Fibroblast growth factor-23 regulates parathyroid hormone and 1α-hydroxylase expression in cultured bovine parathyroid cells

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Abstract

Fibroblast growth factor-23 (FGF23) is a circulating factor that decreases serum levels of inorganic phosphate (Pi) as well as 1,25-dihydroxyvitamin D₃. Recent studies also suggest a correlation between serum levels of FGF23 and parathyroid hormone (PTH) in patients with chronic kidney disease. It is, however, unknown whether FGF23 directly modulates PTH expression, or whether the correlation is secondary to abnormalities in Pi and vitamin D metabolism. The objective of the current study was therefore to elucidate possible direct effects of FGF23 on bovine parathyroid cells in vitro. Treatment of parathyroid cells with a stabilized form of recombinant FGF23 (FGF23(R176Q)) induced a rise in early response gene-1 mRNA transcripts, a marker of FGF23 signaling. FGF23(R176Q) potently and dose-dependently decreased the PTH mRNA level within 12 h. In agreement, FGF23(R176Q) also decreased PTH secretion into conditioned media. In contrast, FGF23(R176Q) dose-dependently increased 1α-hydroxylase expression within 3 h. FGF23(R176Q) did not affect cell viability nor induce apoptosis, whereas a small but significant increase in cell proliferation was found. We conclude that FGF23 is a negative regulator of PTH mRNA expression and secretion in vitro. Our data suggest that FGF23 may be a physiologically relevant regulator of PTH. This defines a novel function of FGF23 in addition to the previously established roles in controlling vitamin D and Pi metabolism.

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Introduction

Fibroblast growth factor-23 (FGF23) is a circulating phosphaturic factor that plays a critical role in renal phosphate (Pi) reabsorption and vitamin D metabolism (ADHR–Consortium 2000, Shimada et al. 2001). Its physiological importance is exemplified by numerous activating and inactivating mutations in the human FGF23 gene, causing two clinical disorders of disturbed Pi homeostasis: autosomal dominant hypophosphatemic rickets (ADHR, OMIM#193100; ADHR–Consortium 2000) and hyperphosphatemic familial tumoral calcinosis (HFTC, OMIM#211900; Benet-Pages et al. 2005, Larsson et al. 2005). Elevated FGF23 levels are also associated with several other disorders of hypophosphatemia or dysfunctional regulation of vitamin D, such as autosomal recessive hypophosphatemic rickets (ARHR; Feng et al. 2006, Lorenz-Depiereux et al. 2006), X-linked hypophosphatemic rickets (XLH; Liu et al. 2003, Riminucci et al. 2003), tumor-induced osteomalacia (TIO; Shimada et al. 2001, White et al. 2001b), fibrous dysplasia (FD; Riminucci et al. 2003), and linear nevus sebaceous syndrome (LNSS; Hoffman et al. 2005).

The regulation of Pi and the production of 1,25-dihydroxyvitamin D₃ (1,25(OH)₂D₃) mainly occur in the kidney, although the physiological source of FGF23 production is bone (Riminucci et al. 2003, Mirams et al. 2004, Sitara et al. 2004). In states of hyperphosphatemia, such as in chronic kidney disease (CKD) and hypoparathyroidism, FGF23 expression is induced, giving rise to increased serum FGF23 levels (Larsson et al. 2003a, Gupta et al. 2004). The compensatory rise in FGF23 causes a decrease in renal Pi reabsorption and diminished production of 1,25(OH)₂D₃ due to decreased expression of 25-hydroxyvitamin D₃-1α-hydroxylase (1α(OH)ase; Shimada et al. 2001). Serum levels of FGF23 continuously increase as renal function declines in CKD (Imanishi et al. 2004, Larsson et al. 2004, Shigematsu et al. 2004), at least in part, due to the manifest hyperphosphatemia. In end-stage renal disease (ESRD), FGF23 concentrations are therefore typically increased a 1000-fold or more when compared with healthy individuals (Imanishi et al. 2004, Larsson et al. 2004, Shigematsu et al. 2004). Elevated FGF23 in CKD has been proposed to play a role in the development of secondary hyperparathyroidism (Kazama et al. 2005, Nakanishi et al. 2005).

