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Stimulation of Insulin-like Growth Factor Receptor 1 Expression and Its Phosphorylation in Dog Mandibles by β -TCP

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It has been reported that β -TCP can stimulate bone formation, but the mechanisms are not well understood. The enhancement of bone formation and IGFs gene expression in bone defects of Beagle dog mandibles by β -TCP were reported. IGFs are the most abundant growth factors produced by osteoblasts, and exert important effects on the proliferation and differentiation of osteoblasts. However, the mechanism of activation of IGF signaling by β -TCP has not been elucidated. In this study, an implant drill was used to make bone defects in Beagle dog mandibles, and β -TCP was filled into the bone defects. The effect of β -TCP on IGF receptor 1 (IGF1R) gene expression was analyzed by RT-PCR and real-time

PCR. Moreover, the gene products in mandibles were examined by immunohistochemistry. Increased mRNA levels of IGF1R gene were observed in β -TCP implanted samples compared with controls. The enhancement of IGF1R mRNA levels by β -TCP was confirmed by RT-PCR and real-time PCR. Immunohistochemical staining revealed increased IGF1R protein expression and phosphorylation in β -TCP-implanted bone tissue. Taken together, the stimulation of IGF1R expression and phosphorylation by β -TCP might be a part of the mechanism of accelerating bone formation.

Key words: dog mandible, β -TCP, insulin-like growth factor receptor 1 (IGF1R), IGF signaling

Introduction

The osteogenic potential of autogenous bone graft is due to the retention of osteogenic precursor cells with the ability to proliferate and differentiate to osteoblasts¹⁾. The number of clinicians performing en-

dosseous dental implants, whether immediately following tooth extraction or after a period of time, is rapidly increasing. However, on many occasions, clinicians encounter insufficient bone due to a number of reasons including injury, eradicated tumor masses, or progressive periodontal diseases. To overcome this difficulty, many bone grafts have been developed

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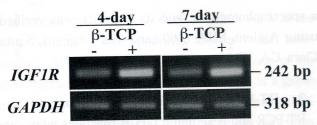


Fig. 1 RT-PCR analysis of IGFR1 gene expression The amplification of each DNA band intensity of IGFR1 gene was greater in β -TCP implanted dog mandibles than in the control. Each GAPDH was used as an internal control.

retrieval and endogeneous peroxidase blocking (30 min), and rinsed with phosphate-buffered saline (PBS). Anti-IGF1R (signal way antibody) and anti-IGF1R Phospho-Tyr1161 (abm) rabbit polyclonal antibodies were used, and anti-IGF1R Phospho-Tyr1161 (abm) rabbit polyclonal antibodies were used. After overnight incubation at 4C, the specimens were rinsed with PBS and incubated at room temperature for 1 h with secondary antibody conjugated to Alexa Flour 488 donkey anti-rabbit IgG (H+L) (Molecular Probes, Inc., OR, USA). After rinsing with PBS, all specimens were color-developed with ProLong Gold Antifade Reagent with DAPI (Molecular Probes, Inc., OR, USA). The immunostaining of all specimens was performed simultaneously to ensure the same antibody reaction and DAPI exposure conditions. The cells were visualized using a confocal laser scanning microscope (BZ-8000, Keyence Corporation, Osaka, Japan) by DAPI nuclei staining. The merged image represents the localization of IGF1 and IGF2 in cells. Original magnification = $\times 20$; Bar = $50 \mu m$.

5. Statistical analyses

Significant differences were analyzed by Student's t-test. P<0.05 was considered to be statistically significant and p<0.01 highly significant.

Results

First, we examined the gene expression of IGF1R by RT-PCR in mandible bone tissues. An increase in

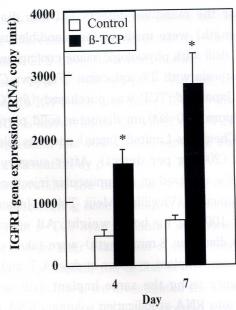


Fig. 2 Real-time PCR analysis of IGFR1 gene expression The level of IGFR1 gene expression relative to the level of GAPDH mRNA expression was quanitified. The data was converted to mRNA copy unit. Differences between control and β -TCP group were determined using Student's t-test. *, p<0.01, n = 3.

the amplified DNA band intensity of IGF1R gene was seen in β -TCP implanted mandibles compared with the untreated control. In contrast, mRNA levels of GAPDH, the housekeeping gene control, showed no change between β -TCP and control groups.

