

Review Article

Current Understanding on the Molecular Basis of Chondrogenesis

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Abstract. Endochondral bone formation involves multiple steps, consisting of the condensation of undifferentiated mesenchymal cells, proliferation and hypertrophic differentiation of chondrocytes, and then mineralization. To date, various factors including transcription factors, soluble mediators, extracellular matrices (ECMs), and cell-cell and cell-matrix interactions have been identified to regulate this sequential, complex process. Moreover, recent studies have revealed that epigenetic and microRNA-mediated mechanisms also play roles in chondrogenesis. Defects in the regulators for the development of growth plate cartilage often cause skeletal dysplasias and growth failure. In this review article, I will describe the current understanding concerning the regulatory mechanisms underlying chondrogenesis.

Key words: chondrocyte, transcription factors, growth factors, extracellular matrix, differentiation

Introduction

In mammals, most of the skeleton including the long bones of the limbs and the vertebral columns is formed through endochondral bone formation, which consists of the mesenchymal condensation of undifferentiated cells, proliferation of chondrocytes and differentiation into hypertrophic chondrocytes, followed by mineralization (1–3). Proliferating chondrocytes form orderly parallel columns in the growth

plates, and are characterized by the expression of type II, IX, and XI collagen (Col II, IX and XI) and proteoglycans such as aggrecan. When chondrocytes differentiate, they become hypertrophic and begin to produce a high level of alkaline phosphatase and type X collagen (Col X). Eventually, the terminally differentiated chondrocytes undergo apoptosis, and the cartilaginous matrix is mineralized and replaced by bone (1–3). These mature chondrocytes express vascular endothelial growth factor (VEGF) and matrix metalloproteinases (MMPs) (4, 5). VEGF induces blood vessel invasion, and MMPs aid in the degradation of the cartilaginous matrix (4, 5). Accumulating evidence provided by human diseases, mouse models and cell studies has identified a number of factors to be involved in the regulation of proliferation and differentiation of chondrocytes (Fig. 1). Among them are various transcription factors, soluble growth factors, ECMs, and epigenetic factors. In this review

Received: August 13, 2013

Accepted: September 13, 2013

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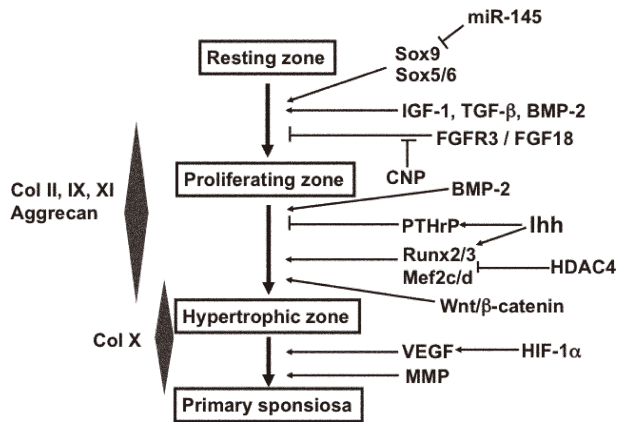


Fig. 1. Molecular network controlling the development of growth plate cartilage.

article, I will provide an updated overview of the molecular mechanisms regulating the development of growth plate cartilage.

Transcription Factors Involved in Chondrogenesis

Among the transcription factors involved in chondrogenesis, SOX9 has been the most extensively studied. SOX9 is a member of the Sox family of transcription factors characterized by a high-mobility-group-box DNA binding motif related to that of the sex-determining factor SRY, and is a responsible molecule for campomelic dysplasia characterized by severe skeletal malformation (6, 7). Evidence provided by mouse models has also revealed that Sox9 is indispensable for chondrogenesis. Sox9 begins to be expressed at the mesenchymal osteochondrogenitor stage, and transactivates several genes specific to proliferating chondrocytes such as *Col2a1* encoding Col II (8, 9). Sox5 (L-Sox5) and Sox6 were shown to cooperate with Sox9 to activate the chondrocyte-specific enhancers in these genes (10, 11). The activating transcription factor (ATF)/cyclic AMP response element binding protein (CREB) family and the AP1 family member c-Fos are required to maintain the proliferative capacity of early chondrocytes (12, 13).

