

Dexamethasone Promotes Osteoclastogenesis by Inhibiting Osteoprotegerin Through Multiple Levels

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Abstract Increased bone fragility attributed to osteopenia is a serious side effect of glucocorticoid treatment. Glucocorticoid-induced bone loss is caused primarily by hypofunction and apoptosis of osteoblasts, and secondarily by accelerated bone resorption. To explore the mechanism whereby dexamethasone (Dex) stimulates osteoclastogenesis in the coculture system, we analyzed the effect of Dex on the expression of both mouse osteoprotegerin (OPG) and receptor activator of NF- κ B ligand (RANKL). Dex reduced OPG transcripts and OPG protein secretion by the ST2 osteoblastic cells. Since mainly the c-Jun homodimer maintains the steady-state transcription of the OPG gene, we examined the effect of Dex on c-Jun signaling in ST2 cells. Western blotting disclosed that Dex decreased the amount of phospho-c-Jun protein (p-c-Jun) and, correspondingly, the amount of the phosphorylated p46 isoform of Jun N-terminal kinase (JNK). The amount of phospho-SEK1 also decreased after Dex treatment, while the amounts of phospho-ERK and p38 remained constant. Among mitogen-activated protein (MAP) kinase inhibitors, the JNK inhibitor mimicked the inhibitory effect of Dex on OPG promoter activity. On the other hand, Dex treatment per se showed a nominal increase of RANKL gene expression. A part of Dex-mediated OPG gene suppression was achieved by the suppression of β -catenin signaling. We speculate therefore that the bone resorptive action of Dex is mediated mainly by the inhibition of OPG by transrepressing the OPG gene through the AP-1 site, with a reduction (mediated mainly by the decrease in the p46 isoform of JNK) in the proportion of p-c-Jun in a JNK-dependent manner. *J. Cell. Biochem.* 103: 335–345, 2008. © 2007 Wiley-Liss, Inc.

Key words: osteoprotegerin; dexamethasone; promoter; transrepression; c-Jun

Glucocorticoids (GCs) exert a multitude of effects on the immune response and are anti-inflammatory and immunosuppressive when administered therapeutically [Langenegger and Michel, 1999; Riccardi et al., 2000; Pitzalis et al., 2002]. Although GCs are used extensively to relieve inflammatory diseases, increased bone fragility attributed to osteopenia is a serious side effect of GC treatment. It is

generally accepted that GC-induced bone loss is caused primarily by hypofunction and apoptosis of osteoblasts; GCs induce a 30% increase in osteoblast and osteocyte apoptosis [Weinstein et al., 1998]. At the same time, an increase in bone resorption markers (such as urinary deoxypyridinoline (DPD) excretion) is observed during GC therapy [Ardissone et al., 2002], indicating that accelerated bone resorption is also attributed to GC-induced bone loss.

Osteoclasts, derived from hematopoietic precursors of the monocyte/macrophage lineage, are multinucleated giant cells specialized in resorbing bone. Osteoclast precursors must interact with osteoblasts/stromal cells to differentiate into mature osteoclasts [Suda et al., 1992, 1999]. The protein involved in this interaction has been identified as receptor activator of NF- κ B ligand (RANKL), also known as osteoclast differentiation factor (ODF) or tumor necrosis factor-related activation-induced cytokine (TRANCE) [Simonet et al., 1997; Wong

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et al., 1997b; Lacey et al., 1998; Nakagawa et al., 1998; Quinn et al., 1998; Yasuda et al., 1998]. A subset of osteoblasts/stromal cells, at the same time, secrete osteoprotegerin (OPG), a soluble member of the TNF receptor superfamily, that acts as a decoy receptor for RANKL and thereby prevents its interaction with the cognate receptor RANK [Anderson et al., 1997; Wong et al., 1997a; Kong et al., 1999]. OPG strongly inhibits osteoclast differentiation, survival, and function in vitro and bone resorption in vivo [Akatsu et al., 1998; Bucay et al., 1998; Hakeda et al., 1998]: mice lacking OPG show severe early onset of osteoporosis [Mizuno et al., 1998], whereas transgenic animals overexpressing OPG show osteopetrosis [Simonet et al., 1997]. RANKL and OPG are therefore the two final regulators of osteoclastogenesis, and many of the regulators of bone metabolism regulate bone volume by modulating osteoclastogenesis through this RANKL–OPG axis [Horwood et al., 1998; Murakami et al., 1998; Takai et al., 1998; Vidal et al., 1998; Brandstrom et al., 1998a,b; Nagai and Sato, 1999; Hofbauer et al., 2000]. Among these bone-seeking factors, $1\alpha,25$ dihydroxyvitamin D₃ ($1\alpha,25(\text{OH})_2\text{D}_3$) alone [Hofbauer et al., 1998; Kondo et al., 2004] or in combination with dexamethasone (Dex) [Nagai and Sato, 1999] efficiently accelerate osteoclastogenesis by regulating the RANKL–OPG axis in a reciprocal manner. The effect of Dex per se on the RANKL–OPG axis varies, however, according to the nature or origin of osteoblastic/stromal cells. Dex upregulates the OPG gene in calvaria, a membranous bone that is resistant to GC-induced bone loss in the organ culture system [Swanson et al., 2006]. On the other hand, it downregulates OPG and upregulates RANKL reciprocally, thus increasing the RANKL/OPG ratio in the in vitro system using cultured human osteoblastic cell lines [Hofbauer et al., 1999; Harding et al., 2006].

