

# EVOLUTION OF VERTEBRATE CARTILAGE DEVELOPMENT

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## Abstract

Major advances in the molecular genetics, paleobiology, and the evolutionary developmental biology of vertebrate skeletogenesis have improved our understanding of the early evolution and development of the vertebrate skeleton.

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These studies have involved genetic analysis of model organisms, human genetics, comparative developmental studies of basal vertebrates and nonvertebrate chordates, and both cladistic and histological analyses of fossil vertebrates. Integration of these studies has led to renaissance in the area of skeletal development and evolution. Among the major findings that have emerged is the discovery of an unexpectedly deep origin of the gene network that regulates chondrogenesis. In this chapter, we discuss recent progress in each these areas and identify a number of questions that need to be addressed in order to fill key gaps in our knowledge of early skeletal evolution.

## 1. INTRODUCTION

The vertebrate skeleton consists of two predominant tissue types: cartilage and bone. Although generally considered a vertebrate character, cartilage is found across a broad range of animal taxa, indicating a long and complex evolutionary history (Hall, 2005). Cartilage differs from bone in several ways; cartilage has a lower metabolic rate, is mostly avascular, and contains different cellular and extracellular components that give it unique structural properties. Classically, true cartilage was defined by three criteria (1) it contains chondrocytes suspended in rigid matrix, (2) the matrix has a high content of collagen, and (3) the matrix is rich in acidic polysaccharides (Person and Mathews, 1967). The proposal that the cartilage of some vertebrates, such as lampreys and hagfishes, is noncollagenous led to a revision of this definition to substitute “fibrous proteins” for “collagen” (Cole and Hall, 2004a); however, recent work has shown that these jawless fishes also have collagen-based cartilage (Ohtani *et al.*, 2008; Zhang and Cohn, 2006; Zhang *et al.*, 2006). Such studies of cartilage in nontetrapod lineages have revealed that a deeply conserved genetic system underlies a diverse array of cartilage types. These discoveries have enhanced our understanding of the early evolution of cartilage and raised new questions about the homologies of animal connective tissues. Here, we review these advances in the context of skeletal developmental genetics and the evolutionary history of vertebrates, and discuss how changes to developmental and genomic programs may have contributed to the origin of the vertebrate skeleton.

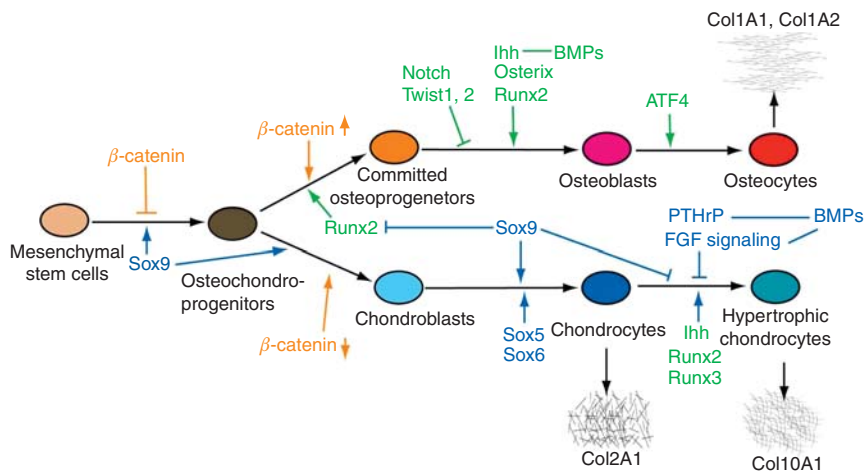
## 2. SKELETAL CELL LINEAGE DETERMINATION AND THE SKELETOGENIC GENE NETWORK

Vertebrate cartilage and bone are composed of three major cell lineages, chondrocytes, osteoblasts, and osteoclasts. The former two cell types are derived from common mesenchymal progenitor cells, whereas

