Forum Original Research Communication

Activation of the Mouse Heme Oxygenase-1 Gene by 15-Deoxy- $\Delta^{12,14}$ -Prostaglandin J₂ Is Mediated by the Stress Response Elements and Transcription Factor Nrf2

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ABSTRACT

The mechanism of heme oxygenase-1 (ho-1) gene activation by 15-deoxy-\(\Delta^{12}\).14-prostaglandin J, (15d-PGJ,) was examined. 15d-PGJ, stimulated expression of HO-1 mRNA and protein and of a mouse ho-1 gene promoter/luciferase fusion construct (HO15luc) in a dose-dependent manner in mouse hepatoma (Hepa) cells. H015luc expression was not effected by troglitazone, a peroxisome proliferator-activated receptor- γ (PPAR- γ) ligand, but induction by 15d-PGJ, was abrogated by the antioxidant N-acetylcysteine. The primary 15d-PGJ, responsive sequences were localized to a 5' distal enhancer (E1) and identified as the stress-response element, previously shown to mediate ho-1 activation by several agents, including heme and heavy metals. Treatment of Hepa cells with 15d-PGJ, stimulated stress-response element-binding activity as judged by electrophoretic mobility shift assays. Antibody "supershift" experiments identified NF-E2 related factor 2 (Nrf2), but not Fos, Jun, or activating transcription factor/cyclic AMP response element binding protein transcription factors, within the 15d-PGJ,-induced complexes. Similarly, a dominant-negative mutant of Nrf2, but not of c-Jun or c-Fos, abrogated 15d-PGJ,-stimulated E1 transcription activity. Finally, prior induction of HO-1 in RAW264.7 mouse macrophages by 15d-PGJ₂ attenuated cell death caused by diesel exhaust particle extracts. These results demonstrate that induction of mouse HO-1 expression by 15d-PGJ, is independent of PPAR- γ but dependent on oxidative stress, is regulated by the oxidative stress-activated transcription factor Nrf2, and provides cytoprotective activity. Antioxid. Redox Signal. 4, 249–257.

INTRODUCTION

ROSTAGLANDINS (PGs), oxygenated metabolites of arachidonic acid, are produced in response to a variety of extracellular stimuli and regulate cellular growth, differentiation, and homeostasis (36, 48). Conventional PGs of the D, E, F, and I classes exert their effects via stimulation of G proteincoupled, seven-transmembrane receptors. On the other hand, cyclopentenome PGs—characterized by the presence of an α,β -unsaturated ketone in the cyclopentenome ring—do not appear to bind to membrane receptors and are actively transported into

cells (35), where they exert a unique spectrum of biological effects including antitumor and antiviral activities, cessation of cell growth, and stimulation of osteogenesis (11, 37). These effects of cyclopentenome PGs, such as PGA_2 and PGJ_2 , can be attributed in part to their ability to stimulate expression of proteins involved in multiple cellular processes including gene transcription [p53 (30) and c-Fos (15)], cell-cycle progression [p53 and p21/WAF1/CiP (19)], and stress management [heatshock proteins (39, 47) and heme oxygenase-1 (HO-1) (26)].

HO-1, a ubiquitous stress-responsive protein, and one of the most prominent proteins induced by Δ^{12} -PGJ₂ (26, 27), is

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a key enzyme in heme metabolism, initiating the oxidative cleavage of heme to yield carbon monoxide, iron, and biliverdin; the latter is subsequently reduced to bilirubin in a non-rate-limiting step. Evidence accumulated over the past decade suggests that HO-1 functions as a cytoprotective enzyme, largely as a consequence of the antioxidant activities of biliverdin and bilirubin and the pleiotropic effects of carbon monoxide (8, 32). The biological importance of HO-1 activity, and presumably its inducibility, are most dramatically demonstrated by the physiological abnormalities, including growth retardation, anemia, leukocytosis, and tissue iron deposition, resulting from HO-1 deficiency (42, 43, 50).