Recent studies have shed light on FGF23 signaling. It has been demonstrated that Klotho is a permissive receptor co-factor for FGF23, converting FGR1 (IIIc) into a native FGF23-specific receptor (Urakawa et al. 2006). Klotho null mice also display a marked elevation of serum Fgf23, although...
their phenotype closely resembles that of Fgf23 knockout mice, presenting further evidence of Klotho as a regulator of FGF23 signaling (Kurosu et al. 2006, Urakawa et al. 2006). Importantly, Klotho is abundantly expressed in parathyroid glands (Ito et al. 2007). This has raised the question whether FGF23 may exert direct effects on parathyroid glands. In a physiological context, a relationship between FGF23 and PTH is also plausible due to their overlapping capacity to diminish renal Pi reabsorption and counter-regulatory effects on 1α(OH)ase. Finally, a covariation of FGF23 and PTH has been observed in vivo in early and late stages of CKD (Shigematsu et al. 2004, Westerberg et al. 2007).

In the current study, we sought to elucidate potential regulatory effects of FGF23 on PTH and 1α(OH)ase expression in vitro, using bovine parathyroid cells.

Materials and Methods

Preparation of bovine parathyroid glands and cell culture

Bovine parathyroid glands were obtained from healthy adult cattle within minutes after slaughter as previously described (Segersten et al. 2002). The glands were minced with scissors and cell suspensions were prepared by collagenase digestion at 37°C in a shaking incubator in F-10 medium (pH 7.4) containing 1m g collagenase, 0.05 mg/ml DNase I, 1.25 mM CaCl₂, and 1-5% BSA. The incubation was carried out for 2 h, interrupted by repeated pipette aspirations. After filtration through a nylon mesh, cells were centrifuged through 25% modified Eagle’s medium (DMEM)-medium containing 10% fetal calf serum (FCS) and penicillin–fungizone plusL-glutamine (PFL). The cells were kept in an incubator at 37°C in 5% CO₂ and 95% O₂ cycling conditions were: a) 95°C, 3 min; b) 40 times: 95°C, 1 min; c) 95°C, 3 min; d) 55°C, 1 min; e) 80 times: +0.5°C, starting from 8°C, 3 min; and f) 80°C, 1 min. Reactions were performed in triplicates and repeated two to four times.

RNA extraction

In accordance with EZNA Total RNA Isolation Protocol (Omega Biotek, Doraville, GA, USA), total RNA was extracted and on-membrane DNase I digestion was performed. Electrophoresis on 1% agarose gel was run to check for RNA degradation. NanoDrop ND-1000 Spectrophotometer (NanoDrop Technologies, Wilmington, DE, USA) was used to estimate concentration as well as to obtain the purity A₂₆₀/A₂₈₀ ratio (≥ 1.99). A representative group of samples was further analyzed by Agilent 2100 Bioanalyzer (Agilent Technologies, Santa Clara, CA, USA) to confirm adequate RNA integrity. RNA was kept at −70°C.

cDNA synthesis

Superscript II Reverse Transcriptase and Oligo (dT)-primers (Invitrogen) were used for reverse transcription from 0.6–1 μg total DNased RNA. cDNA was kept at −20°C.

Real-time PCR analysis

A total volume of 25 μl per PCR was used: 12.5 μl (2X) iQ SYBR Green Supermix containing fluorescein (Bio-Rad); 2.5 μl (2 μM) Primer Fwd; 2.5 μl (2 μM) Primer Rev; 5-5 μl sterile H₂O; and 2 μl cDNA. The iCycler, MyiQ Single Color Real-Time PCR Detection System (Bio-Rad) was used and the cycling conditions were: a) 95°C, 3 min; b) 40 times: 95°C, 15 s; 54–60°C (Tₘ depending on the primers), 1 min; c) 95°C, 1 min; d) 55°C, 1 min; and e) 80 times: +0.5°C, starting from 55°C, 10 s, for melt-curve determination. All samples, including non-template negative controls, were amplified in duplicates. All assays were run three to four times. The sequences of bovine PTH and GAPDH primer pairs have previously been described (Segersten et al. 2002). Primer sequences for bovine 1α(OH)ase were as follows: F: 5’–ATC-CCCAAAATAACGCTGGT-3’ and R: 5’–GCTGGAC-GAAAAGAGATTGG-3’.