osteoclasts are of hematopoietic origin. After condensation, mesenchymal cells start to differentiate into chondrocytes. These chondrocytes may remain as cartilage throughout life, or the cartilage template may undergo hypertrophy and eventually be replaced by bone, a process termed endochondral ossification. Alternatively, the mesenchymal cells may differentiate directly into bone, through a process termed intramembranous ossification, as seen in the membrane bones of the skull, such as the calvaria. In both intramembranous and endochondral ossification, osteoblasts first aggregate as mesenchymal condensations (Karsenty and Wagner, 2002; Yang and Karsenty, 2002; Zelzer and Olsen, 2003). The cell fate decisions made by aggregating mesenchymal cells are regulated by a skeletogenic gene network (Fig. 2.1), and understanding the hierarchy, regulation, and function of these factors is critical to our discussion of the evolution of skeletogenic mechanisms. Below, we review the major components of this network and describe their functions and interactions during embryonic development of the skeleton.

## 2.1. Sox9

As cells in mesenchymal condensations begin to differentiate into chondrocytes, the earliest marker of chondrogenesis is *Sox9*, a member of the vertebrate SoxE family that contains a high-mobility-group (HMG)-box



**Figure 2.1** Schematic representation of gene network that directs mesenchymal cells along chondrogenic (bottom) and osteogenic (top) differentiation pathways. Arrows indicate positive regulation, lines indicate interaction, and bars indicate negative regulation. Data represented in this schematic are taken from multiple sources cited in the text. The scheme depicts hierarchical arrangement of genes in the network and does not necessarily indicate direct transcriptional regulation at each step.

DNA-binding domain (Fig. 2.1) (Healy *et al.*, 1996; Wright *et al.*, 1995). *Sox9* directly regulates expression of two genes that code for major matrix proteins, type II collagen (*Col2 $\alpha$ 1*) and aggrecan, and is required for expression of genes that encode minor matrix proteins, including type IX and XI collagen (Lefebvre and de Crombrughe, 1998; Lefebvre *et al.*, 1997; Liu *et al.*, 2000; Ng *et al.*, 1997; Zhang *et al.*, 2003b; Zhou *et al.*, 1998). Haploinsufficiency of *Sox9* in humans underlies campomelic dysplasia, a congenital malformation of the skeleton characterized by shortening and bowing of the limbs, and similar anomalies occur in mice with loss-of-function mutation in *Sox9* (Foster *et al.*, 1994; Wagner *et al.*, 1994). Reciprocal experiments involving ectopic expression of *Sox9* in chick embryos can induce dermomyotomal or neural crest-derived cells to form cartilage (Healy *et al.*, 1999; Eames *et al.*, 2004). *Sox9* function is enhanced by *Sox5* and *Sox6*, which can bind to *Sox9* and act as cofactors in the activation of *Col2 $\alpha$ 1* (Ikeda *et al.*, 2004; Lefebvre and de Crombrughe, 1998; Lefebvre *et al.*, 1998, 2001; Smits and Lefebvre, 2003; Stolt *et al.*, 2006). The *Sox5/6/9* trio also has been shown to bind S100A1 and S100B, two novel targets that mediate the trio's ability to inhibit chondrocyte differentiation (Saito *et al.*, 2007). *Sox9* can form complexes with the CREB-binding protein CBP/P300, and the association of these proteins may be required for chondrocyte-specific expression of *Col2 $\alpha$ 1* (Tsuda *et al.*, 2003). Interestingly, the chondrogenic activity of TGF $\beta$ /Bmp signaling (described below) may be mediated, at least in part, by the ability of Smad3 to promote binding of *Sox9* with the CBP/P300 coactivator (Furumatsu *et al.*, 2005). These interactions may account for the ability of *Sox9* to activate *Col2 $\alpha$ 1* in some cell lineages (e.g., limb bud, sclerotome, and cranial neural crest) but not others (e.g., genital ridge).