To confirm the enhancement of IGF1R gene expression by β -TCP, RT-PCR analysis was carried out. Figure 2 shows that significantly higher levels of IGF1R DNA amplified bands were observed compared with the control. In contrast, mRNA levels of GAPDH, the housekeeping gene control, showed no change between β -TCP and control groups.

To examine the phenotypic expression of IGF1R, we performed immunofluorescence staining for IGF1R in Beagle mandible tissues. As shown in Fig. 3, the staining for IGF1R was found in granulation tissue-forming processes in the mandibles, which showed markedly positive immunostaining in the β -TCP implanted samples, whereas weak staining was

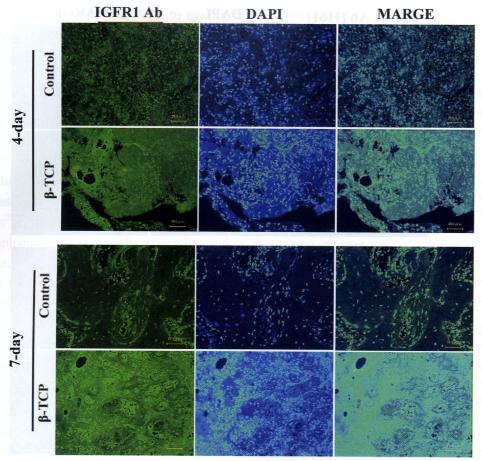


Fig. 3 Immunostaining for IGFR1 at day 4 and day 7 after surgery The nuclei were counter-stained with ProLong A Gold antifade reagent with DAPI. The cells were visualized using confocal laser scanning microscopy. The merged image represents the localization of IGF1 and IGF2 in cells. Original magnification = $\times 20$; Bar = $50 \, \mu \text{m}$.

observed in the control group. Enhanced staining around the cells presumably represents deposits of IGF1R in the β -TCP implanted specimen. When parallel non-treated specimens were stained as controls, a barely visible fluorescence was observed.

Next, we examined IGF1R phosphorylation in the β -TCP. As shown in Fig. 4, the staining for phosphorylated IGF1R was markedly positive in the β -TCP implanted samples compared with the control group. After β -TCP implantation, the osteoblastic niche contained accumulated tyrosine-phosphorylated IGF1R protein. These observations suggested that the osteoblastic niche mediates the IGF1-receptor signal to its intracellular signaling molecules.

Discussion

IGF1 and IGF2 are important regulators of bone formation and promote both the proliferation and differentiation of osteoblast precursor. The expression level of IGF1 and IGF2 was also increased at a relatively early stage in the β -TCP-implanted group compared with the control¹⁷⁾. IGFs are the most abundant growth factors and exert important effects on the proliferation, differentiation, and apoptosis of osteoblasts¹⁸⁾. In this study, we demonstrated that β -TCP enhanced IGF1R mRNA and protein expression followed by phosphorylation of IGF1R in dog mandibles.

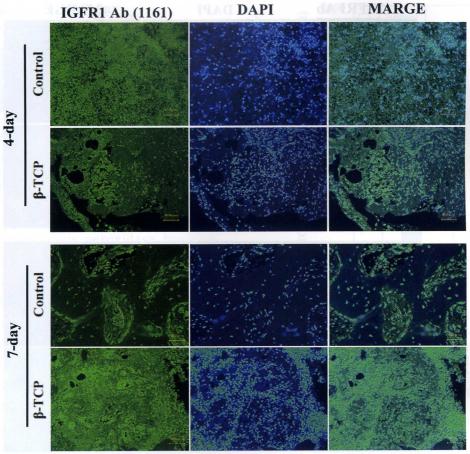


Fig. 4 Immunostaining for phosphorylated IGFR1 at day 4 and day 7 after surgery The nuclei were counter-stained with ProLong A Gold antifade reagent with DAPI in accordance with the manufacturer's instructions. The cells were visualized using confocal laser scanning microscopy (BZ-8000, Keyence Corporation, Osaka, Japan). The merged image represents the localization of IGF1 and IGF2 in cells. Original magnification = $\times 20$; Yellow bar = $50 \, \mu m$.