As is the case with most inducers, stimulation of HO-1 expression by Δ^{12} -PGJ, is presumably regulated at the level of gene transcription (27, 38), but the molecular mechanism of ho-1 gene activation by Δ^{12} -PGJ, is still incompletely understood. Koizumi et al. (27) have localized the Δ^{12} -PGJ₂responsive sequence of the rat ho-1 gene to a promoter region between residues -810 and -600. They have further identified the critical sequence, CATGTG, as an element that conforms to the consensus E-box motif, CANNTG, a recognition site for a large family of basic/helix-loop-helix transcription factors. Interestingly, although the mouse and rat ho-1 gene promoter sequences in this region are highly conserved, the corresponding mouse element, TATGTG, no longer conforms to an E-box motif. Furthermore, in our analysis of the mouse ho-1 gene, we have been unable to identify any agent that transmits ho-1 gene inducibility solely through this promoter region. Rather, induction by most agents is mediated by two distal enhancers, E1 and E2, located approximately 4 and 10 kbp upstream of the transcription initiation site, respectively (3, 4, 8). Taken together, these observations point to the existence of additional or alternative mechanisms for ho-1 gene activation by PGJ₂. Data presented in this report indicate that the E1 enhancer is essential for ho-1 gene activation by 15deoxy- $\Delta^{12,14}$ -prostaglandin J_2 (15d-PGJ₂), a metabolite of Δ^{12} -PGJ₂, and that this induction is mediated by the stress response elements (StREs) (18) and the NF-E2 related factor 2 (Nrf2) transcription factor. Additional studies indicate that prior stimulation of HO-1 expression by 15d-PGJ₂ attenuates cell death induced by diesel exhaust particle (DEP) extracts.

MATERIALS AND METHODS

Materials

PGs were obtained from Sigma Chemical Co. (St. Louis, MO, U.S.A.) or Calbiochem-Novabiochem Corp. (La Jolla, CA, U.S.A.). DEP extracts were prepared as previously described (16).

Plasmids

The construction of plasmids pHO15luc and its corresponding mutants [Δ E1, Δ E2, and Δ (E1+E2)] (6), pE1-luc and its corresponding mutants (1, 6), and the dominant-negative mutants (DNMs) of Nrf2 and c-Jun (5) have been described. The MafK DNM (29) and the A-Zip type mutant of c-Fos (40) were kindly provided by Drs. Stuart Orkin (Harvard University) and Chuck Vinson (NCI).

Cell culture, transfection, and enzyme assays

Mouse hepatoma (Hepa) and macrophage (RAW264.7) cells were cultured in a humidified atmosphere at 37°C in Dulbecco's modified Eagle's medium (Life Technologies Inc., Grand Island, NY, U.S.A.) containing 0.45% glucose and 10% fetal bovine serum (Mediatech, Herndon, VA, U.S.A.), with 50 µg/ml gentamycin. Stable transfections were carried out by the calcium phosphate precipitation technique as previously described (1, 2). Transient transfections were carried out either by the calcium phosphate precipitation technique or by using Effectene Transfection Reagent (Qiagen, Valencia, CA, U.S.A.) according to the manufacturer's recommendation. Transfection efficiency was monitored by co-expression of E. coli β-galactosidase encoded by plasmid pCMV/β-gal. Preparation of cell extract and measurement of reporter enzyme activities were carried out as described (2). Additional details are provided in the figure legends.

RNA and protein blot analyses

Total RNA was isolated by the procedure of Chomczynski and Sacchi (9), and RNA dot blot analysis was carried out as previously described (6). Hybridization signals were quantified using a Storm Phosporimager (Molecular Dynamics, Sunnyvale, CA, U.S.A.). Western blot analysis for HO-1 was carried out as previously described (14) using monoclonal or polyclonal anti-rat HO-1 antibodies (StressGen Biotech, Victoria, BC, Canada) and the ECL detection system (Amersham Pharmacia Biotechnology, Piscataway, NJ, U.S.A.).

Electrophoretic mobility shift assay (EMSA)

Hepa cells were seeded (4 \times 10⁶ cells/10-cm plate) and cultured for 40-48 h in complete medium and an additional 24 h in serum-free medium. Cells were treated with vehicle or 25 μM 15d-PGJ, in serum-free medium for 3 h and then collected for preparation of whole-cell extracts (13). A doublestranded oligonucleotide (IDT Inc., Coraville, IA, U.S.A.) containing the sequence 5'-TTTTATGCTGTGTCATGGTT-3' (core StRE sequence underlined) was used as probe in EMSA reactions using conditions previously reported (13). In antibody supershift assays, 1 µl of preimmune serum or anti-MafG serum (kindly provided by Dr. V. Blank, Lady Davis Institute for Medical Research, Montreal, Quebec, Canada) or 2 µg of preimmune IgG or antitranscription factor IgG (Santa Cruz Biotechnology, Santa Cruz, CA, U.S.A.) was added to the reaction mixture and incubated for 20 min at room temperature prior to electrophoresis.