## 2.2. Runx2

The vertebrate *Runx2* gene [also known as *PEBP2A* (*polyoma enhancer-binding protein 2A*), *Osf2* (*osteoblast-specific factor 2*), *AML3* (*acute myelogenous leukemia 3*), and *Cbfa1* (*core-binding factor alpha 1*)] is an ortholog of the fly *runt* gene and a master regulator of osteoblast differentiation (Fig. 2.1) (van Wijnen *et al.*, 2004). In addition to its role in osteoblast differentiation (Ducy *et al.*, 1997, 1999; Komori *et al.*, 1997; Otto *et al.*, 1997), *Runx2* is required for chondrocyte hypertrophy (Fig. 2.1). In *Runx2*-null mice, the entire skeleton remains cartilaginous due to the maturational arrest of osteoblasts, and there is a failure of chondrocyte hypertrophy (Inada *et al.*, 1999; Kim *et al.*, 1999; Takeda *et al.*, 2001). Reciprocally, ectopic expression of *Runx2* in chick head mesenchyme can drive excess bone formation and ectopic chondrocyte hypertrophy (Eames *et al.*, 2004). Haploinsufficiency of *Runx2* in humans causes cleidocranial dysplasia, a rare skeletal malformation characterized by short stature, distinctive facial features and

narrow, sloping shoulders associated with defective or absent clavicles (Mundlos and Olsen, 1997a,b; Mundlos *et al.*, 1996). *Runx1* and *Runx3*, two genes closely related to *Runx2*, also are expressed in chondrocytes and participate in the progression of chondrocytes to the hypertrophic stage (Karsenty, 2008; Levanon *et al.*, 2001; Lian *et al.*, 2003; Smith *et al.*, 2005; Stricker *et al.*, 2002; Wang *et al.*, 2005).

### 2.3. Interaction of *Sox9* and *Runx2*

Several lines of evidence have shown that in many cases, condensed mesenchymal cells have chondrogenic and osteogenic potential, since they express both *Sox9* and *Runx2* (Bi *et al.*, 1999; Ducky *et al.*, 1997; Eames and Helms, 2004; Otto *et al.*, 1997; Yamashiro *et al.*, 2004). Moreover, cultured embryonic cells may form both bone and cartilage (Fang and Hall, 1997; Toma *et al.*, 1997; Wong and Tuan, 1995). Inactivation of *Sox9* in the cranial neural crest-derived mesenchymal cells blocks cartilage differentiation, but this also leads to ectopic expression of osteoblast-specific genes such as *Runx2*, *Osterix*, and *Col1 $\alpha$ 1* (Mori-Akiyama *et al.*, 2003). Conversely, it was reported that in *Osterix* mutants, ectopic chondrocytes formed at the expense of the bone collar in long bones and in some membrane bones (Nakashima *et al.*, 2002). These data support the idea that the common skeletal mesenchymal progenitors have three possible differentiation fates in the skeleton, chondrogenesis, intramembranous ossification or endochondral ossification (it is noteworthy, however, that these mesenchymal cells also can take on other, nonskeletal cell fates, such as adipose tissue) (Karsenty, 2003; Karsenty and Wagner, 2002). In mesenchymal osteochondrogenic progenitors, removal of *Sox9* will abolish cartilage and endochondral bone formation, indicating that *Sox9* is required for skeletal differentiation (Akiyama *et al.*, 2005). Experiments in chick embryos demonstrated that higher levels of *Sox9* will commit cells to chondrogenesis, whereas higher levels of *Runx2* will push them toward osteogenesis (Fig. 2.1) (Eames *et al.*, 2004). *Sox9* has been shown to be dominant to *Runx2* (Zhou *et al.*, 2006), which suggests that if these transcription factors are expressed at similar levels, then skeletal progenitor cells may differentiate preferentially into cartilage.