In this study, we explored the mechanism whereby Dex stimulates osteoclastogenesis in the coculture system (using osteoblastic/stromal cells and bone marrow macrophages) by analyzing the effect of Dex on mouse OPG gene expression in osteoblasts. We used bone-marrow-derived osteoblastic/stromal cell line ST2 that corresponds to precursor osteoblastic cells in trabecular bone which is highly susceptible to GC-induced bone loss. We focused particularly on three major transcriptional mechanisms—

AP-1 [Kondo et al., 2004], Runx2 [Thirunavukarasu et al., 2000], and the Wnt/ β -catenin signaling pathway [Glass et al., 2005]—that regulate OPG gene expression.

MATERIALS AND METHODS

Cell Culture and In Vitro Osteoclast-Like Cell Formation

Mouse bone marrow stromal cell line ST2 and C6 cells, established from the calvariae of *runx*-deficient mice, were cultured and maintained in α MEM (Sigma) supplemented with 10% fetal bovine serum (FBS, GIBCO-BRL). Both ST2 and C6 cells are categorized as immature mesenchymal cell lines capable of differentiating into osteoblastic cells. All cultures were maintained at 37°C in a humidified atmosphere of 95% air and 5% CO₂. Mouse bone marrow mononucleated cells ($10^5/\text{cm}^2$), prepared as previously described [Kitazawa et al., 1995], were cocultured with ST2 cells ($10^4/\text{cm}^2$) in the presence of $1\alpha,25(\text{OH})_2\text{D}_3$ (10^{-8} M) and dexamethasone (10^{-8} M) in multiwell plates (Becton Dickinson). At the end of the culture period, the cells were stained for tartrate resistant acid phosphatase (TRAP) with a commercial kit (Sigma), and the number of osteoclast-like TRAP positive multinucleated (more than 3) cells was counted.

Northern Blot Analysis

Total RNA was extracted from ST2 cells by RNazol (Tel-Test, Inc., Friendswood, TX). RNA samples (10 μ g) were separated by denaturing electrophoresis in formaldehyde-agarose gels and stained with ethidium bromide. Total RNA was transferred onto Hybond N+ nylon membranes (Amersham Biosciences Corp., Piscataway, NJ) and immobilized by UV cross-linking. A 1,004 bp cDNA fragment from OPG and a 250 bp cDNA fragment from RANKL were generated by RT-PCR with the following pairs of primers.

- OPG sense: 5'-GAATGGACAACCCAGGAA-ACCC-3';
- OPG antisense: 5'-GTGCTTGAGGGCATA-CATCAGG-3';
- RANKL sense: 5'-TCCTAACAGAATATCA-GAAGACAG-3';
- RANKL antisense: 5'-AGGCTTGCCCTCGCT-GGGCCACATC-3'.

The sequence of OPG and RANKL cDNA was confirmed by direct sequencing. The cDNA fragments of OPG, RANKL, and GAPDH were labeled with [α - 32 P]dCTP by the random primer technique (Random Primer DNA labeling kit, TaKaRa, Japan). The membranes were hybridized with the labeled probe in $5\times$ SSPE, $5\times$ Denhardt's solution, 0.5% SDS, and $1\times$ Background Quencher (Molecular Research Center, Cincinnati, OH) at 60°C for 16 h, washed in $2\times$ SSPE containing 0.1% SDS, in $1\times$ SSPE containing 0.1% SDS, and in $0.1\times$ SSPE containing 0.1% SDS and then analyzed with image analyzer BAS2000 (FUJIX, Tokyo, Japan). The density of each band was analyzed with Image Gauge software (FUJIX, Tokyo, Japan).

Quantitative Real-Time PCR

Total RNA (1 μg) isolated from each cell line was reverse transcribed to produce cDNA, which was then amplified and quantified by the ABI PRISM 7300 Real-Time PCR system (Applied Biosystems, Foster city, CA) using a set of primers and probes (assay ID: mouse RANKL (Mm00441908_m1), mouse OPG (Mm00435452_m1), mouse Runx2 (Mm00501578_m1), and mouse β -catenin (Mm004803033_m1)) purchased from Applied Biosystems. The amount of mRNA was quantified relative to that of GAPDH in each reaction according to the manufacturer's protocol (Applied Biosystems).

OPG ELISA Assay

The amount of OPG protein secreted into the culture medium by ST2 cells was analyzed by a sandwich ELISA procedure, with the use of ANALYZA (TECHNE Corporation, MN) according to the manufacturer's instructions.

Transient Transfection Study

Nested deletion mutants generated by restriction enzyme sites (OPG: Luc-1487, Luc-1125, Luc-697, Luc-116; RANKL: Luc-1005, Luc-723, Luc-524, Luc-276) were ligated to a promoterless and enhancerless pGL3-Basic vector plasmid (Promega) as previously described [Kitazawa et al., 1999; Kitazawa and Kitazawa, 2002; Kondo et al., 2004]. For site-directed mutagenesis of the putative AP-1 binding site ($-293/-287$), the AP-1 core element (TGACTGA, $-293/-287$) in Luc-1487 was replaced with CTCCCTC by a recombinant PCR strategy as previously described [Kondo

et al., 2004]. Plasmid DNA was purified with EndoFree Plasmid Maxi kit (QIAGEN). Each plasmid construct was cotransfected with the phRG-TK vector (Promega) into ST2 cells via liposome-mediated transfection, using Lipofectamine Reagent (Invitrogen), according to the manufacturer's instructions. pGL3-Control vector (Promega) was also transfected as a positive control. Transfected cells were cultured in α MEM (ST2) supplemented with 10% FBS. The cells were harvested 48 h after transfection, and luciferase activity from cell lysates was determined with a luminometer (Model ATP-3010, Advantec, Japan). The transcription efficiency of each construct was standardized by the activity of Renilla luciferase and of a basal luciferase construct.