Analysis of cell death using flow cytometry

RAW264.7 cells were plated (1 \times 10⁵ cells/well of sixwell plate) and cultured for 16 h. Cells were pretreated with vehicle, 15d-PGJ₂ (0.53 μ M), tin protoporphyrin (SnPP, 7.5 μ g/ml), or both 15d-PGJ₂ and SnPP for 48 h. The culture medium was then replaced with medium containing the same agents in the presence or absence of DEP extract (100 μ g/ml), and the cells were cultured for an additional 16 h. During exposure to DEP, the 15d-PGJ₂ concentration was increased to 1.6 μ M. Cells were collected by scraping, washed

in phosphate-buffered saline, and stained with propidium iodide (PI, 1 µg/ml). Flow cytometric analysis was performed using a FACScan (Becton Dickinson, Mountain View, CA, U.S.A.) equipped with a 488-nm argon laser. Forward and side scatters were used to gate out cellular debris. PI fluorescence was analyzed in FL-2 channel. The data were analyzed using CellQuest software (Becton Dickinson).

RESULTS

$15d-PGJ_2$ stimulates the expression of HO-1 mRNA and protein in mouse Hep cells

Treatment of Hepa cells with 15d-PGJ₂ for 3 h stimulated HO-1 mRNA accumulation in a dose-dependent manner (Fig. 1A). The steady-state level of HO-1 mRNA, normalized to the amount of ribosomal protein S3 mRNA, increased \sim 30-fold at the highest concentration (20 μ M) of 15d-PGJ₂ tested. A similar accumulation of HO-1 protein was also observed after exposure to 20 μ M 15d-PGJ₂ (Fig. 1B).

15d- PGJ_2 stimulates ho-1 promoter activity in Hepa cells

Reasoning that induction of HO-1 expression by 15d-PGJ_2 is regulated at the level of gene transcription, we examined the expression of HO15luc, a firefly luciferase gene under the control of a 15-kbp mouse ho-1 promoter fragment. Based on luciferase activity measurements, 15d-PGJ_2 stimulated expression of the stably integrated HO15luc gene in a dose-dependent manner (Fig. 1) and to a similar extent to that observed with the endogenous ho-1 gene (Fig. 2). This response was relatively specific for 15d-PGJ_2 as no induction or only minimal induction was observed with other PGs, including PGA_1 , PGA_2 , PGE_1 , PGE_2 , and PGF_α . Unless otherwise indicated, subsequent studies were carried out at a 15d-PGJ_2 concentration of $25 \ \mu M$, a level at which no cytotoxicity was observed under our experimental conditions (data not shown).

15d-PGJ₂ stimulates mouse ho-1 gene activation through a peroxisome proliferator-activated receptor- γ (PPAR- γ)-independent pathway

15d-PGJ, is a natural ligand of PPAR-γ, a member of the nuclear receptor superfamily of ligand-dependent transcription factors that is also activated by antidiabetic thiazolidinediones, such as troglitazone (10). To determine if ho-1 gene induction is mediated by PPAR-γ, we examined the effect of troglitazone on HO15luc expression. As shown in Fig. 3A, troglitazone, up to a concentration of 10 μM, had no significant effect on luciferase activity. In addition to functioning as a PPAR-γ ligand, 15d-PGJ₂ is also known to produce cellular oxidative stress (28). To examine the role of oxidative stressdependent signaling on ho-1 gene activation, we measured the effect of N-acetylcysteine (NAC), an antioxidant and glutathione precursor, on HO15luc induction. Treatment of Hepa cells with varying concentrations of NAC decreased 15d-PGJ₂-induced luciferase activity in a dose-dependent manner with essentially complete inhibition observed at 4 mM NAC