When β -TCP is mixed with the blood clot and surrounded by the bony walls of the alveolar socket, osteogenic cells, including undifferentiated mesenchymal cells, start migrating from the bone surface between and over the surface of β -TCP. The β -TCP particles attract osteoprogenitor cells that migrate into the interconnecting micropores of the bone substitute material during 6 months²⁰⁾, and β -TCP particles in the extraction sockets are clinically osteoconductive. The β -TCP implanted group showed a higher bone formation rate at 4 and 7 days, although this difference between the β -TCP and control groups seemed to disappear by day $14^{16)}$. These findings suggest that tissue healing and bone formation

occurred at a relatively early stage, and the gene expression of COL1A1, ALP, OPN and TGF- β_2 was increased and RANKL and IFN expression decreased in the β -TCP-implanted group¹⁶⁾.

Concerning the IGF signaling system, the mature heterotetrameric IGF1R conformation, structurally a and b subunits of the receptors, reside entirely extracellularly and include a cysteine-rich region and potential N-linked glycosylation sites. The cysteine-rich domain of the IGF1R is known to be important for high-affinity IGF1 binding¹⁹⁾. The b subunit constitutes the transmembrane domain and the cytoplasmic portion contains a tyrosine kinase domain. The inside of this catalytic region participates in the

transfer of the phosphate moiety of ATP to specific substrates, and upon ligand activation, the receptors undergo a conformational change that leads to ATP binding and autophosphorylation of the tyrosine kinase domain²⁰⁾. This event enhances the kinase activity of the receptors and leads to downstream signal transduction and engaging in biological activity such as proliferation and differentiation²⁰⁾. Interestingly, mice lacking the IGF1R exhibited delayed appearance of their ossification centers and delayed epiphyseal maturation²¹⁾. Taken together, our findings suggest that the enhancement of IGF1R expression and its phosphorylation is a part of the mechanism of accelerating bone formation by β -TCP through activation of IGF signaling. The activation of IGF signaling by β -TCP may act either in an autocrine and/or paracrine fashion to promote an increase of bone formation. The present findings suggest the therapeutic potential of IGF signaling for bone regeneration in dental implant therapy. We consider that IGF/IGF1R signaling may be used in future, not only for the improvement of new bone formation in dental implant therapy, but also for the development of diagnostic screening in a wide array of biomaterials.

Conclusion

 β -TCP enhanced IGF1R expression and its phosphorylation in dog mandible tissues. This finding suggests that the induction of IGF signaling through the enhancement of IGF1R expression and its phosphorylation in mandible tissues might be a part of the mechanism of accelerating bone formation by β -TCP.

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 β -TCP は骨形成を促進すると報告されているが、その機序については不明な点が多い、ビーグル犬の下顎骨の骨欠損部に β -TCP を填入することで骨形成を促進され、また、顎骨組織中の IGF 遺伝子の発現増大が報告されている、IGF は、骨芽細胞で豊富に産生され、細胞増殖、分化に重要な役割を発揮する成長因子である。しかし、 β -TCP による顎骨の IGF シグナリングの活性化の機序については不明である。本研究では、インプラントドリルでビーグル犬下顎骨に骨欠損を作成して β -TCP を填入し

た. そして IGF 受容体 1 (IGF1R) の遺伝子発現への影響 について RT-PCR およびリアルタイム PCR 法を応用して調べ, さらにタンパク質発現を免疫組織学的に検証した.

その結果、対照群に比べて、IGF1R 遺伝子の発現が β -TCP によって促進し、さらに、IGF1R タンパクおよび IGF1R リン酸化の促進が確認された。これらのことから、 β -TCP による IGF1R 遺伝子発現およびリン酸化は骨形成促進の機序の一部であることが示唆される。