Nonidet P-40 (Kodak). The PRs and associated eluted proteins were resolved by 10% polyacrylamide gel electrophoresis on 7.5% gels, transferred to nitrocellulose, and immunoblotted with the antibodies against PRs, Sp1, or CBP/p300 described above. The protein bands were detected by enhanced chemiluminescence (Amersham Corp.).

RESULTS

Progesterone Activates the p21 Promoter through an Sp1 Site—We recently demonstrated that in PR-positive T47D breast cancer cells, a pulse of progesterone induces one round of cell division. The cells then enter a period of prolonged growth arrest, during which they are resistant to the proliferative effects of a second dose of progesterone (1). The cells are not resistant to other mitogenic signals, however, because they can reenter the mitotic cell cycle in response to epidermal growth factor. Furthermore, during the arrested state the cells express functional PRs, which following treatment with a second dose of progesterone can activate transcription of a synthetic promoter/reporter (1) and can promote cellular differentiation and accumulation of lipid vesicles (26). Cells arrested by one dose of progesterone express high levels of p21, and the levels rise further following a second dose of progesterone given 48 h after the first (1).

To determine whether progesterone regulates p21 transcriptionally, a luciferase reporter gene driven by 2320 nt of the p21 promoter (Fig. 1A) was transfected into PR-positive T47DCO cells that had been pre-treated with ethanol or 30 nM progesterone for 48 h, then re-treated with ethanol or progesterone for another 48 h (Fig. 1B). Luciferase activity increased 2.3-fold in cells harvested 48 h after progesterone treatment, and 11.7-fold in cells receiving two sequential 48-h progesterone treatments. If progesterone is removed after 48 h, but the cells are not harvested for another 48 h, luciferase transcription continues and rises to 6.3-fold above controls. Since the half-life of progesterone is 3–4 h (27) and of luciferase is 90 min (28), we speculate that secondary signals prolong p21 transcription.

Similarly, in PR-negative HeLa cells transfected with an expression vector encoding PR A, 24 h of progesterone increases luciferase activity driven by the proximal 2320 nt of the

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p21 promoter, 2–3-fold (Fig. 2). To map the progesterone-responsive region, a set of sequentially truncated promoter constructs driving the luciferase gene was transfected into HeLa cells transiently expressing PR A and treated with progesterone for 24 h (Fig. 2). Progressive 5'-truncation led to a decrease in basal activity, but the 2–3-fold induction by progesterone was maintained through a construct that retained only 154 nt at the 3'-end of the promoter. However, when sequences between −154 and −61 were deleted, the progesterone response was abolished, suggesting that PR effects are mediated from this region.

The region between −154 and the transcription start site lacks PReS or AP-1 binding sites, through which progesterone responses could in theory be transmitted (29). On the other hand, this region contains four consensus Sp1 binding sites, and downstream of −61 there are two more Sp1 sites and a TATA box (Fig. 3). Since PR responsiveness maps downstream of −154, this region was analyzed in detail using a series of 60-bp constructs, spanning nt −93 to −33 of the promoter (p21P93-S, WT), in which 10-bp blocks were progressively mutated (Fig. 3; p21P93-S, mut 1–6) (16). The wild-type construct retains progesterone sensitivity narrowing the PR-responsive region to the 32 nt lying between −93 and −61 (Fig. 3). Mutations that destroy the Sp1-3 and Sp1-4 binding sites within this region (p21P93-S, mut 2 and 3) abolish progesterone induction. Mutation of Sp1-3 (p21P-S, mut 2) appears to produce a general loss of basal transcriptional activity. Therefore this site, coupled with Sp1-4 (p21P-S, mut 3) located between nt −70 and −65, encompasses the PR-responsive element. Interestingly, neither mutation of the Sp1-5 or Sp1-6 sites further downstream nor mutation of the TATA box, eliminate the progesterone response. TATA box-independent transcription of the p21 promoter has been previously reported (21). We find, however, that fusion of nt −117 to −61, which contains the progesterone-responsive region, directly upstream of the luciferase transcription start site, produces an inactive promoter (not shown), suggesting that proper spacing between the upstream Sp1 sites and the transcription start site must be maintained, as shown also by Prowse et al. (19), and/or that along with the Sp1 sites, the proximal 94 nt of the promoter are necessary for PR function.