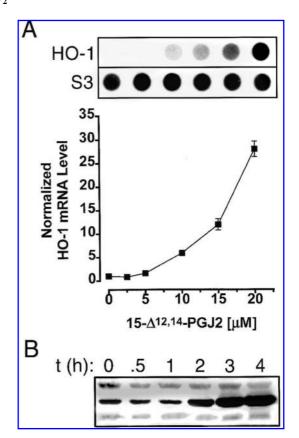


FIG. 1. 15d-PGJ, stimulates accumulation of HO-1 mRNA (A) and protein (B) in Hepa cells. (A) Hepa cells (5×10^5) cells/well of six-well plate) were cultured for 48 h in complete medium and for 24 h in serum-free medium and subsequently treated with the indicated concentrations of 15d-PGJ, for 3 h. Total RNA was isolated, and 5-µg portions were blotted onto a nylon membrane. The membrane was hybridized to a radiolabeled rat HO-1 cDNA probe, stripped, and reprobed with a radiolabeled rat ribosomal protein S3 cDNA. Signals were quantified using a phosphorimager, and relative HO-1 mRNA levels, normalized to S3 mRNA, are presented. The data represent the average and range of two independent experiments. (B) Hepa cells were cultured as in A and treated with 20 μM 15d-PGJ, for the indicated times. Twenty-microgram portions of whole-cell extracts were electrophoresed on a 15% polyacrylamide gel, transferred to nitrocellulose membranes, and subjected to western blotting using a polyclonal anti-rat HO-1 antibody.

(Fig. 3B). Interestingly, under similar conditions, hememediated induction of HO15luc (Fig. 3B) was not affected by NAC. This divergent effect of NAC was also observed with induction of the endogenous ho-1 gene by $15d-PGJ_2$ and heme (data not shown).

Identification of the StREs as the 15d-PGJ₂-responsive elements of the mouse ho-1 gene

Previous studies (3, 4) from our laboratory have identified two enhancer regions, E1 and E2, located approximately 4 kbp and 10 kbp upstream of the transcription initiation site, respectively, as the primary loci responsible for *ho-1* gene activation

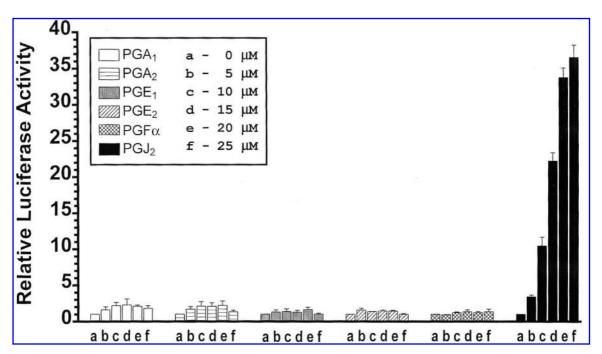


FIG. 2. 15d-PGJ₂ stimulates *HO15luc* expression. *HO15luc* stable transfectants of Hepa cells were plated (2×10^5 cells/well of 12-well plate), cultured as described in the legend to Fig. 1, and treated for 5 h with the indicated concentrations of the designated PGs. Aliquots representing 10% of the cell extracts were used for measurement of luciferase activity, which was normalized to protein content. Normalized activity in vehicle-treated cells was arbitrarily assigned a value of 1. Data are presented as means \pm SD (n = 3).

in response to multiple agents, including heme and heavy metals. To determine the role of these regions in 15d-PGJ_2 -dependent gene activation, we tested the expression of HO15luc mutants lacking one or both enhancers. Targeted deletion of the 161-bp E2 enhancer or a 521-bp fragment containing the 268-bp E1 enhancer reduced basal luciferase activity by $\sim 70\%$, but

no additional dimunition was observed when both enhancers were excised (Fig. 4A). Deletion of E1 or E2 also diminished 15d-PGJ₂-dependent luciferase activity, by approximately 80% and 25%, respectively, indicating a greater importance of E1 in this response. The double mutant promoter, Δ (E1+E2), was only minimally responsive to 15d-PGJ₂ (1.5-fold induction).