### 2.4. Parathyroid hormone-related protein and Indian hedgehog

During long bone growth, chondrocyte proliferation and differentiation is tightly regulated by a negative feedback loop between Indian hedgehog (Ihh) and parathyroid hormone-related protein (PTHrP) (Fig. 2.1) (Karp *et al.*, 2000; Lanske *et al.*, 1996; St-Jacques *et al.*, 1999; Vortkamp *et al.*, 1996). PTHrP is a peptide hormone that is secreted by the most distal perichondrium, and its G protein-coupled receptor, *PPR*, localizes to the

proliferative prehypertrophic zone. PTHrP acts to maintain proliferation and to inhibit differentiation (St-Jacques *et al.*, 1999). In humans, activating mutations of *PPR* cause Jansen's metaphyseal chondrodysplasia, which involves delayed skeletal differentiation and abnormal growth plates (Schipani *et al.*, 1995). Loss-of-function mutations in *PTHrP* in mice result in dwarfism due to accelerated hypertrophy (Karaplis *et al.*, 1994; Lanske *et al.*, 1996). *Ihh* is expressed along with *PPR* in the prehypertrophic zone and controls expression of *PTHrP* (Vortkamp *et al.*, 1996). Deletion of *Ihh* results in reduced chondrocyte proliferation and failure of perichondral osteoblast formation, ultimately leading to dwarfism. In the *Ihh*-null mutants, *PTHrP* expression is lost (Razzaque *et al.*, 2005; St-Jacques *et al.*, 1999), and *Ihh* overexpression results in upregulation of *PTHrP*, promoting proliferation and delaying hypertrophy. PTHrP feeds back to negatively regulate *Ihh* expression. This *Ihh*-PTHrP feedback loop maintains the balance between proliferation and differentiation (Kronenberg, 2006). Very recent work has shown that *Ihh* can promote chondrocyte hypertrophy independently of PTHrP (Mak *et al.*, 2008). *Bapx1* (Nk3.2) is a downstream target of *Ihh*-PTHrP loop and, at least in part, mediates chondrocyte hypertrophy (Provot *et al.*, 2006). Interestingly, *Runx2* and *Runx3* can induce *Ihh* expression (St-Jacques *et al.*, 1999; Yoshida *et al.*, 2004) and *Ihh* can feed back to inhibit *Runx2* expression through the PKA pathway (Iwamoto *et al.*, 2003; Li *et al.*, 2004).

## 2.5. Wnt signaling

The canonical Wnt pathway is a key regulator for mesenchymal cell lineage determination (Fig. 2.1). *Wnt* genes are vertebrate orthologs of the *Drosophila wingless* gene, and there are 19 known *Wnt* genes in humans (Logan and Nusse, 2004; Miller, 2002). This group of secreted molecules is highly conserved in metazoan animals ranging from cnidarians to humans, and they have critical functions both in normal development and tumorigenesis (Kusserow *et al.*, 2005; Lee *et al.*, 2006; Logan and Nusse, 2004; Prud'homme *et al.*, 2002). Wnt proteins that bind to Frizzled receptors transduce the input into the cell together with the coreceptor, LDL receptor-related protein 5/6 (LRP5/6). There are at least three intracellular pathways for Wnt signaling; the canonical pathway mediated by  $\beta$ -catenin, the Ca-PKC pathway, and the planar cell polarity pathway (Miller, 2002). Interestingly, *Sox9* also interacts with  $\beta$ -catenin. *Sox9* can inhibit  $\beta$ -catenin-dependent promoter activation through the interaction between HMG-box and Armadillo repeats. *Sox9* also promotes degradation of  $\beta$ -catenin by ubiquitination or the proteasome pathway (Akiyama *et al.*, 2004).

Canonical Wnt signaling has been implicated in skeletal development (Bodine *et al.*, 2004; Boyden *et al.*, 2002; Gong *et al.*, 2001; Hartmann and Tabin, 2001; Kato *et al.*, 2002; Little *et al.*, 2002; Rawadi *et al.*, 2003).