Immunoblotting

ST2 cells were treated with Dex (10^{-8} M) for 5 min, 10 min, 30 min, 1, 3, 6, 12, 24 h, and the treated cells in 100 mm culture dishes were then lysed with 0.5 ml lysis buffer (50 mM Tris-HCl, pH 8.0, 100 mM NaCl, 0.2% Nonidet P-40, 0.2% sodium deoxycholate, 0.1% SDS, and 50 $\mu\text{m}/\text{ml}$ aprotinin) and a protease inhibitor cocktail tablet (Boehringer Mannheim). The lysates were centrifuged at $15,000g$ for 10 min at 4°C and the supernatants were stored at -80°C . Equal amounts of protein were separated by SDS-PAGE, electrotransferred to nitrocellulose membranes (Trans-Blot) from Bio-Rad Laboratories (Hercules, CA), and immunoblotted with primary antibodies against c-Jun and c-Fos (from Santa Cruz Biotechnology) and phospho-c-Jun (Ser63), phosphorylated Jun N-terminal kinase (phospho-JNK (Thr183/Tyr185)), phosphorylated SAPK/Erk kinase (phospho-SEK1/MKK4 (Thr261)), phosphorylated p44/42 MAP Kinase (Erk1 and Erk2) (phospho-p44/42 MAP Kinase (Thr202/Tyr204)), phosphorylated p38 MAP Kinase (phospho-p38 MAP Kinase (Thr180/Tyr204)), β -catenin, and phosphorylated β -catenin (phospho- β -catenin (Ser33/37/Thr41)) (from Cell Signaling Technology). Detection of immunocomplexes was carried out with the enhanced chemiluminescence (ECL) kit and Hyperfilm ECL from Amersham.

Mitogen-Activated Protein (MAP) Kinase Inhibitors

To assess their effect on OPG promoter activity (Luc-1487), the transfected cells were treated with three MAP kinase inhibitors: JNK

inhibitor (SP600125, BIOMOL Research Labs, 50 μ M), ERK inhibitor (PD98059, Calbiochem, 10 μ M), and p38 inhibitor (SB203580, Calbiochem, 30 μ M).

Transfection of Small Interfering (si)RNA

SiRNA against mouse Runx2 was synthesized by Ambion. Silencer Negative Control siRNA (Ambion) was used as a nonspecific control. For the transfection of siRNA, the cells were washed and resuspended in Opti-MEM (GIBCO). SiRNA was transfected into ST2 cells with the use of siPORT Amine Transfection Agent (Ambion) according to the manufacturer's instructions. The cells were then cultured for an additional 48-h before quantitative real-time PCR.

Statistical Analysis

Data are expressed as means \pm SD. Statistical analyses were carried out by Student's *t*-test. The level of significance was taken to be $P < 0.05$.

RESULTS

Coculture of ST2 Cells and Mouse Bone Marrow Macrophages

With Dex alone and with $1\alpha,25(\text{OH})_2\text{D}_3$ and Dex, ST2 cells supported the formation of TRAP-positive multinucleated cells (Fig. 1A,B). The expression of OPG transcripts was suppressed by treatment with Dex alone and with Dex and $1\alpha,25(\text{OH})_2\text{D}_3$ (Fig. 1C).

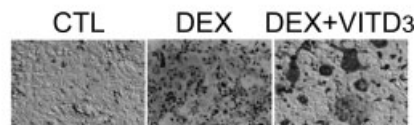
Dose Response and Time Course of OPG Protein Production After Dex Treatment Assessed by ELISA

ELISA showed that the secretion of OPG protein into the culture medium decreased significantly after the treatment of ST2 cells with as little as 10^{-9} M of Dex (Fig. 2A); moreover, this strong inhibitory effect of Dex was observed as early as 6-h after the treatment and lasted for at least 48-h (Fig. 2B) during which no cytotoxic effect was observed.

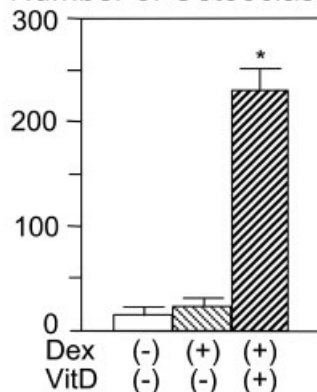
OPG and RANKL mRNA Expression in ST2 Cells

Northern blot analysis showed that a 24-h treatment with Dex (10^{-9} M) suppressed the OPG mRNA expression in ST2 cells (Fig. 3, upper panel), whereas it slightly increased the expression of RANKL mRNA (Fig. 3, lower panel) in a reciprocal manner.