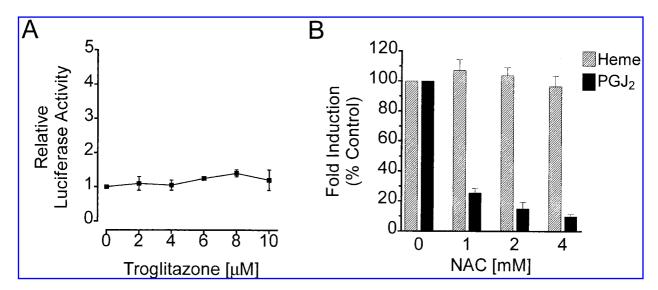


FIG. 3. Induction by 15d-PGJ₂ is inhibited by the antioxidant NAC. HO15luc-transfected Hepa cells were plated and cultured as described in the legend to Fig. 2. Cells were treated for 5 h with the indicated concentrations of troglitazone (A) or 25 μ M 15d-PGJ₂ or 10 μ M heme (B). NAC, at the indicated concentrations, was added 30 min prior to and during the entire incubation period. Luciferase activity was normalized to protein content, and data are presented as means \pm SD (n = 3). For experiments depicted in B, average induction by 15d-PGJ₂ and heme was 28.7- and 32.7-fold above vehicle-treated cells, respectively.

Because of its apparently greater importance, the activity of E1 was examined in more detail. As shown in Fig. 4B, expression of an E1-driven luciferase reporter gene, pE1Luc, was increased >10-fold in response to 15d-PGJ₂. Among other cis-elements (1), the E1 enhancer contains three distinct StREs (Fig. 4B), which have been identified as the dominant inducer-responsive elements within this region (1, 6). Mutation of each of the StREs individually diminished 15d-PGJ₂responsiveness to varying degrees; the StRE1 or StRE3 mutant (M1 and M3, respectively) exhibited 30-40% of native E1 activity, whereas mutation of StRE2 (M2) almost completely abolished inducibility. As would then be expected, the triple mutant (M123) could not be activated by 15d-PGJ₂. From these results we conclude that all three StREs contribute to 15d-PGJ2-dependent E1 transcription activity, but that StRE2 is essential for this response.

Treatment of Hepa cells with $15d-PGJ_2$ stimulates StRE2-binding activity

EMSA reactions using a StRE2 probe and whole-cell extracts from Hepa cells were carried out to identify DNA-binding proteins potentially responsible for 15d-PGJ₂-mediated *ho-I* gene induction. One prominent, specific StRE2-protein complex (Fig. 5, lane 2, "A") was detected when using extracts from vehicle [dimethyl sulfoxide (DMSO)]-treated cells. Treatment with 15d-PGJ₂ substantially increased the level of complex A (or a distinct complex comigrating with complex A) and also stimulated formation of a second complex (lane 3, "B"). Complex B was not detected in all experiments and may result from the degradation of the protein(s) in complex A. The consensus core StRE, (T/C)GCTGAGTCA, resembles the consensus binding sites for the activator protein-1 (AP-1) (Jun–Jun or Jun–Fos dimers), cyclic AMP response element binding protein

(CREB)/ activating transcription factor (ATF), Maf, and Cap 'N' Collar-basic/leucine zipper (CNC-bZIP) families of transcription factors, which function as obligate dimers. "Supershift" EMSA reactions using antibodies directed against one or more members of these protein families were carried out to identify specific StRE-binding proteins (StRE-BPs) and potential 15d-PGJ₂-responsive transcription factor(s). Of several factors tested, only Nrf2, a CNC-bZIP protein, was identified in the 15d-PGJ₂-induced complex(es) (Fig. 5).

DNMs of Nrf2 and MafK attenuate gene activation by 15d-PGJ₂

Consistent with the EMSA results, overexpression of an Nrf2 DNM significantly reduced both basal and 15d-PGJ₂-stimulated pE1Luc expression to 25% and 8%, respectively, of that observed in corresponding control cells (Fig. 6). MafK, like other small Maf proteins, dimerizes most prominently with CNC-bZIP proteins (14, 17, 20, 23). A MafK DNM, which would be expected to dimerize with Nrf2 but inhibit subsequent DNA binding of the dimer (29), also diminished both basal and induced E1 activities (70% and 19%, respectively, of control levels). Conversely, DNMs of AP-1 constituents, c-Jun and c-Fos, slightly enhanced pE1Luc expression, indicating that Jun and Fos proteins may actually function as weak repressors of E1-dependent ho-1 gene regulation.