Several lines of evidence have revealed that the canonical Wnt pathway regulates skeletogenic cell fate determination through a cell-autonomous mechanism to induce osteoblast differentiation and to repress chondrocyte differentiation (Fig. 2.1) (Day *et al.*, 2005; Glass *et al.*, 2005; Hill *et al.*, 2005; Hu *et al.*, 2005; Rodda and McMahon, 2006). When  $\beta$ -catenin is conditionally removed from skeletogenic mesenchyme using the *Prx1-Cre* allele, osteoblast differentiation arrests, and neither cortical nor membrane bone forms (although this can be rescued by *Ihh* and *Bmp2*). Similar phenotypes were found when  $\beta$ -catenin was deleted from the skeletal primordium using *Dermo1-Cre* and *Col2a1-Cre* mouse lines, in which ectopic chondrocytes formed at the expense of osteoblasts (Day *et al.*, 2005; Hu *et al.*, 2005). Moreover, micromass cell culture experiments showed that  $\beta$ -catenin levels can control the expression of *Sox9* and *Runx2* *in vitro* (Day *et al.*, 2005). Collectively,  $\beta$ -catenin controls early osteochondroprogenitor differentiation into chondrocytic or osteoblastic lineages. High levels of  $\beta$ -catenin lead to osteogenic differentiation and low levels lead to chondrogenic differentiation (Day *et al.*, 2005; Hill *et al.*, 2005). The process is summarized in Fig. 2.1. These studies suggest that variation in skeletal composition, both developmentally and evolutionarily, may be accomplished by tinkering with the temporal and spatial expression of canonical Wnt signals.

## 2.6. Fibroblast growth factor signaling

Fibroblast growth factors (Fgfs) and their receptors are also critical regulators of chondrocyte proliferation and differentiation (Fig. 2.1). In humans and mice, there are 22 Fgf genes and 4 Fgf receptors (Fgfr), many of which are involved in skeletal development, including those that signal through Fgfr1, Fgfr2, and Fgfr3 (Ornitz and Marie, 2002). Fgf9 has been shown to regulate differentiation of hypertrophic chondrocytes and to direct vascularization of the limb skeleton (Hung *et al.*, 2007). *Fgf18* is expressed in the perichondrium, and it signals to the chondrocytes through Fgfr3. *Fgfr1* is found in prehypertrophic and hypertrophic zone, and *Fgfr2* and *Fgfr3* are expressed, respectively, in perichondral cells and in the proliferating zone. Each of the three receptors has a unique function. Human genetic studies first revealed the importance of Fgf signaling in skeletal development, when *Fgfr3* mutations were shown to underlie achondroplasia, hypochondroplasia, and thanatophoric dysplasia (Olsen *et al.*, 2000). In *Fgfr3*-null mice, the proliferative rate is accelerated, which causes the chondrocyte column length to be increased (Colvin *et al.*, 1996; Deng *et al.*, 1996). Moreover, activating mutations in mouse *Fgfr3* cause reduced proliferation and increased apoptosis of chondrocytes (Sahni *et al.*, 1999). These studies suggested that Fgfr3 is a negative regulator of proliferation in the growth plate, and this process is mediated through STAT1–P21 pathway (Sahni *et al.*, 1999). As with Fgfr3, conditional removal of Fgfr1 in chondrocytes results in

expansion of the hypertrophic chondrocyte zone, indicating that *Fgfr1* is also a negative regulator of proliferation (Jacob *et al.*, 2006).