A ST2 and BMM coculture



B Number of Osteoclasts



C Realtime PCR

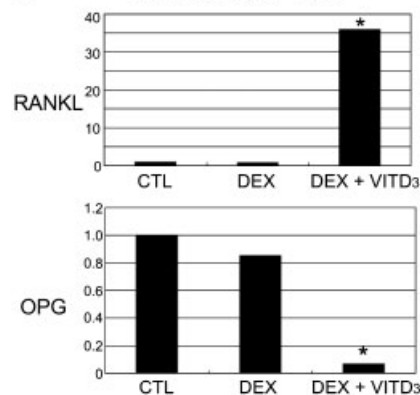


Fig. 1. Coculture of ST2 cells and mouse bone marrow macrophages (BMM). **A,B:** Mouse bone marrow macrophages ($10^5/\text{cm}^2$) and ST2 cells ($10^4/\text{cm}^2$) were cocultured with and without 10 nM $1\alpha,25(\text{OH})_2\text{D}_3$ and dexamethasone (Dex) for 7 days and then stained for TRAP. With Dex alone (middle panel) and with $1\alpha,25(\text{OH})_2\text{D}_3$ and Dex (right panel), ST2 cells supported the formation of TRAP-positive multinucleated cells. The number of osteoclast-like TRAP-positive multinucleated (more than 3 nuclei) cells was counted (B). **C:** By quantitative RT-PCR, in the presence of 10 nM Dex and $1\alpha,25(\text{OH})_2\text{D}_3$, RANKL mRNA increased significantly. On the other hand, the expression of OPG transcripts was suppressed by treatment with Dex alone and with Dex and $1\alpha,25(\text{OH})_2\text{D}_3$. Results are expressed as the relative mRNA amount standardized by GAPDH.

Promoter Activity of Each Deletion Construct (OPG)

A series of deletion constructs of the mouse OPG promoter (Luc-116, Luc-697, Luc-1125, Luc-1487) was transfected into ST2 cells and

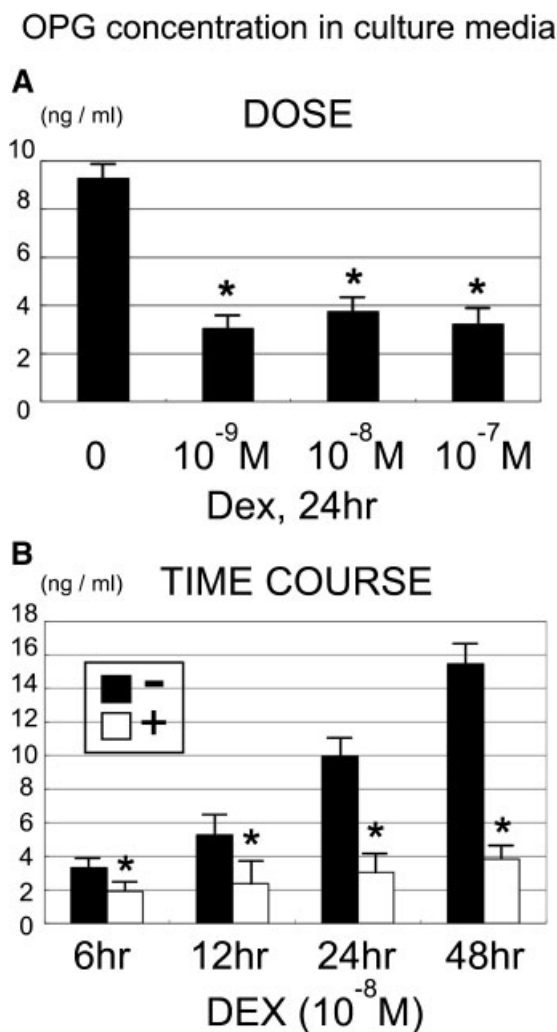


Fig. 2. Dose response and time course of OPG protein production after Dex treatment assessed by ELISA. To assess the effect of Dex on OPG at the protein level, the amount of OPG protein secreted by ST2 cells was measured. The cells were treated with either the vehicle (ethanol) or Dex. The secretion of OPG protein decreased after treatment with as little as 10^{-9} M of Dex (**A**). The strong inhibitory effect of Dex on OPG secretion was observed as early as 6 h after treatment and lasted for at least 48 h (**B**). * $P < 0.05$ versus non-treated cells.

subjected to luciferase assay. Mirroring Northern blot analysis, Dex reduced the promoter activity of Luc-1487 to 50% (Fig. 4A). Furthermore, introduction of mutation to the AP-1 site (-293/-287) showed a reduction in luciferase activity and completely nullified the inhibitory effect of Dex on the promoter (Fig. 4B).

Promoter Activity of Each Deletion Construct (RANKL)

A series of deletion constructs of the mouse RANKL promoter (Luc-1005, Luc-723, Luc-524

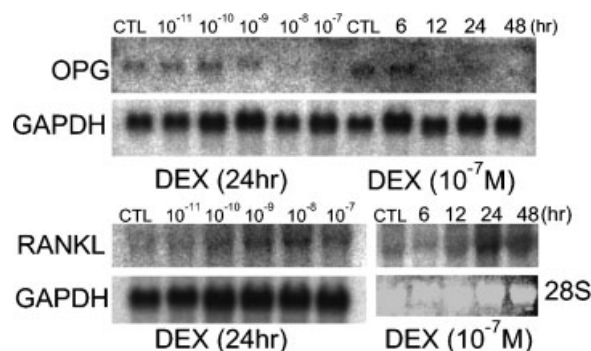


Fig. 3. OPG and RANKL mRNA expression in ST2 cells. Northern blot analysis showed that a 24-h treatment with Dex (10^{-7} M) suppressed the expression of the OPG gene in ST2 cells (**upper panel**). On the other hand, Dex (10^{-7} M) slightly increased the expression of RANKL mRNA in a reciprocal manner (**lower panel**).