Hypertrophic maturation of chondrocytes requires the Runt domain family transcription factors Runx2 and Runx3 as well as a decrease in the expression and/or activity of the Sox proteins. *Runx2/Runx3*-double knockout mice lack hypertrophic chondrocytes (14, 15). It has been reported that Runx2 directly transactivates the genes *Ihh* (*Indian hedgehog*), *Col10a1* encoding Col X, and *MMP13* (15–17). Recently, it has also been shown that Sox9 suppresses the expression of Runx2 and β -catenin signaling, which inhibits the hypertrophic change of chondrocytes (18). A basic helix-loop-helix type transcription factor, Twist-1 functions as another repressor of Runx2 in the perichondrium (19). Other transcription factors, such as MADS-box transcription factors Mef2c and Mef2d (myocyte enhancer factor 2c and 2d), Msx2, the AP1 family member Fra2, and FoxA family transcription factors, also facilitate chondrocyte hypertrophy (20–25). The transcription factor hypoxia-inducible factor-1 α (HIF-1 α) is one of the major regulators of the hypoxic response in mammals and plays a role in chondrocyte survival and gene regulation for VEGF, which induces blood vessel invasion into cartilage (26, 27). Thus, a complex transcriptional network governs the process of chondrogenesis from chondrocytic commitment to terminal differentiation.

Soluble Regulators of Chondrogenesis

Fibroblast growth factors (FGFs) play critical roles in chondrogenesis by activating signaling through FGF receptors (FGFRs), as indicated by a spectrum of human chondrodysplasias and dwarfism caused by gain-of-function mutations in the *FGFR3* gene (28–31). Among the FGFRs, *Fgfr3* is expressed in cells undergoing mesenchymal condensation and proliferating chondrocytes. On the other hand, *Fgfr1* is expressed in prehypertrophic and hypertrophic chondrocytes (32–34). It has been suggested that FGFR3-mediated signaling negatively regulates chondrocyte proliferation and differentiation (35–

37). In FGFR3-related chondrodysplasias such as achondroplasia, constitutive activation of FGFR3 results in the activation of the downstream ERK and STAT pathways (28). Although various FGFs are expressed in cartilage, FGF18 is suggested to be a physiological ligand for FGFR3 in chondrocytes, because of similar histology in the growth plates between *Fgf18*-knockout mice and *Fgfr3*-knockout mice (38, 39).

Ihh is a secreted signaling molecule, expressed by prehypertrophic chondrocytes. A line of evidence provided by genetically altered mouse models has revealed that Ihh increases the expression of parathyroid hormone-related protein (PTHrP) in perichondrial cells and chondrocytes at the ends of long bones, which delays chondrocyte hypertrophy through the PTH/PTHrP receptor expressed in proliferating chondrocytes. Thus, Ihh and PTHrP function in a local negative feedback loop to regulate the onset of hypertrophic differentiation (40). In addition, it is also reported that Ihh stimulates the proliferation and maturation of chondrocytes independently of PTHrP, in which activation of Wnt and bone morphogenetic protein (BMP) signaling is suggested to be involved (41–43).

The importance of C-type natriuretic peptide (CNP) signaling in chondrogenesis was shown by the severe dwarfism of *CNP*-knockout mice (44, 45). CNP exerts its signal mainly through the receptor NPR2, which is also called guanylyl cyclase B (GC-B), and *Npr2*-null mice display a similar phenotype to *CNP*-knockout mice (46). Based on the mouse studies, it has been suggested that CNP promotes endochondral bone growth through several mechanisms, including the stimulation of chondrocyte proliferation and hypertrophy and an increase in ECM production (44–46). In humans, loss-of-function mutations in the *NPR2* gene cause acromesomelic dysplasia, type Maroteaux, characterized by severe dwarfism (47, 48), while a gain-of-function type mutation in the gene has been identified in a family with skeletal overgrowth (49), which indicates that the CNP/NPR2 signaling pathway

plays a role in the development of growth plate cartilage both in humans and mice. The similarity in the skeletal phenotype between CNP-deficient mice and human achondroplasia has suggested that CNP/NPR2 signaling is promising as a new therapeutic target for the dwarfism associated with skeletal dysplasia (46). It has been shown that the signaling evoked by CNP inhibits the FGF-induced activation of the ERK pathway (46). The p38MAPK pathway and PI3K/Akt pathway are also suggested to be involved in the regulation of chondrocyte development by CNP (50).

Other soluble factors such as Wnts, bone morphogenic proteins (BMPs), transforming growth factor-beta (TGF- β), insulin-like growth factors (IGFs) and thyroid hormone are also involved in chondrogenesis (51–53) but are not further discussed here.

Regulation of Chondrogenesis by the ECM

The ECM provides a cell type-specific microenvironment. As chondrocytes mature, they produce abundant ECM proteins such as collagens and proteoglycans, and the cell-matrix interactions come to have more important roles than in the earlier stages of chondrogenesis, when the cell-cell interaction via adhesion molecules such as N-cadherin and N-CAM is involved in cellular condensation and subsequent chondrogenesis (54, 55). The ECM is recognized and bound by integrins and cell surface transmembrane receptors. Integrins occur as dimers of an α subunit and a β subunit, and the binding of ligands to integrins leads to transduction of signaling from the ECM to intracellular effectors (56). Chondrocytes express several integrin subunits, and it has been reported that chondrocyte-specific $\beta 1$ integrin-knockout mice exhibited a chondrodysplasia-like phenotype (57, 58). In these mice, growth plates exhibited unorganized proliferative columns and an abnormal cell shape due to the loss of adhesion to Col II, and the isolated chondrocytes displayed

reduced proliferation (58). Integrin-linked kinase is one of the components of the complex whose formation is triggered by the activation of integrin-mediated signaling, and knockout of its gene resulted in a chondrodysplasia-like phenotype similar to that of chondrocyte-specific $\beta 1$ integrin-knockout mice (59). These results suggest the importance of integrin-mediated signaling from the ECM in chondrogenesis.

