

## Signaling Networks in RUNX2-Dependent Bone Development

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### ABSTRACT

RUNX2 is an essential transcription factor for osteoblast differentiation and chondrocyte maturation. SP7, another transcription factor, is required for osteoblast differentiation. Major signaling pathways, including FGF, Wnt, and IHH, also play important roles in skeletal development. RUNX2 regulates *Sp7* expression at an early stage of osteoblast differentiation. FGF2 upregulates *Runx2* expression and activates RUNX2, and gain-of-function mutations of FGFRs cause craniosynostosis and limb defect with upregulation of *Runx2* expression. Wnt signaling upregulates *Runx2* expression and activates RUNX2, and RUNX2 induces *Tcf7* expression. IHH is required for *Runx2* expression in osteoprogenitor cells during endochondral bone development, and RUNX2 directly regulates *Ihh* expression in chondrocytes. Thus, RUNX2 regulates osteoblast differentiation and chondrocyte maturation through the network with SP7 and with FGF, Wnt, and IHH signaling pathways during skeletal development. *J. Cell. Biochem.* 112: 750–755, 2011. © 2010 Wiley-Liss, Inc.

**KEY WORDS:** RUNX2; FGF; WNT; SP7; IHH, OSTEOBLAST; CHONDROCYTE

**R**UNX2 is an essential transcription factor for osteoblast and chondrocyte differentiation [Komori, 2005]. RUNX2 belongs to the Runx family, which consists of RUNX1, RUNX2, and RUNX3. These transcription factors form heterodimers with C/EBPβ and bind the consensus sequence, TGPYGGPY. These transcription factors act as master regulators in different cell lineages with some overlapping functions. RUNX1 is essential for hematopoietic stem cell differentiation and is involved in acute myeloid leukemia. RUNX3 plays important roles in the growth regulation of gastric epithelial cells and in neurogenesis, and is related to gastric cancer. RUNX1 and RUNX3 are required for thymocyte development, and RUNX3 has a redundant function with RUNX2 in chondrocyte differentiation in a late stage. In this review, the focus is on the interaction of RUNX2 with major signaling pathways, including FGF, Wnt, and IHH, and on SP7, another essential transcription factor for osteoblast differentiation, during bone development.

### SP7 AND RUNX2

SP7 is a zinc finger-containing protein which belongs to the Sp/KLF (Kruppel like factor) family of transcription factors [Nakashima et al., 2002]. *Sp7*-deficient (*Sp7*<sup>-/-</sup>) mice are unable to form bone due to the arrest of osteoblast differentiation. Their mesenchymal

cells condense in the perichondrial region, where bone normally forms, and express genes for chondrocyte markers but not bone matrix proteins. Therefore, SP7 is essential for osteoblast differentiation, and *Runx2*<sup>+</sup>*Sp7*<sup>-</sup> mesenchymal cells (preosteoblasts) are able to differentiate into osteoblasts or chondrocytes [Nakashima et al., 2002]. As *Runx2* is expressed in mesenchymal cells in *Sp7*<sup>-/-</sup> mice, SP7 is a downstream molecule of RUNX2. BMP and IGF mediate *Sp7* expression via MAPK and protein kinase D pathways and RUNX2 [Celil and Campbell, 2005]. Further, BMP induces *Sp7* expression in a manner dependent on RUNX2 and independent of RUNX2 through MSX2 [Matsubara et al., 2008] (Fig. 1).

In contrast to RUNX2, the induction of osteoblast differentiation by SP7 is dependent on the cells and culture conditions in vitro [Kim et al., 2006; Maehata et al., 2006; Tu et al., 2006; Fu et al., 2007; Kurata et al., 2007; Kaback et al., 2008; Matsubara et al., 2008; Kärner et al., 2009; Tominaga et al., 2009]. Thus, additional factors are required for SP7-dependent osteoblast differentiation. Although osteoblast-specific deletion of *Sp7* using the 2.3 kb *Col1a1* promoter Cre transgenic mice resulted in osteopenia due to the inhibition of osteoblast differentiation in adult mice [Baek et al., 2009], the important role of SP7 should be in the early stage of osteoblast differentiation. In addition to capacity for the induction of osteoblast differentiation, RUNX2 is involved in vascular invasion