Luc-185) was transfected into ST2 cells and subjected to luciferase assay (Fig. 5). Dex slightly increased RANKL promoter activity. Deletion mutant studies suggested that Dex upregulated RANKL through the putative GRE half sites (-642/-628) or the AP-1 sites in the promoter.

Phosphorylation of MAP Kinase and Effects of MAP Kinase Inhibitors On Promoter Activity (OPG)

Since the mutation of the AP-1 site negated Dex-driven OPG suppression and since AP-1 is a major downstream effector for MAPK, we focused on the mitogen-activated protein (MAP) kinase signaling cascade. In agreement with the transient transfection studies, Western blot analysis (Fig. 6A) showed that the amount of phosphorylated c-Jun protein (p-c-Jun) decreased 1hr after treatment of ST2 cells with Dex, whereas the total amount of c-Jun protein decreased after 12 h. Corresponding to the decrease of p-c-Jun, the amount of phosphorylated p46 isoform of JNK decreased significantly 30 min after Dex treatment, whereas that of phosphorylated p54 isoform decreased after 12 h. The amount of phosphorylated SEK1 also decreased significantly 30 min after Dex treatment. In contrast, the amounts of p-ERK and p-p38 remained constant. The transfected cells were treated with three MAP kinase inhibitors: JNK inhibitor (SP600125), ERK inhibitor (PD98059) and p38 inhibitor (SB203580) to assess their effect on OPG promoter activity (Fig. 6B). Of these, only the

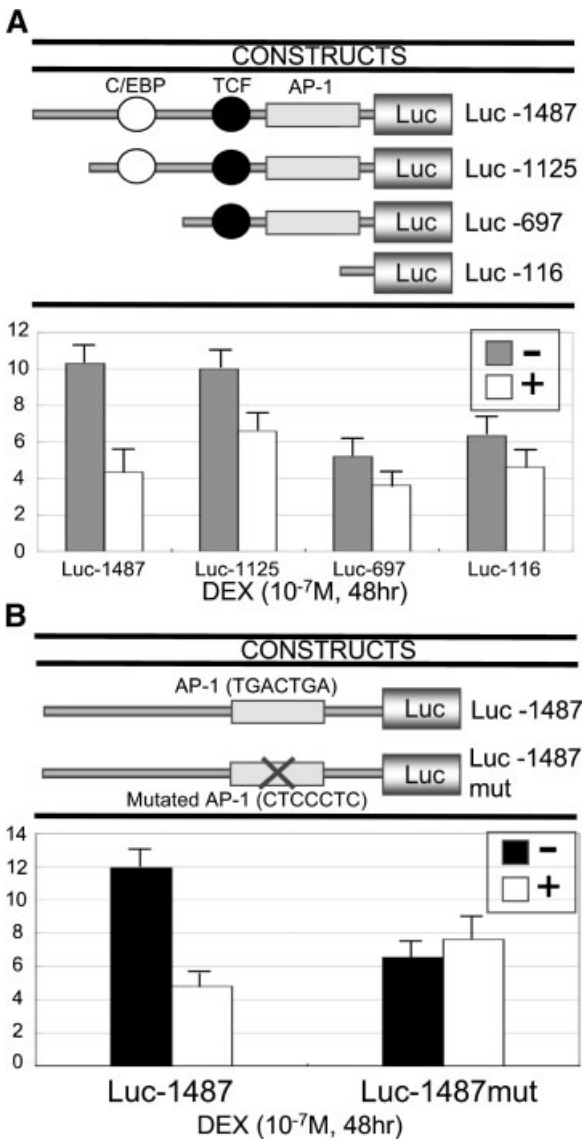


Fig. 4. Promoter activity of each deletion construct (OPG). A series of deletion constructs of the mouse OPG promoter (Luc-116, Luc-697, Luc-1125, Luc-1487) was transfected into ST2 cells and subjected to luciferase assay. Transfected cells were treated with Dex to assess its effect on OPG promoter activity. Mirroring Northern blot analysis, Dex reduced the promoter activity of Luc-1487 to 50% (A). Furthermore, introduction of mutation to the AP-1 site showed a reduction in luciferase activity and completely nullified the inhibitory effect of Dex on the promoter (B).

JNK inhibitor (SP600125) mimicked the inhibitory effect of Dex.

Involvement of Runx2 and β -Catenin Signaling in Dex-Mediated OPG Suppression

Because Runx2 and β -catenin signaling pathways are reportedly involved in OPG expression

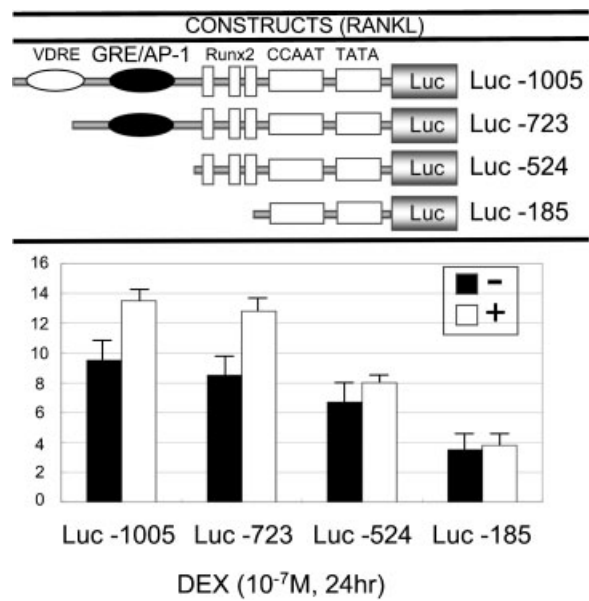


Fig. 5. Promoter activity of each deletion construct (RANKL). A series of deletion constructs of the mouse RANKL promoter (Luc-1005, Luc-723, Luc-524, Luc-185) was transfected into ST2 cells and subjected to luciferase assay. Transfected cells were treated with Dex to assess its effect on RANKL promoter activity. Dex slightly increased RANKL promoter activity. Deletion mutant studies suggested that Dex upregulated RANKL through the putative GRE half sites (-642/-628) or the AP-1 sites in the promoter.