The *SLC26A2* gene encodes a sulfate transporter responsible for sulfate uptake by chondrocytes. Mutations in this gene have been identified in a form of chondrodysplasia called diastrophic dysplasia, which is characterized by undersulfation of cartilaginous proteoglycans. Similar to patients with diastrophic dysplasia, *dttd* mice harboring a knock-in *Slc26a2* mutation were reported to exhibit undersulfation of glycosaminoglycans such as chondroitin (60). It has been also reported that mice lacking the gene encoding chondroitin sulfate *N*-acetylgalactosaminyltransferase 1 (CSGalNAcT-1), an enzyme involved in the initiation of the biosynthesis of chondroitin sulfate, have shorter, disorganized chondrocyte columns in the growth plates with a rapid catabolism of aggrecan (61).

Another function of the cartilaginous ECM is regulation of chondrogenesis through binding, storage, and release of soluble factors. For example, most of FGFs bind to heparan sulfate proteoglycans and bind to FGFRs in the context of heparan sulfate proteoglycans to trigger signal transduction. Analysis of mice lacking sulfate-modifying factor 1 (*Sumf1*) has suggested that desulfation of proteoglycans regulates chondrocyte proliferation and differentiation by limiting FGF signaling (62).

Vinculin is a major component of the focal adhesion complex and functions in adhesion and/or signaling between the extracellular microenvironment and the cell via integrins and cadherins. Although little is known about its tissue-specific functions, we have recently identified vinculin as having profound roles in

chondrogenesis (63). Knockdown of vinculin in primary chondrocytes and organ cultures of metatarsal explants resulted in reduced expression of *Col2a1*, *aggrecan*, *Col10a1*, and *Runx2*. Moreover, knockdown of *vinculin* abrogated IGF-I-induced growth of metatarsal explants. The upregulation of *Col2a1* and *aggrecan* expression by IGF-I was also cancelled by the knockdown. These results suggest that vinculin regulates the expression of chondrocyte-specific genes by orchestrating the signaling from the ECM and soluble factors such as IGF-I (63).

Epigenetic Control of Chondrogenesis

Recent studies have uncovered the roles of epigenetic mechanism in chondrogenesis. Among the histone deacetylases (HDACs), HDAC4 has been shown to prevent the premature chondrocyte hypertrophy by inhibiting the activity of *Runx2/3* and *Mef2c/d* transcription factors (20, 21, 64). HDAC1 and HDAC2 mediate the repression of some cartilage-specific genes including *Col2a1* (65). These findings suggest that histone modification influences the process of endochondral bone formation.

DNA methylation is also involved in the regulation of cartilage-specific genes. For example, it was reported that the demethylation of 2 CpG sites in the *COL10A1* promoter was correlated with induction of the *COL10A1* gene during the chondrogenic differentiation of human mesenchymal stem cells (66).

MicroRNAs as Novel Regulators of Chondrogenesis

MicroRNAs (miRNAs) are a class of ~22 nucleotide noncoding RNAs that regulate the expression of other genes at the posttranscriptional level. The critical roles of miRNAs in chondrogenesis were first indicated by the severe skeletal growth defects in mice lacking *Dicer*, an enzyme required for miRNA synthesis (67). In the growth plates of *Dicer*-

knockout mice, proliferation of chondrocytes was decreased, while differentiation was accelerated (67). Since then, an increasing number of specific miRNAs has been identified to have roles in chondrocyte differentiation. Mice lacking miR-140 showed a mild short stature and age-related osteoarthritis-like changes, suggesting that miR-140 regulates both the development and homeostasis of cartilage (68). miR-145 was reported to directly target Sox9 and regulate chondrogenic differentiation of mesenchymal stem cells (69), while miR-199a was shown to be responsive to BMP and to regulate chondrogenesis by targeting Smad1 (70). These findings indicate the importance of miRNA-mediated regulation of chondrogenesis.

Conclusion

In this review, I have overviewed the current knowledge concerning the molecular mechanisms underlying the development of growth cartilage. The proliferation and differentiation of chondrocytes is elaborately controlled by various factors, and their defects are often associated with growth failure and skeletal dysplasias. Further clarification of the molecular basis of cartilage development may lead to the discovery of new therapeutic targets for these conditions.

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