Relative gene expression was calculated according to the comparative Cₜ method (2−ΔΔCₜ) by Livak & Schmittgen (2001).
ELISA measurements

To determine FGF23 protein concentration, conditioned media from transfected COS-7 cells were analyzed by an intact FGF23 ELISA (Kainos laboratories, Tokyo, Japan; Yamazaki et al. 2002). This ELISA detects only the intact, biologically active, portion of the protein. For measurement of secreted PTH protein, a bovine intact PTH ELISA was used (Immuntupics, San Clemente, CA, USA) according to the manufacturer’s instructions. To determine PTH protein secretion, parathyroid cells were treated at various concentrations of FGF23 for 24 h, followed by two 1×PBS washes and addition of fresh serum-free medium to the cells. After 4 h, conditioned media were collected for subsequent PTH measurements. Secreted PTH concentrations were corrected for total protein content in the wells, determined using a NanoDrop ND-1000 Spectrophotometer. Secreted protein levels were measured from triplicate wells in two separate experiments.

Flow cytometry analysis

Parathyroid cells were trypsinized and diluted with 1×PBS and divided into two 5 ml FACS tubes (measured in duplicates). The cells were centrifuged, washed by, and resuspended in FACS buffer: 2% FCS, 0.05% NaN3, 2.5 mM CaCl2, and 1×PBS. After a second centrifugation, the cells were resuspended in 100 µl FACS buffer, and 5 µl anti-Annexin V-FITC-conjugated antibodies were added. They were left for 20–30 min in darkness at room temperature. After a second wash, 5 µl propidium iodide (PI) was added. Non-treated cells were used as FACS controls: a) without FITC or PI, b) only FITC, and c) only PI. Low flow speed and a limit of 50 000 cells were set for each measurement. Identical settings were used at later measurements. Total apoptosis was defined as the sum of early (FITC) and late (FITC and PI) apoptosis. FACS results were derived from two separate experiments.

Tritium-labeled thymidine incorporation

In order to estimate the proliferation of the cells, 1 µCi [³H]thymidine was added to each well 12 h before harvesting. After incubation, medium was removed and unincorporated [³H]thymidine was precipitated with 500 µl cold trichloroacetic acid for 20 min. This procedure was repeated twice. Cells were then lysed in 1 ml 10% NaOH and 0.5% Triton X. The radioactivity was measured in a β-counter. Proliferation data were obtained from three separate experiments and all samples were run in triplicates.

Statistical analysis

GraphPad Prism Version 3.03 software (GraphPad Software Inc., San Diego, CA, USA) was used for statistical data analysis. Unpaired t-tests were performed, and the results are shown as arithmetic means ±S.E.M. A P value of <0.05 was considered statistically significant.

Results

Homology analysis of human and bovine FGF23 revealed 83% identity at the nucleotide level and 84% identity at the amino acid level (data not shown). Functionally important motifs, such as the 176RXXR179 site (ADHR-Consortium 2000), were preserved allowing human recombinant FGF23 protein to be used in the experiments. In addition, we used mutant FGF23(R176Q) protein in all experiments in order to increase FGF23 stability (White et al. 2001a). The short-term biological potency of FGF23(R176Q) and wild-type FGF23 are similar based on previous studies on renal Pi transport (Shimada et al. 2002). To determine the effect of FGF23 on parathyroid cells, we used a well-established system of primary isolates of bovine parathyroid cells.

As expected, we found by RT-PCR that the FGF23 receptor cofactor Klotho was expressed in the parathyroid cells as previously reported in mice (Ito et al. 2007; data not shown). To further validate our assay system, we analyzed the effect of FGF23(R176Q) treatment on the Egr-1 mRNA expression, a reported marker of FGF23 signaling (Urakawa et al. 2006). FGF23(R176Q) treatment evoked an increase in Egr-1 mRNA after 60 min, suggesting a direct effect of FGF23(R176Q) on parathyroid cells (Fig. 1).