[Thirunavukkarasu et al., 2000; Glass et al., 2005], we tested the effect of Dex on these two factors. Dex treatment downregulated the Runx2 transcript and the β -catenin protein (Fig. 7A). Real-time RT-PCR analysis of Runx2-deficient mouse-derived stromal cell line C6 revealed that while steady-state transcription of the OPG gene in C6 cells was 2 times that in ST2 cells (Fig. 7B), Dex reduced OPG expression to the same extent (84% and 81%, respectively) in both cells (Fig. 7B). Although Dex reduced Runx2 expression in ST2 (Fig. 7A), Runx2 knockdown, established by the transfection of Runx2 siRNA, showed a nominal reduction in OPG mRNA expression in ST2 cells (Fig. 7B), indicating that the inhibitory effect of Dex on OPG expression is independent of Runx2. On the other hand, OPG promoter activity of Luc-1487 was reduced to 70% in ST2 cells treated with LiCl (Fig. 7C), an agonist of the β -catenin signaling pathway, indicating that the Wnt- β -catenin signaling pathway is partially involved in the Dex-mediated down-regulation of OPG.

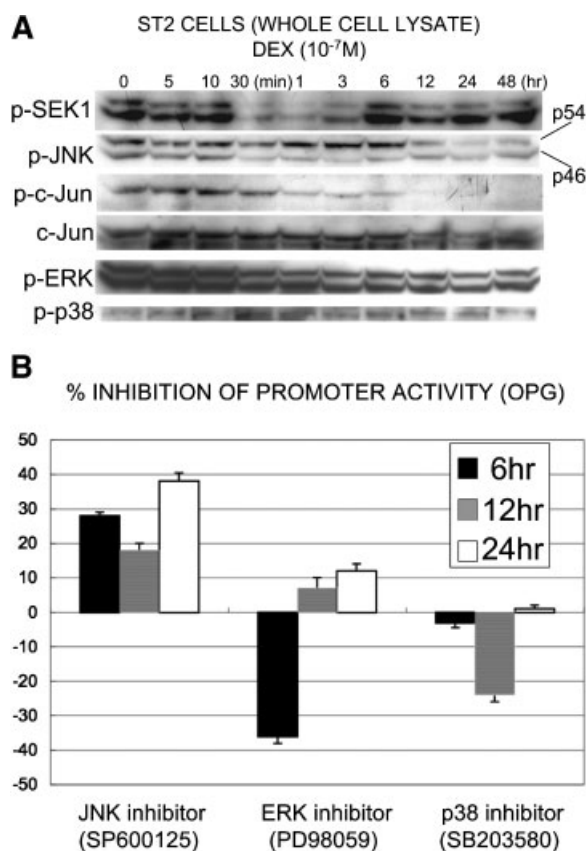


Fig. 6. Phosphorylation of MAP kinase and effects of MAP kinase inhibitors on promoter activity (OPG). **A:** ST2 cells were treated with Dex (10^{-7} M) for 5 min, 10 min, 30 min, 1, 3, 6, 12, 24, 48 h, and whole cell lysates prepared from the treated cells were subjected to Western blot analysis. The antibodies used were against c-Jun, phospho-c-Jun (serine 63), phosphorylated Jun N-terminal kinase (JNK, threonine 183/tyrosine 185), phosphorylated SAPK/Erk kinase (SEK1, threonine 261), phospho-p44/42 MAP Kinase (p-ERK, threonine 202/tyrosine 204) and phosphorylated p38 MAP Kinase (p-p38, threonine 180/tyrosine 182). In agreement with the transient transfection studies, the amount of phosphorylated c-Jun protein (p-c-Jun) decreased 1hr after treatment of ST2 cells with Dex, whereas the total amount of c-Jun protein decreased after 12 h. Corresponding to the decrease of p-c-Jun, the amount of phosphorylated p46 isoform of JNK decreased significantly 30 min after Dex treatment, whereas that of phosphorylated p54 isoform decreased after 12 h. The amount of phosphorylated SEK1 also decreased significantly 30 min after Dex treatment. In contrast, the amounts of p-ERK and p-p38 were constant. **B:** The transfected cells were treated with three MAP kinase inhibitors: JNK inhibitor (SP600125), ERK inhibitor (PD98059), and p38 inhibitor (SB203580) to assess their effect on OPG promoter activity (Luc-1487). Only the JNK inhibitor (SP600125) mimicked the inhibitory effect of Dex. The inhibitory effect of each MAP kinase inhibitor is expressed as % inhibition of promoter activity. Results are expressed as means \pm SD of three assays.