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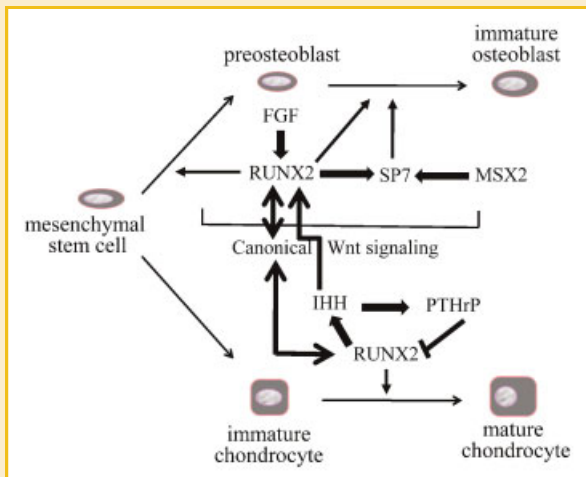


Fig. 1. RUNX2 plays important roles in osteoblast differentiation and chondrocyte maturation. RUNX2, SP7, and canonical Wnt signaling are essential for osteoblast differentiation. RUNX2 induces *Sp7* expression in preosteoblasts; FGF induces *Runx2* expression and activates RUNX2 in the osteoblast lineage; Wnt induces *Runx2* expression and activates RUNX2, while RUNX2 induces *Tcf7* expression in osteoblast and chondrocyte lineages; RUNX2 induces *Ihh* expression in chondrocytes; and *Ihh* induces *Runx2* expression in osteoprogenitor cells.

into the cartilage [Sun et al., 2001; Zelzer et al., 2001; Himeno et al., 2002; Javed et al., 2005; Conen et al., 2009; Sun et al., 2009]. Osteoblast precursors expressing the reporter gene under the control of *Sp7* promoter, located in the perichondrium prior to vascular invasion of the cartilage, give rise to trabecular osteoblasts, osteocytes, and stromal cells inside the developing bone. Throughout translocation, some precursors were found to intimately associate with invading blood vessels, in pericyte-like fashion [Maes et al., 2010]. Therefore, SP7 may also be involved in the invasion of blood vessels into the developing bone.

## FGF SIGNALING AND *Runx2*

Four fibroblast growth factor receptor (FGFR) genes have been identified in mammals (*FGFR1-4*), each encoding an extracellular domain composed of two or three extracellular immunoglobulin-like (Ig) loops, a transmembrane segment, and an intracellular tyrosine kinase. The affinity and specificity of FGFR1-3 are regulated by tissue-specific alternative splicing, which occurs in the region encoding the carboxyl-terminal half of Ig domain III creating different isoforms, IIIb and IIIc. The receptor isoforms have distinct ligand-binding specificity. For FGFR2, the mesenchymal-based ligands (FGF7 and FGF10) activate only FGFR2b, which is expressed overlying the epithelium, whereas epithelium-based ligands (FGF2, 4, 6, 8, 9) bind to mainly mesenchyme-expressed FGFR2c [Itoh and Ornitz, 2004; Beenken and Mohammadi, 2009; Turner and Grose, 2010]. Signaling from FGFR1, FGFR2, and FGFR3 plays important roles in skeletal development by regulating the proliferation and differentiation of osteoblasts and chondrocytes [Colvin et al., 1996; Deng et al., 1996; Naski et al., 1998; Partanen et al., 1998; Chen et

al., 1999; Eswarakumar et al., 2002; Yu et al., 2003; Valverde-Franco et al., 2004; Li et al., 2005; Verheyden et al., 2005; Jacob et al., 2006]. *Fgfr1c*, *Fgfr2b*, *Fgfr2c*, and *Fgfr3c* are expressed in mesenchymal cells in the calvaria [Iseki et al., 1999; Rice et al., 2000; Johnson et al., 2000], and gain of function mutations in *FGFR1*, *FGFR2*, and *FGFR3* genes cause craniosynostosis syndromes, such as Apert, Crouzon, Pfeiffer, and Muenke syndromes and Thanatophoric dysplasia [Cohen, 2004].

Gain-of-function mutations of *Fgfr1* and *Fgfr2* in mice enhanced *Runx2* expression. In mice carrying a P250R mutation in *Fgfr1*, which is orthologous to the Pfeiffer syndrome mutation in humans, premature fusion of calvarial sutures occurred accompanying the marked increase in *Runx2* expression [Zhou et al., 2000]. Mutant mice carrying C342Y replacement in *Fgfr2c*, equivalent to a mutation associated with Crouzon and Pfeiffer syndromes in humans, showed enhanced *Runx2* expression, and *Fgfr2c* loss-of-function mutant mice showed reduced *Runx2* expression [Eswarakumar et al., 2002, 2004]; however, the induction of *Runx2* by *Fgfr2*-activating mutants is controversial in vitro. Overexpression of *Fgfr2c* with or without the S253W mutation equivalent to the Apert mutation enhanced *Runx2* mRNA expression [Tanimoto et al., 2004], whereas overexpression of neither C342Y nor S252W mutant in a murine osteoblastic cell line increased *Runx2* mRNA and protein [Mansukhani et al., 2005]. From the findings with *Fgfr* mutant mice, however, RUNX2 seems to be involved in the pathogenesis of craniosynostosis caused by gain-of-function mutations of FGFRs.