Pretreatment with 15d-PGJ₂ protects RAW264.7 macrophages from DEP extract-induced cell death

Because HO-1 is known to possess cytoprotective activity, we tested the ability of 15d-PGJ₂-induced HO-1 to protect RAW264.7 cells from subsequent DEP extract-mediated cell death. As observed with Hepa cells, treatment of RAW264.7

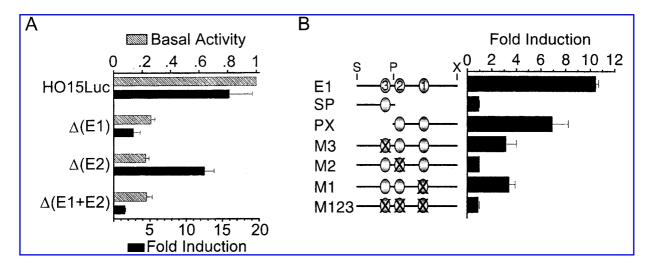


FIG. 4. Identification of StREs as 15d-PGJ₂-responsive *cis*-elements. Hepa cells were plated (5 × 10⁵ cells/well of six-well plate) 24 h prior to transient transfection of pHO15luc and its corresponding mutants (A) or pE1Luc (E1) and its derivatives (B). Transfection was carried out for 6 h by the calcium phosphate co-precipitation method with DNA mixtures consisting of (per well) 2.5 μg of the luciferase plasmid and 2.5 μg of pCMV/β-gal. Cells were cultured overnight in complete medium and for 24 h in serum-free medium prior to treatment with vehicle or 25 μM 15d-PGJ₂ in serum-free medium for 5 h. Luciferase activities were normalized with the corresponding β-galactosidase activities, and data are presented as means ± SD (n = 3). In B, StREs and their relative positions are indicated by numbered ovals; StRE mutations are marked by ovals with crosses. S (Sac I), P (Pvu II), and X (Xba I) represent restriction endonuclease sites in the E1 fragment.

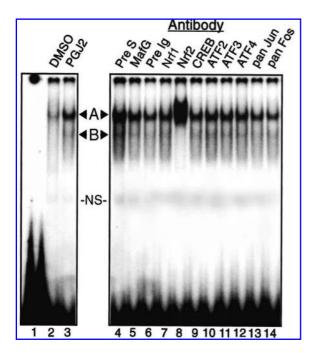


FIG. 5. 15d-PGJ₂ stimulates StRE2 binding activity. EMSA reactions were carried out as described in Materials and Methods using an StRE2 probe and extracts prepared from Hepa cells treated with vehicle (DMSO) or with 25 μ M 15d-PGJ₂ for 3 h. Preimmune serum ("Pre S"), preimmune IgG ("Pre Ig"), or antibodies directed against the indicated transcription factors were used in antibody supershift analysis. The gels were autoradiographed for 24 h. NS, nonspecific.

cells with 15d-PGJ $_2$ (1.6 μ M), but not with PGB $_2$, stimulated HO-1 protein accumulation (Fig. 7A) without appreciably affecting cell viability (Fig. 7B). DEP extract (50 μ g/ml) treatment also increased the amount of HO-1 protein, but prolonged exposure to a higher concentration of DEP extract (16 h, 100 μ g/ml) reduced cell viability by ~70%. Pretreatment with 15d-PGJ $_2$ reversed this cell mortality by slightly >50% (71% versus 32% dead cells). This cytoprotective effect of 15d-PGJ $_2$ was effectively blocked by cotreatment with the HO inhibitor SnPP, providing support for a role of HO-1 in the protective response. Consistent with this role, SnPP by itself reduced cell viability by 22% in this experiment, presumably by inhibiting basal HO activity.

DISCUSSION

Confirming results from previous studies (27) using Δ^{12} -PGJ₂, a precursor of 15d-PGJ₂, we show that the latter directly induces HO-1 expression in mouse liver and macrophage cell lines. Given the comparable levels of stimulation of the endogenous *ho-1* gene (Fig. 1) and the stably transfected *HO15Luc* fusion gene (Fig. 2), it appears that this induction is regulated primarily at the level of gene transcription, at least in Hepa cells. We have further characterized this mechanism by identifying the 15d-PGJ₂-responsive *cis*-elements and *trans*-factor: the StREs and Nrf2, respectively.

We have previously demonstrated that the StREs, in one or both of the enhancers, regulate *ho-1* induction by a diverse array of agents, including the substrate heme, 12-*O*-tetrade-canoylphorbol 13-acetate, lipopolysaccharide, various electrophiles, hyperoxia, DEP extract, and heavy metals such as cadmium, zinc, mercury, and cobalt (for reviews, see 8, 13, 31). Although structurally and chemically diverse, these inducers share the ability to produce cellular oxidative stress. Inclusion of 15d-PGJ₂ in this group further highlights the dominant role of the StRE in inducer-dependent, mouse *ho-1* gene regulation.