DISCUSSION

GC-induced bone loss is now interpreted primarily as hypofunction and apoptosis of osteoblasts during the progressive phase, and secondarily as accelerated bone resorption especially during the rapid or early phase. Although the latter process is a major therapeutic target of GC-induced bone loss, its precise mechanism is not fully understood. In this study, we analyzed the effect of Dex on mouse OPG and RANKL expression and found that Dex accelerated osteoclastogenesis mainly by suppressing OPG expression at both transcriptional and protein secretion levels of ST2 osteoblasts.

Dex treatment per se, and in combination with $1\alpha,25(\text{OH})_2\text{D}_3$, reciprocally regulated RANKL and OPG mRNA expression, although its exclusive effect on RANKL and OPG was small (Fig. 1). Additionally, OPG secretion into the culture media was modulated by as little as 10^{-9} M of Dex and as early as 6 h after treatment (Fig. 2), indicating, as is often the case with GC function, that Dex modulates OPG expression at multiple levels—from mRNA transcription to protein secretion. Since three major transcriptional mechanisms, namely AP-1 [Kondo et al., 2004], Runx2 [Thirunavukkarasu et al., 2000], and the canonical Wnt/ β -catenin signaling pathway [Glass et al., 2005], regulate OPG gene expression, we extended our study to explore Dex function on the OPG gene at the transcriptional level, with special focus on the three mechanisms above.

First, as we have reported [Kondo et al., 2004], mainly the c-Jun homodimer binds to the AP-1 site in the mouse OPG promoter and maintains steady-state transcription of the OPG gene. Several mechanisms by which GCs inhibit AP-1 activity have been proposed [Hirasawa et al., 2003]: (1) suppression of the activation of JNK; (2) competitive reduction of the interaction between AP-1 and the transcriptional coactivator CREB binding protein (CBP) or p300 via the interaction of glucocorticoid receptor (GR) with CBP/p300; (3) inhibition of the binding of AP-1 to DNA by direct binding of GR to AP-1; and (4) induction of the inhibitory protein, glucocorticoid-induced leucine zipper (GILZ). In the first mechanism, it is hypothesized that GR disrupts the binding of JNK to c-Jun resulting in the inhibition of the phosphorylation of c-Jun by JNK [Hirasawa et al.,