Inactivation of *Fgfr1* in osteo-chondro-progenitor cells resulted in delayed osteoblast differentiation, while inactivation of *Fgfr1* in differentiated osteoblasts accelerated differentiation and increased bone mass [Jacob et al., 2006]. Inactivation of *Runx2* in differentiated osteoblasts also showed similar phenotypes [Maruyama et al., 2007], suggesting that RUNX2 is induced and activated by FGFR1 signaling; however, adult mice with inactivation of *Fgfr1* in osteo-chondro-progenitor cells also showed increased bone mass. Thus, FGFR1 signaling may not be able to induce and activate RUNX2 at the stage of commitment to the osteoblast lineage, because proliferating osteoprogenitor cells express *Fgfr2* but not *Fgfr1*, and *Fgfr1* is upregulated during osteoblast differentiation in calvarial development [Iseki et al., 1999]. Each FGFR seems to have specific and redundant functions at a different stage of osteoblast differentiation through differential expression during osteoblast differentiation.

FGFR signaling also plays an important role in limb development, and gain-of-function mutations of FGFRs cause limb defects [Wilkie et al., 2002]. Apert syndrome, which is a gain-of-function mutation of *FGFR2*, shows limb defects, including broad first digits, complex bony syndactyly, symphalangisms, and radio-humeral or -ulnar synostosis [Wilkie et al., 2002], and osteoblastic cells derived from digital bone show enhanced osteoblast differentiation [Tanimoto et al., 2004]. Pfeiffer syndrome also shows limb defects including broad thumbs, symphalangisms, and radio-humeral or -ulnar synostosis [Wilkie et al., 2002]. *Fgfr2c* mutant mice with the gain-of-function mutation (C342Y) showed multiple joint fusions with excessive bone formation, and *Runx2* expression was upregulated in chondrocytes, the perichondrium, and periosteum

[Eswarakumar et al., 2004]. As the overexpression of *Runx2* in chondrocytes causes multiple joint fusions with excessive bone formation [Ueta et al., 2001], RUNX2 may also be involved in the pathogenesis of limb defects caused by gain-of-function mutations of FGFRs.

FGF2 enhanced *Runx2* mRNA expression through the PKC pathway [Kim et al., 2003]. FGF2 phosphorylated RUNX2 through the MAPK pathway and enhanced transcriptional activity of RUNX2 [Xiao et al., 2002; Ge et al., 2009; Li et al., 2010]; ERK-dependent phosphorylation stabilized RUNX2 protein [Park et al., 2010], and craniosynostosis resulting from *FGFR2* with the S252W substitution was rescued by treatment with U0126, an inhibitor of MEK1/2 [Shukla et al., 2007]. RUNX2 is also activated through the PI3K-Akt pathway [Fujita et al., 2004]. *Fgf2*-deficient mice show decreased bone mass and bone formation, and *Fgf18*-deficient mice show a delay of osteogenic differentiation in the long bones and cranium [Montero et al., 2000; Liu et al., 2002; Ohbayashi et al., 2002]. Although *Runx2* mRNA expression was maintained in *Fgf18*-deficient mice, RUNX2 activity may have been reduced in mice. Thus, FGF2 enhances *Runx2* mRNA expression and activates RUNX2, and FGF18 may have similar activities (Fig. 1).