The StRE resembles the binding site for several families of basic leucine zipper (bZIP) transcription factors: AP-1, CREB/ATF, Maf, and CNC-bZIP. Indeed, we have previously shown that one or more members of each of these bZIP subfamilies binds to the StRE (4, 6, 8, 13, 14). The existence of multiple StRE-BPs provides a mechanism for inducerspecific or inducer-selective regulation of the ho-1 gene via a single type of element. Although all potential StRE-BPs were not examined in the present study, the antibody "supershift" analysis in conjunction with the DNM experiments strongly implicate Nrf2 in 15d-PGJ₂-mediated ho-1 gene activation. Conversely, these experiments rule out the role of AP-1 proteins in this response as the pan-Jun and pan-Fos antibodies would recognize all members of each of their respective families. To the best of our knowledge, this is the first report demonstrating that Nrf2 is a 15d-PGJ₂-responsive transcription factor.

Nrf2, like Fos proteins, is incapable of forming homodimers (14, 34) and dimerizes most prominently with small

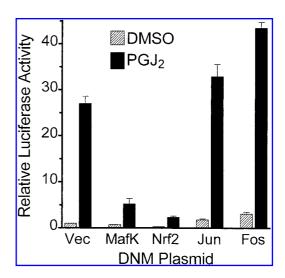


FIG. 6. DNMs of Nrf2 and MafK inhibit pE1-Luc induction by 15d-PGJ₂. Hepa cells were plated (2 × 10⁵ cells/well of 12-well plate) and transfected (Effectene method) 24 h later with DNA mixtures consisting of (per well) 150 ng of pE1-Luc, 50 ng of pCMV/β-gal, and 300 ng of the empty vector ("Vec") or the indicated DNM expression plasmid. After a 24-h incubation period, cells were treated with vehicle (DMSO) or 25 μM 15d-PGJ₂ in serum-free medium for 5 h. Luciferase activities were normalized with the corresponding β-galactosidase activities and are presented relative to the activity in vehicle-treated, vector-transfected cells. Data are means \pm SD (n = 3).

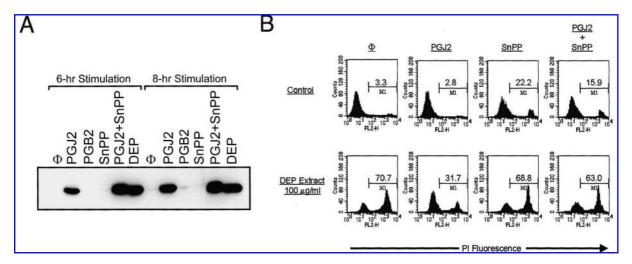


FIG. 7. Pretreatment with 15d-PGJ₂ protects RAW264.7 macrophages from cell death by DEP extract. (A) RAW264.7 cells were plated (2×10^6 cells/well of six-well plates), cultured for 16 h, and treated with vehicle (ϕ), 15d-PGJ₂ (PGJ2, 1.6 μ M), PGB2 (5μ M), SnPP (7.5 μ g/ml), or DEP extract (50μ g/ml) for 6 or 8 h. HO-1 protein was detected by immunoblotting. (B) Cell culture and treatment and flow cytometry were carried out as described in Materials and Methods. Results from a typical experiment (out of three) are presented. The percentage of cells exhibiting PI staining under each experimental condition is indicated.

Maf proteins (14, 17, 20, 33). We have recently provided evidence for a role of Nrf2–MafG heterodimers in *ho-1* gene induction by cobalt in Chinese hamster ovary cells (13), but were consistently unable to detect MafG in the 15d-PGJ₂-induced StRE2–protein complex of Hepa cells, even though this protein is sufficiently expressed in these cells (unpublished observation). It is conceivable that Nrf2 dimerizes with other small Maf proteins, such as MafK and MafF, to mediate *ho-1* gene activation. Recently, we have identified ATF4 as an Nrf2 dimerization partner (14), but ATF4 was also not detected in the StRE2–protein complex(es). Additional studies will be necessary to define more precisely the dimeric nature of the StRE-BP(s) responsible for *ho-1* gene activation in response to 15d-PGJ₂.