## 2.7. Bone morphogenetic protein signaling

Bone morphogenetic proteins (BMPs) and their receptors play multiple roles in chondrocyte differentiation and proliferation, and have been reviewed extensively elsewhere (Li and Cao, 2006; Pogue and Lyons, 2006). *Bmp7* is found mainly in the proliferating chondrocytes, whereas *Bmp2–Bmp5* are expressed primarily in the perichondrium (Lyons *et al.*, 1995; Minina *et al.*, 2001), although hypertrophic chondrocytes also express *Bmp2* and *Bmp6* (Solloway *et al.*, 1998). These distinctive expression patterns suggest that each of these Bmps has a unique function. The relationship of Bmp and Indian hedgehog is somewhat unclear. Although *in vitro* experiments in chick and mouse and *in vivo* studies in chick showed that Bmp receptor IA is an upstream regulator of *Ihh*, other *in vivo* and *in vitro* studies in mouse failed to detect changes in *Ihh* following activation of Bmp receptors or treatment with Bmp protein (Kobayashi *et al.*, 2005; Seki and Hata, 2004; Zhang *et al.*, 2003a). Different experimental approaches also have led to curious findings regarding the function of BmpR1A and BmpR1B. Studies in the chick limb suggested that BmpR1A and BmpR1B may have very different functions (Zou *et al.*, 1997), although more recent studies in mice found them to be interchangeable (Kobayashi *et al.*, 2005). Kobayashi *et al.* (2005) used multiple experimental strategies to overexpress *BmpR1A* in chondrocytes and found that BmpR1A has different roles at different stages of cartilage development. According to their findings, constitutive activation of *BmpR1A* stimulates chondrocyte hypertrophy and also promotes differentiation of prechondrogenic mesenchyme into chondrocytes.

## 3. STRUCTURE OF VERTEBRATE CARTILAGE MATRIX

### 3.1. Collagens

Most of the connective tissues of vertebrates are formed from extracellular fibers, matrix, and ground substance. For example, up to 90% of the dry weight of cartilage is extracellular matrix (Hardingham and Fosang, 1992). In jawed vertebrates, cartilage extracellular matrix typically is composed of mucopolysaccharides (in the form of proteoglycans) deposited within a meshwork of collagen fibers (Bruckner and van der Rest, 1994). Collagens are the main components of animal extracellular matrix (Exposito *et al.*, 2002), and the expansion of this gene family within the vertebrate clade coincided with evolution of a broad range of vertebrate skeletal tissues. For example, 29 different collagen genes have been identified in humans thus far



(Soderhall *et al.*, 2007), and the resultant proteins can be divided into two major groups, fibrillar and nonfibrillar collagens. The fibrillar collagen proteins, in which multiple collagen fibrils are assembled into collagen fibers, are further divisible into three clades, designated A, B, and C (Aouacheria *et al.*, 2004). Clade A collagens are the major fibril-forming collagens, including types I, II, III, and V (Aouacheria *et al.*, 2004). Clade A fibril procollagens consist of an N-propeptide, an N-telopeptide, a triple helix, a C-telopeptide, and a C-propeptide (from N- to C-terminus). The triple helix domain consists of a Gly-X-Y triplet repeat, with X and Y usually being proline and hydroxyproline. The propeptide is removed during the maturation of collagen through posttranslational processing by N- and C-proteinase (Exposito *et al.*, 2002; Kadler *et al.*, 1996). Type II collagen is encoded by *Col2a1*, and nearly 40 years ago this was shown to be the major matrix protein found in cartilage (Miller and Matukas, 1969). Each type II collagen fibril is made of three identical chains that provide tensile strength and a scaffolding network for proteoglycans (van der Rest and Garrone, 1991). Cartilage also contains minor collagens type IX and XI, which belong to the clade B fibrillar collagen family and participate in the process of fibril formation (Eyre *et al.*, 2004; Kadler *et al.*, 1996; Li *et al.*, 1995). Different types of cartilage are characterized by different combinations and quantities of collagen proteins. In addition, the profile of collagen expression can be dynamic during skeletal development. During long bone development, for example, the major matrix protein found in proliferative cartilage is type II collagen, whereas type X collagen is most abundant during the hypertrophic stage and type I collagen dominates bony matrix (Olsen *et al.*, 2000).