Involvement of CBP/p300 in PR Regulation of the p21 Promoter—Recently, Missero et al. (30) demonstrated that keratinocyte differentiation associated with an increase in p21 levels is abolished by overexpression of the E1A oncoprotein. E1A binds CBP/p300, therefore titration of CBP/p300 into the keratinocytes restored p21 expression (30). To determine whether CBP/p300 is important in the induction of p21 by progesterone, HeLa cells were cotransfected into HeLa cells with either progesterone (100 nM) or ethanol vehicle for 24 h. Relative luciferase units were corrected for transfection efficiency based on β-galactosidase activity.
from the −2320 bp promoter. This mutant also increases basal transcription of the p21 promoter, which is similar to its effects on p15 promoter activity previously described (31). Interestingly, overexpression of wild-type E1A also abolishes progesterone regulation of the PRE2-TATAa3 promoter, yet fails to alter progesterone-regulated transcription of the Sp1-Luc (32) promoter (not shown). This suggests that the ability of E1A overexpression to block progesterone-induced transcription is promoter specific and not necessarily Sp1-dependent.

**PR Bind Sp1 and p300**—Since the PR-dependent induction of p21 involves Sp1 and CBP/p300 in a region of the p21 promoter lacking a PRE, we postulated that PRs are tethered to the promoter through Sp1 and/or CBP/p300. To test this hypothesis, HeLa cells were stably transfected with expression vectors encoding flag-tagged PR A or B. The cells were treated or not with the progesterin R5020, and nuclear extracts were prepared. PRs and associated proteins were immunoprecipitated from nuclear extracts with an anti-flag M2 affinity gel, then eluted from the resin with a flag peptide, and detected by immunoblotting. Fig. 5A (top) shows expression of the PR A-or B-isoforms in nuclear extracts from untreated or R5020-treated PR-positive HeLa cells. Low levels of A receptors can be immunopurified from nuclear extracts with anti-flag resin even in the absence of ligand (lane 2), and the levels increase further after ligand addition (lane 1). In the absence of ligand, no B receptors can be precipitated from nuclear extracts (lane 4), but high levels are purified following ligand treatment (lane 3). Fig. 5A (bottom) shows that Sp1 co-immunoprecipitates with the anti-flag antibody and is eluted by the flag peptide only from extracts that contain PRs. Similarly, no Sp1 is present in immunoprecipitates of nuclear extracts from PR-negative HeLa cells (not shown).

Interactions between PRs and CBP/p300 are shown in Fig. 5B. Using R5020-treated PR-negative HeLa cells, or HeLa cells expressing flag-tagged PR B, nuclear extracts were immunoprecipitated with an anti-CBP/p300 antibody or the anti-flag resin-bound antibody, and copurified proteins were detected with anti-CBP/p300 or anti-PR antibodies. CBP (p265) and p300 can be immunoprecipitated with the anti-CBP/p300 antibody from PR-negative HeLa cells, but PR B are absent (lane 1), and no nonspecific binding is seen with the anti-flag antibody control (lane 2). However, in HeLa cells expressing flag-tagged PR B, high levels of B receptors co-immunoprecipitate with the anti-CBP/p300 antibody (lane 3) and in the reciprocal assay, p300 is co-immunoprecipitated with B receptors using the anti-flag antibody (lane 4).

**DISCUSSION**

In breast cancer cells, a transient pulse of progesterone has biphasic effects; it accelerates proliferation in the first cell cycle then arrests cells at the G1/S boundary of the second cycle (1, 9). A second dose of progesterone prolongs the growth arrest. We have proposed that the arrested cells are poised to enter a proliferative or differentiative pathway, depending on the nature of other cellular signals. This model calls for the convergence and integration of signals from the cell surface and cytoplasm with those in the nucleus. Since the progesterone-induced growth arrest is accompanied by a 10–15-fold increase in the levels of p21 (1) and this protein is a key player in determining cell fate (12), we speculated that integration of divergent signals occurs at the p21 promoter. To that end we sought to understand the mechanisms by which progesterone regulates the levels of p21.

We show here that a transient pulse of progesterone increases transcription from the p21 promoter 2–3-fold (Figs. 1 and 2), which rises to approximately 12-fold in cells receiving a second hormone dose (Fig. 1). The progesterin-responsive element maps to the Sp1-3 and Sp1-4 sites located between −84 and −65 nt. This suggests that progesterone induction is p53-
interaction may account for the ability of Sp1 to activate tran-

sition (Fig. 6). The former is more likely since p21 promoter regulation by TGF-β in keratinocytes is also CBP/p300-dependent (31).

In sum, we have demonstrated a novel mechanism by which PRs can regulate gene transcription through a promoter that lacks canonical PREs. Instead, we suggest that PRs are brought to the DNA by binding to Sp1. It is possible that other Sp1-responsive genes (39, 40) can be similarly regulated. Fur-

thermore, we have demonstrated this unusual regulation using the promoter of the p21 gene. This cyclin-dependent kinase inhibitor is a key intermediary protein in the pathway that determines whether cells proliferate or differentiate (10, 11), and it is therefore a target of regulation by multiple signaling molecules. We speculate that the proliferative versus differentiative fate of progeste gene regulatory functions is controlled by interactions between PRs and other transcription factors localized on the p21 promoter.

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