15d-PGJ, is known to regulate target gene expression by at least two general mechanisms: activation of PPAR-γ and/or activation of the stress-response pathway. The identification of StREs, as opposed to a sequence similar to the consensus PPAR- γ binding site (10, 24), as the active *cis*-elements argues that induction of ho-1 by 15d-PGJ, proceeds primarily via a PPAR-γ-independent pathway. This conclusion is further strengthened by the observations that the synthetic PPAR-γ ligand troglitazone does not influence ho-1 promoter activity, but that induction by 15d-PGJ, is completely abrogated by the antioxidant NAC. The insensitivity of the mouse ho-1 promoter to troglitazone is consistent with the observations of Kasai et al. (23) who reported that whereas 15d-PGJ₂ and its precursors, PGJ2 and PGD2, readily stimulate HO-1 mRNA accumulation in human thyrocytes, troglitazone and pioglitazone, another antidiabetic thiazolidinedione, are without effect. In contrast to these results, Kitamura et al. (25) reported a stimulatory effect of both 15d-PGJ₂ and antidiabetic thiazolidinediones on HO-1 expression in primary rat glial cells, thus providing evidence for a role of PPAR-γ in ho-1 gene regulation. It is conceivable that the latter pathway is operative in a cell-specific manner.

Cyclopentenone PGs have been implicated in the resolution of acute inflammatory reactions (12). Indeed, 15d-PGJ₂ inhibits the production of proinflammatory cytokines and inducible nitric oxide synthetase in activated monocytes by negatively interfering with the transcription factors (e.g., AP-1, nuclear factor-κB, STAT) that regulate the corresponding genes (22, 45). Such interference could arise by either PPAR-γ dependent (45) or -independent mechanisms (46). In addition to inhibiting proinflammatory pathways, 15d-PGJ₂ could conceivably promote resolution of inflammation by activating antiinflammatory systems. HO-1 and particularly Nrf2 may be important participants in this effector arm of 15d-PGJ₂ function. For instance, in a carrageenan-inducedmodel of acute pleurisy, elevation of HO-1 expression suppresses, whereas inhibition of HO enzymatic activity potentiates, the inflammatory response (49). Furthermore, overexpression of HO-1 in RAW cells attenuates lipopolysaccharide-induced tumor necrosis factor-\alpha production, and this inhibitory response can be mimicked by administration of exogenous carbon monoxide, which also inhibits the expression of other proinflammatory cytokines, including interleukin-1\beta and macrophage inflammatory protein-1β (41). Although our studies with the macrophage cells only examined the cytoprotective capability of 15d-PGJ₂-induced HO-1, it is likely that the cytoprotective, antioxidant, and antiinflammatory activities of HO-1 are not mutually exclusive properties. If this is the case, and given that accumulating evidence points to Nrf2 as an important regulator of gene-encoding proteins with antioxidant and xenobiotic detoxification functions (21), activation of Nrf2 may provide an even more significant mechanism for manifestation of the various biological effects, including antiproliferation, antitumorogenesis, and osteogenesis, of cyclopentenone PGs in general and 15d-PGJ, in particular. For instance, Nrf2-deficient mice exhibit a significantly higher burden of benzo[a]pyrene-induced gastric neoplasia and reduced chemoprotective efficacy than wild-

type animals (44). Furthermore, using gene array analysis, Beck *et al.* (7) have recently shown that expression of Nrf2 is up-regulated during osteoblast differentiation. Further studies will be necessary to establish more conclusively the role of Nrf2 in manifestation of the various cellular and biological effects of cyclopentenone PGs.

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ABBREVIATIONS

AP-1, activator protein-1; ATF, activating transcription factor; CNC-bZip, Cap 'N' Collar–basic/leucine zipper; CREB, cyclic AMP response element binding protein; DEP, diesel exhaust particle; DMSO, dimethyl sulfoxide; DNM, dominant-negative mutant; 15d-PGJ₂, 15-deoxy-Δ^{12,14}-prostaglandin J₂; EMSA, electrophoretic mobility shift assay; HO, heme oxygenase; NAC, *N*-acetylcysteine, Nrf2, NF-E2 related factor 2; PG, prostaglandin; PI, propidium iodide; PPAR, peroxisome proliferator-activated receptor; SnPP, tin protoporphyrin IX; StRE, stress response element; StRE-BP, stress response element binding protein.

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