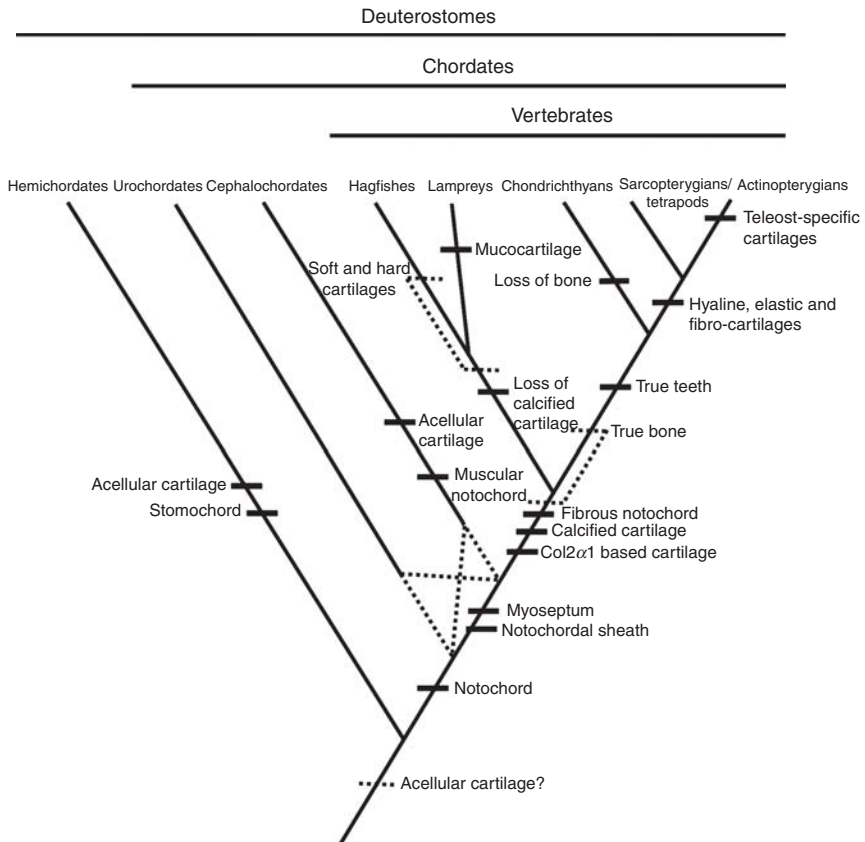
### 3.2. Proteoglycans

Proteoglycans are the second-most abundant proteins (after the fibrillar collagens) in cartilage matrix. Glycosaminoglycan side chains of proteoglycans become heavily sulfated, which increases their retention of water, giving cartilage its characteristic resistance to compression. Chondroitin sulfate was shown to be the predominant glycosaminoglycan in cartilage, and one of its substrates, aggrecan, was found to be the most abundant cartilage proteoglycan (Doege *et al.*, 1991). Deposition of aggrecan has been considered a hallmark of chondrogenesis (although it is also present in aorta, intervertebral disks, and tendons) (Schwartz *et al.*, 1999). Aggrecan not only contributes to the physical properties of cartilage, but also it protects cartilage collagen from degradation by stabilizing collagen protein (Pratta *et al.*, 2003). In addition to the large aggregating proteoglycan aggrecan, there are many small leucine-rich proteoglycans in cartilage, including biglycan, decorin, fibromodulin, lumican, and epiphygan, which have a variety of functions in cartilage development and maintenance (Iozzo, 1998; Knudson and Knudson, 2001). Chondrocytes also express cell surface

proteoglycans, such as syndecans and glypican, which can bind growth factors during cell–cell and cell–matrix interactions (Iozzo, 1998; Song *et al.*, 2007).