Subsequently, we determined the effect of FGF23(R176Q) on PTH mRNA expression. At 400 pg/ml (equivalent to approximately 286 nM) FGF23(R176Q), the PTH mRNA level was significantly decreased (P<0.05) when compared with control-treated cells at 12 h (Fig. 2a) as determined by real-time RT-PCR. The maximal observed effect was detected at 24 h (P<0.01) and sustained for at least 48 h.

Figure 1 Egr-1 is an early response gene and a marker of FGF23 signaling. A rise in Egr-1 mRNA was observed 60 min after treatment with 400 and 2000 pg/ml FGF23(R176Q), supporting a direct effect of FGF23 on parathyroid cells. Error bars indicate mean ±S.E.M.
In order to determine the concentrations required for reducing the PTH mRNA level, we treated the parathyroid cells for 24 h at various concentrations of FGF23(R176Q), ranging from 100 to 2000 pg/ml (Fig. 2b). FGF23(R176Q) reduced the PTH mRNA level in a dose-dependent manner (Fig. 2b) in the concentration range of 400–2000 pg/ml. To exclude the possibility that control-conditioned media (from mock-transfected cells) regulated the PTH mRNA level, we performed a dose–response treatment with control-conditioned media serially diluted in nonconditioned media. This revealed no effect on PTH mRNA expression (data not shown). In summary, our data suggest that FGF23(R176Q) dose-dependently decreases the PTH mRNA level.

We further examined whether FGF23(R176Q) displayed a regulatory effect on PTH secretion. For this purpose, conditioned media from FGF23(R176Q)- and control-treated parathyroid cells were analyzed for PTH concentrations, using a bovine intact PTH ELISA. Importantly, FGF23(R176Q) dose-dependently decreased the secretion of PTH protein at 24 h when compared with control-treated cells in the concentration range of 700–2000 pg/ml (Fig. 3).

Since several previous studies have shown that FGF23 decreases the expression of 1α(OH)ase expression in kidneys (Shimada et al. 2001, 2002, 2004a,b,c, Bai et al. 2004, Larsson et al. 2004, Sitar et al. 2004), we investigated the effect of FGF23(R176Q) treatment on parathyroid 1α(OH)ase expression. Notably, FGF23(R176Q) increased 1α(OH)ase mRNA level within 3 h and the effect sustained for 24 h (Fig. 4a). The effect was dose dependent in the concentration range of 400–2000 pg/ml (Fig. 4b).

We also examined parathyroid cell number, viability, apoptosis, and proliferation. At a FGF23(R176Q) concentration of 2000 pg/ml for 24 h, we did not observe significant effects on total cell number (data not shown) or viability (Fig. 5a) when compared with control-treated cells. Similarly, we did not detect any significant effect on apoptosis (Fig. 5b), whereas a small but significant increase in cell proliferation was observed (Fig. 5c). The proportion of cells expressing PTH was ∼90–95% at 0–48 h, independent of FGF23(R176Q) treatment (data not shown).

Discussion

Previous extensive studies have shown that FGF23 is a key regulator of PTH expression (ADHR-Consortium 2000, Shimada et al. 2001). Maintenance of mineral ion homeostasis is a complex process involving several hormonal systems and target tissues, including bone, kidney, and parathyroid glands. Observational data supporting a correlation between FGF23 and PTH in vivo (Shigematsu et al. 2004, Kazama et al. 2005, Nakaniishi et al. 2005), and the presence of the FGF23 receptor cofactor Klotho in parathyroid glands (Ito et al. 2007) prompted us to elucidate whether FGF23 directly modulates PTH expression in parathyroid cells. Herein, we demonstrate that FGF23(R176Q) induced a dose-dependent decrease in PTH mRNA level and protein secretion. Our data support a previously unidentified direct link between FGF23
A small but significant increase in cell proliferation was observed with treatment at high concentrations of FGF23(R176Q).

The in vitro system used in the present study provides a novel tool for the study of potential physiological actions of FGF23. However, a limitation of this system is that primary isolated parathyroid cells loose their ability to secrete PTH protein and display decreased PTH mRNA message over time, independent of FGF23 action. Therefore, one has to be careful when extrapolating our in vitro data into in vivo physiology. The presence of Klotho in parathyroid cells, as well as independent associations between serum FGF23 and PTH is important in pathophysiology; however, they may also reflect typical in vivo/in vitro differences.