## Wnt SIGNALING AND RUNX2

Canonical Wnt signals are transmitted through stabilizing  $\beta$ -catenin protein by inhibiting GSK3 $\beta$ -mediated  $\beta$ -catenin phosphorylation. Unphosphorylated  $\beta$ -catenin accumulates in the cytoplasm and translocates to the nucleus where it acts as a co-activator with TCF/LEF transcription factors, including TCF7/TCF1, LEF1, TCF7L1/TCF3, and TCF7L2/TCF4 [Sharpe et al., 2001; Hartmann, 2006; Xu and Kimelman, 2007]. *Ctnnb1*/ $\beta$ -catenin depletion in osteoblast progenitors using *Prrx1* promoter *Cre* transgenic mice or *Twist2/Dermo1* *Cre* knock-in mice and *Ctnnb1* depletion in preosteoblasts using *Sp7* promoter *Cre* transgenic mice result in a complete block of osteoblast differentiation, indicating that *Ctnnb1* is essential for osteoblast differentiation [Day et al., 2005; Hill et al., 2005; Hu et al., 2005; Rodda and McMahon, 2006]. In these conditional knockout mice, *Runx2* is expressed in perichondrial cells surrounding hypertrophic chondrocytes, and these cells differentiate into chondrocytes. *Sp7* is not detected in perichondrial cells whose *Ctnnb1* has been depleted at the osteoblast progenitor stage, whereas *Sp7* is detected in perichondrial cells whose *Ctnnb1* has been depleted at the preosteoblast stage. This result indicates that  $\beta$ -catenin is required for not only *Sp7* expression, but also osteoblast differentiation after the expression of *Sp7*. These findings indicate that RUNX2 is the first transcription factor required for determination of the osteoblast lineage, while SP7 and canonical Wnt signaling further direct the fate of mesenchymal cells to osteoblasts, blocking their differentiation into chondrocytes.

The functions of canonical Wnt signaling in *Runx2* expression and activation are still controversial. Wnt signaling enhances *Runx2* expression through the direct binding of TCF7 or LEF1/ $\beta$ -catenin on the *Runx2* promoter and through DNA binding of SMADs and TCF7L2/ $\beta$ -catenin to their cognate sequences as well as protein-protein interactions between them [Gaur et al., 2005; Dong et al., 2006;

Rodríguez-Carballo et al., 2010]. Further, FHL2, a member of the LIM-only subclass of the LIM protein superfamily, interacts with  $\beta$ -catenin and potentiates  $\beta$ -catenin nuclear translocation and TCF/LEF transcription, resulting in increased *Runx2* expression [Hamidouche et al., 2008]. In contrast, constitutive active  $\beta$ -catenin and BMP2 synergistically stimulated bone formation without altering RUNX2 protein expression [Mbalaviele et al., 2005]. Wnt activates RUNX2 through activation of the PI3K-Akt pathway, and RUNX2 forms a complex with LEF1 or TCF7L2-TCF7L2 and this complex binds the composite-binding site in the *Fgf18* promoter and activates it [Reinhold and Naski, 2007; Ling et al., 2010], whereas LEF1 interacts with RUNX2 and represses RUNX2-induced activation of the osteocalcin promoter [Kahler and Westendorf, 2003].

The expression patterns of Tcf/Lef family genes in endochondral bones are quite different. *Tcf7* is upregulated in prehypertrophic chondrocytes and is also expressed in perichondrium around hypertrophic chondrocytes and in osteoblasts. *Lef1* is expressed in proliferating chondrocytes, *Tcf7l1* is expressed in the whole cartilage, but *Lef1* and *Tcf7l1* are undetectable in osteoblasts. *Tcf7l2* is expressed in proliferating chondrocytes and is highly expressed in hypertrophic chondrocytes and osteoblasts but not in prehypertrophic chondrocytes [Glass et al., 2005; Hu et al., 2005]. *Runx2* is weakly expressed in resting and proliferating chondrocytes and upregulated in prehypertrophic chondrocytes, and is highly expressed in the perichondrium around hypertrophic chondrocytes and in osteoblasts [Inada et al., 1999; Maruyama et al., 2007]. Thus, the expression pattern of *Tcf7* is completely compatible with that in *Runx2*, whereas the expression patterns of *Lef1* and *Tcf7l1* are different from in *Runx2*, and the expression pattern of *Tcf7l2* is partly similar to that of *Runx2*.

Regulation of the expression of Tcf/Lef family genes by RUNX2 was also reported. RUNX2 strongly induced the expression of *Tcf7* and *Lef1* in chondrocyte and osteoblast lineages; the expression of *Tcf7* and *Tcf7l2* was reduced in *Runx2*<sup>-/-</sup> endochondral skeletons; the expression of *Tcf7*, *Lef1*, and *Tcf7l2* was reduced in *Runx2*<sup>-/-</sup> calvaria; and RUNX2 enhanced the reporter activity of *Tcf7* promoter [Mikasa et al., 2010]. Combined with the expression patterns of Tcf/Lef family genes and *Runx2*, RUNX2 regulates at least *Tcf7* expression among Tcf/Lef family genes. Further, RUNX2 regulates *Lef1* $\Delta$ N p2 promoter, which is located within the intron between exons 3 and 4 of *Lef1*, and that overexpression of *Lef1* $\Delta$ N in differentiating osteoblasts induces the expression of osteoblast differentiation genes, *osteocalcin* and *Col1a1* [Hoepfner et al., 2009]. Thus, RUNX2 and Wnt signaling are mutually regulated during skeletal development (Fig. 1).