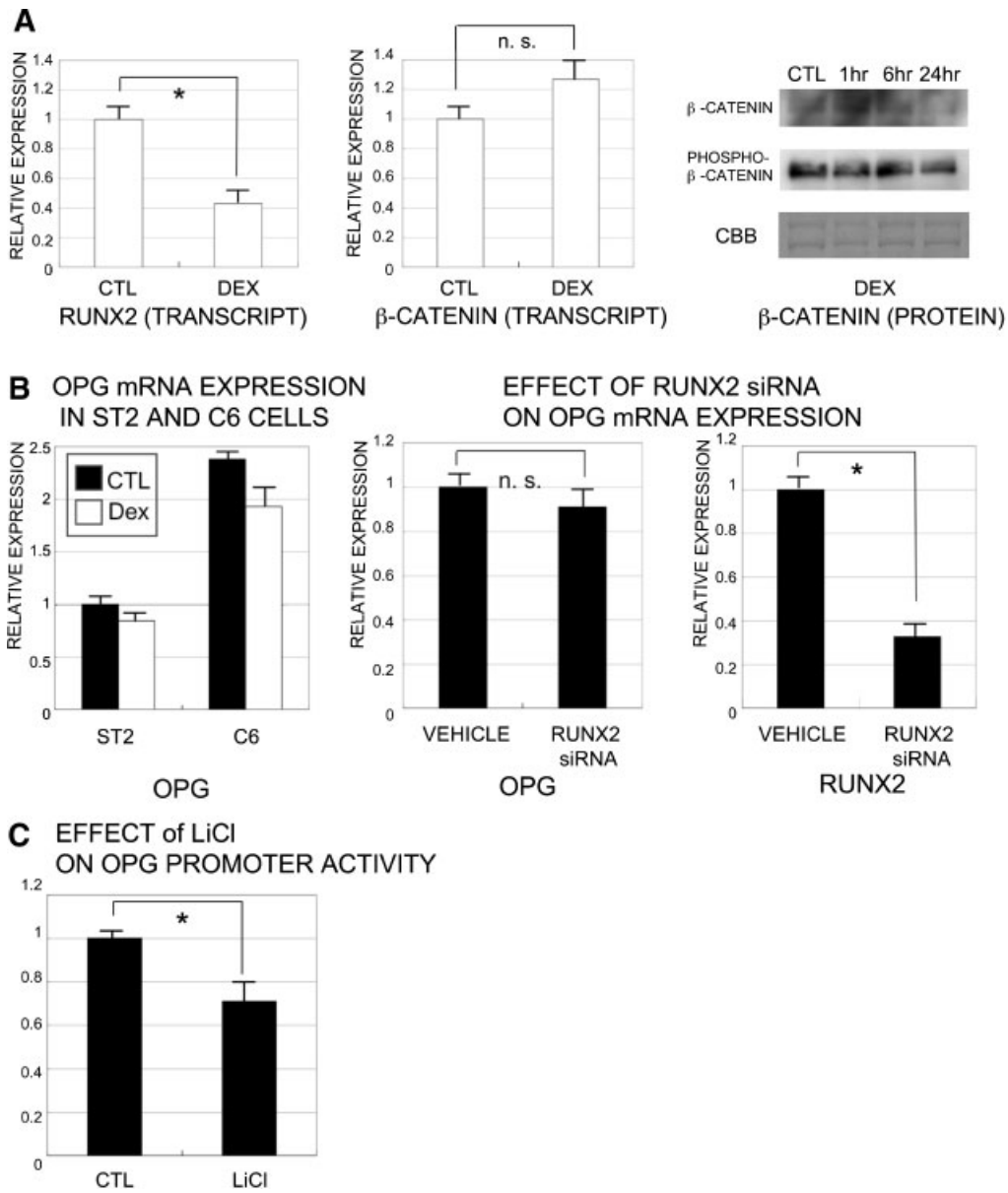


Fig. 7. Involvement of Runx2 and β -catenin signaling in Dex-mediated OPG suppression. **A:** Real-time RT-PCR analysis revealed that Dex decreased Runx2 mRNA expression in ST2 cells (**left panel**). Dex decreased β -catenin protein by a 24-h treatment (**right panel**) although it slightly increased β -catenin mRNA expression. Dex slightly increased phospho- β -catenin protein by a 6-h treatment. **B:** The steady-state transcription of the

OPG gene in C6 cells, established from calvariae of *runx2*-deficient mice, was 2 times that in ST2 cells. Dex reduced OPG expression to the same extent in both cells. The transfection of Runx2 siRNA slightly decreased OPG mRNA expression in ST2 cells. **C:** LiCl (30 μ M), an agonist of the β -catenin signaling pathway, reduced the promoter activity of Luc-1487 to 70%.

2003]. In addition, since GR is phosphorylated by JNK [Rogatsky et al., 1998], Hirasawa et al. [2003] have speculated that the interaction between GR and JNK is involved in the inhibition of the phosphorylation of c-Jun. In the present study, Western blot analysis showed that the amount of phospho-c-Jun protein (p-c-Jun) decreased after the treatment

of ST2 with Dex; correspondingly, the amount of the phosphorylated p46 isoform of JNK decreased as early as 30 min after the treatment, whereas that of p54 decreased after 12 h (Fig. 6A), suggesting that Dex inhibits the c-Jun signaling pathway by suppressing both p46 and p54 isoforms of JNK simultaneously but separately. In contrast, the amounts of p-ERK and

p-p38 remained constant after Dex treatment, suggesting that Dex selectively modulates the JNK pathway in ST2 cells. This was further confirmed by the assessment with MAP kinase inhibitors showing that selective JNK inhibitor SP600125 mimicked the action of Dex on OPG gene promoter activity (Fig. 6B). Our data suggest that Dex negatively regulates OPG by transrepressing the OPG gene through the AP-1 site via a reduction in the proportion of p-c-Jun in a JNK-dependent manner; also the reduction is mediated mainly by the decrease in the p46 isoform. Reportedly, $1\alpha,25(\text{OH})_2\text{D}_3$ also suppresses OPG gene expression via the AP-1 site but in a JNK-independent manner [Kondo et al., 2004]. Taken together, these results may explain the synergistic suppressive action of Dex and $1\alpha,25(\text{OH})_2\text{D}_3$ on OPG expression through both JNK-dependent and JNK-independent pathways.

Second, since the cloning of the human OPG gene promoter region has revealed that Runx2, osteoblast-specific transcription factor, transactivates the gene [Thirunavukkarasu et al., 2000], we tested the effects of Runx2 on mouse OPG gene expression and on the inhibition of OPG by Dex. While the steady-state transcription of the OPG gene in C6 cells was two times that in ST2 cells, Dex reduced OPG expression to the same extent in both cells, indicating that the inhibitory effect of Dex on OPG expression is independent of Runx2. Moreover, Runx2 knock-down by the transfection of Runx2 siRNA showed a minimal effect on OPG mRNA in ST2 cells. Together with the fact that canonical binding elements for Runx2 are not present within the mouse OPG promoter region (1-3261) we have previously tested [Kondo et al., 2004], Runx2 may not be essential for either mouse OPG gene expression or Dex-mediated mouse OPG gene suppression.

As for the third mechanism, OPG expression is regulated by the Wnt- β -catenin signaling pathway through three potential TCF binding sites within the mouse OPG promoter [Glass et al., 2005]. In the present study, because Dex treatment downregulated the β -catenin protein expression (Fig. 7A, right panel), and LiCl, an agonist of the β -catenin signaling, also downregulated OPG promoter activity (Fig. 7C), Wnt- β -catenin signaling may be partially involved in Dex-mediated OPG gene suppression. Indeed, in cultured human osteoblasts, β -catenin protein expression is downregulated

by glucocorticoid treatment through the enhancement of the production of dickkopf-1 [Ohnaka et al., 2005]. A similar mechanism may be involved in Dex-driven OPG suppression in mouse ST2 cells.

On the other hand, Dex slightly increased the expression of RANKL mRNA. Deletion mutant studies suggested that Dex upregulated RANKL through either the putative GRE half sites (-642/-628) or the AP-1 sites in the promoter. We speculate therefore that GCs per se promote osteoclastogenesis mainly by inhibiting OPG and partly by concurrently stimulating RANKL in a reciprocal manner, thereby enhancing bone resorption. Recently, the paper by the Teitelbaum group has shown that glucocorticoids modulate osteoclastogenesis by affecting M-CSF activation of RhoA, Rac, and Vav3 systems in osteoclasts. Also, $Gr^{oc-/-}$ mice are spared the impact of Dex on osteoclasts and their precursors [Kim et al., 2006]. Because M-CSF and the RANKL-OPG axis are two major regulators of osteoclasts, these data show that glucocorticoids play a prominent role in osteoclastogenesis by influencing multiple levels of multiple systems both directly and indirectly.

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