FGF23 regulates PTH expression

and PTH. Because we used an isolated in vitro system, we were able to clarify direct FGF23-mediated effects on PTH expression, as opposed to secondary systemic changes in mineral metabolism.

To evaluate direct effects of FGF23 on parathyroid cells, we investigated expression levels of Egr-1, a marker of FGF23 signaling (Urakawa et al. 2006). In agreement with previous reports, we observed a rise in Egr-1 as early as 1 h after FGF23(R176Q) treatment. In contrast, we noted a significant decrease in PTH mRNA 12 h after FGF23(R176Q) treatment, indicative of a late response gene. Our data strongly suggest a direct effect of FGF23 on PTH expression, although we cannot rule out the possibility that FGF23 may regulate PTH indirectly, by stimulating the release of other locally produced factor(s).

Notably, neither cell number nor viability or apoptosis was affected by treatment at high concentrations of FGF23(R176Q). A small but significant increase in cell proliferation was observed at 24 h, although the biological significance of this finding is unclear. Our data support the assertion that FGF23 does not exert any major stimulatory or inhibitory growth effects on parathyroid cells in vitro at the short term. However, they suggest that the negative effect of FGF23(R176Q) on PTH expression is direct and independent of cell growth and/or survival.

In the present study, we used relatively high doses, i.e. 400–2000 pg/ml FGF23(R176Q) in order to observe effects on the PTH mRNA level or protein secretion. These concentrations are well above the reference range for healthy individuals (Yamazaki et al. 2002) and are typically found in subjects with ESRD (Larsson et al. 2003a) and some TIO and XLH patients (Jonsson et al. 2003). Our data may imply that FGF23 regulation of PTH is important in pathophysiology; however, they may also reflect typical in vivo/in vitro differences.

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Since 1α(OH)ase is expressed in parathyroid glands (Segersten et al. 2002), we investigated the effect of FGF23(R176Q) on its mRNA transcript levels. Interestingly, FGF23(R176Q) dose-dependently increased 1α(OH)ase mRNA level. This indicates a differential regulation of 1α(OH)ase in kidneys and parathyroid glands, since FGF23 is known to potently and rapidly reduce renal expression of 1α(OH)ase (Shimada et al. 2001, 2002). The reason for this discrepancy is unclear, but may speculatively be an attempt of parathyroid glands to locally compensate for decreased serum calcitriol provoked by high circulating FGF23 levels. Further studies are needed to understand the differential expression and determine whether this has any functional importance in vivo.
The etiology of secondary hyperparathyroidism in CKD is multifactorial, but involves alterations in mineral ion homeostasis. The combination of low 1,25(OH)₂D₃ and high Pi in CKD effectively triggers the production of PTH, leading to a gradual development of parathyroid hyperplasia and elevated PTH levels (Fukagawa et al. 2006). Another implication of our study is a plausible role of FGF23 in secondary hyperparathyroidism of CKD, supported by recent studies (Bai et al. 2004, Larsson et al. 2004, Nakanishi et al. 2005). Our data may imply that FGF23, at least in part, has an inhibitory role in secondary hyperparathyroidism of CKD. In support, treatment with appropriate doses of calcitriol increases serum FGF23 (Collins et al. 2005, Ito et al. 2005, Nishi et al. 2005), while effectively preventing or postponing secondary hyperparathyroidism in CKD. In fact, one could speculate that the beneficial effects of calcitriol treatment in CKD may partly be attributed to an increase in FGF23. Of note, secondary hyperplastic glands and adenomas of hyperparathyroidism are phenotypically different when compared with normal parathyroid cells used in our in vitro system and could therefore respond differently to FGF23. Further studies are needed to clarify the role of FGF23 in secondary hyperparathyroidism.

In conclusion, FGF23(R176Q) is a negative regulator of PTH expression; however, it stimulates parathyroid 1α(OH)ase expression in vitro. Our data support the existence of a physiological skeletal-parathyroid endocrine axis and further provide insights into the complex regulation of calcium and Pi homeostasis.

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Disclosure statements

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