## IHH SIGNALING AND RUNX2

In vertebrates, hedgehog signaling is mediated by three GLI transcription factors, GLI1, GLI2, and GLI3, and regulated by several feedback loops. GLI transcription and protein activity are controlled at several different levels by hedgehog signaling. When the levels of the hedgehog ligand are low, GLI2 and GLI3 are processed into truncated N-terminal target repressors. Full-length GLI2 and GLI3 act as target activators, though GLI3 only weakly. High concentra-

tions of the hedgehog ligand downregulate GLI3 at the transcriptional level and also suppress the processing of GLI2 and GLI3 into truncated target repressors. GLI1 is an activator of hedgehog target genes. GLI1 does not undergo proteolytic cleavage and does not function as a repressor [Marigo et al., 1996; Dai et al., 1999; Ruiz and Altaba, 1999; Sasaki et al., 1999; Wang et al., 2000; Ingham and McMahon, 2001]. IHH plays important roles in the regulation of chondrocyte proliferation and differentiation and osteoblast differentiation. *Ihh*-deficient mice show the lack of endochondral bone due to the absence of osteoblasts and *Runx2* expression is absent in the perichondrial cells before vascular invasion [St-Jacques et al., 1999; Hilton et al., 2005]. Further, ectopic expression of *Ihh* in chondrocytes induces *Runx2* expression throughout the perichondrium, although IHH alone is not sufficient to induce bone collar formation throughout it [Long et al., 2004]. Thus, IHH is required for *Runx2* expression in osteoblast precursors during endochondral bone formation but not sufficient for osteoblast differentiation. In *Ihh*<sup>-/-</sup>*Gli3*<sup>-/-</sup> mice, osteoblast differentiation is partly rescued, because *Runx2* and *Col1a1* are expressed in the perichondrium, although *Sp7* expression and activation of canonical Wnt signaling are still absent in the perichondrium before vascular invasion [Hilton et al., 2005]. The repressor form of GLI3 inhibits DNA binding of RUNX2 [Ohba et al., 2008]. Further, IHH upregulates the expression and function of *Runx2* through GLI2 [Shimoyama et al., 2007]. Thus, IHH activates *Runx2* expression by inhibiting the processing of GLI3 to the repressor form and by upregulating the full-length activating form of GLI2. RUNX2 also directly regulates *Ihh* expression in the growth plate [Yoshida et al., 2004]. In the processes of endochondral ossification, RUNX2 plays an important role in chondrocyte maturation, and IHH induces chondrocyte proliferation and inhibits chondrocyte maturation through the induction of parathyroid hormone-related peptide (PTHrP), which inhibits *Runx2* expression through the PKA signaling pathway [Vortkamp et al., 1996; St-Jacques et al., 1999; Enomoto et al., 2000; Takeda et al., 2001; Ueta et al., 2001; Iwamoto et al., 2003; Li et al., 2004]. Thus, in the growth plate, RUNX2 induces chondrocyte maturation and enhances chondrocyte proliferation through the direct induction of *Ihh* expression; IHH induces PTHrP; PTHrP inhibits chondrocyte maturation through the inhibition of *Runx2* expression, forming a negative feedback loop in chondrocyte maturation; and IHH induces *Runx2* expression in the perichondrium and induces osteoblast differentiation (Fig. 1).

## CONCLUDING REMARKS

RUNX2 plays essential roles in osteoblast differentiation and chondrocyte maturation, and RUNX2, SP7, and major signaling pathways, including FGFR, Wnt, and IHH, interact in osteoblast differentiation and/or chondrocyte maturation (Fig. 1). However, it remains to be clarified how *Runx2* expression is regulated in the two lineages and how RUNX2 regulates both osteoblast differentiation and chondrocyte maturation at different stages and locations during bone development. Elucidation of the reciprocal regulation of RUNX2, SP7, and the major signaling pathways at an appropriate

time and space in bone development would reveal why RUNX2 plays critical roles in both osteoblast differentiation and chondrocyte maturation.

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