#### 4. EVOLUTIONARY HISTORY OF THE VERTEBRATE SKELETON

For extant deuterostomes, mapping the key characters of skeletogenesis onto a phylogeny provides a window into the distribution and pattern of skeletal evolution (Fig. 2.2), but what does the fossil record reveal about the evolution of cartilage and bone within vertebrates? Obviously, most preserved specimens will reflect the existence of mineralized tissues, since they are most easily fossilized, but some samples reveal unmineralized cartilage as well. Although studies of invertebrates indicate that cartilage had an earlier origin than did bone in metazoans, it is less clear which of these tissues appeared first in vertebrate skeletal evolution. Conodonts lacked a dermal skeleton and early descriptions of bone in conodonts have been disputed, although their dental elements were rich in dentine and enamel (Donoghue *et al.*, 2006). The 530-million-year-old fossil *Haikouella* is one of the earliest examples of unmineralized vertebrate cartilage, and comparison with modern lamprey cartilage shows striking morphological similarity (Mallatt and Chen, 2003). Jawless fishes dominate the vertebrate fossil record through the upper Paleozoic, and most possessed a heavily armored dermoskeleton, a character that has been lost in lampreys and hagfishes (Sansom *et al.*, 2005). Histological and microscopic studies of dermoskeletons have identified a variety of tissue types, including bone, dentine, and enamel, although neither cartilage nor perichondral bone have been observed (Donoghue and Sansom, 2002; Donoghue *et al.*, 2006; Patterson *et al.*, 1977). Most crown-group vertebrates show few similarities between the mineralized tissues of the teeth and those of the skeleton. Interestingly, the dermal skeletons of early vertebrates were composed of both “dental” and “skeletal” tissue types, and the presence of dentine and enamel in dermal armor has led some investigators to suggest that the evolutionary origin of teeth may be traced to the dermal skeleton (Smith and Johanson, 2003). The earliest examples of mineralized endoskeletons are found in galeaspids and pteraspidomorphs (Donoghue and Sansom, 2002; Donoghue *et al.*, 2006; Janvier, 1996; Stensio, 1927). Galeaspids had dermal armor of unmineralized cartilage and acellular bone. In heterostracans, the dermal skeleton contained dentine, acellular bone, and enameloid tissues. Cellular bone is found in the dermal skeletons of osteostracans, which was combined with dentine in their head shields. The dermoskeleton of thelodonts consisted of scales that were made up of dentine and also may have contained acellular bone (Donoghue and Smith, 2001; Donoghue



**Figure 2.2** Phylogenetic distribution of key skeletogenic characters in deuterostomes. Dotted lines at the base of the cephalochordate and urochordate branches indicate ambiguous positions and these may be transposed. Dotted horizontal bar at base of tree indicates a possible early origin of acellular cartilage in stem deuterostomes (see [Rychel and Swalla, 2007](#)). Alternatively, acellular cartilage may have arisen independently in hemichordates and cephalochordates. Dotted horizontal bar in cyclostome (hagfish + lamprey) clade indicates uncertainty regarding the origin of classically defined “hard” and “soft” cartilage (see [Cole, 1905](#); [Parker, 1883](#); [Zhang and Cohn, 2006](#) for further details).

*et al.*, 2006). The almost exclusively cartilaginous skeletons of extant cyclostomes and sharks have been misinterpreted as evidence that cartilage predated bone in vertebrate evolution; however, this is a derived condition that followed an evolutionary loss of bone ([Carroll, 1988](#); [Daniel, 1934](#); [Donoghue and Sansom, 2002](#); [Goodrich, 1930](#); [Hall, 1975](#); [Janvier, 1996](#); [Maisey, 1988](#); [Moss, 1977](#); [Orvig, 1951](#); [Romer, 1985](#); [Smith and Hall, 1990](#)). The fossil record of sharks shows abundant evidence of exoskeletal

bone (Coates and Sequeira, 2001; Hall, 1975; Maisey, 1988; Moss, 1977; Zangerl, 1966) and limited examples of endoskeletal bone (Coates *et al.*, 1998). Indeed, true bone has persisted in some extant chondrichthyans, in subchondral linings, neural arches, and dermal denticles (Bordat, 1987; Eames *et al.*, 2007; Kemp and Westrin, 1979; Moss, 1970, 1977; Peignoux-Deville *et al.*, 1982; Reif, 1980; Sire and Huysseune, 2003). Thus far, despite the rich diversity of skeletal tissues in the fossil record, the question of whether the earliest vertebrate skeletons were cartilaginous, bony, or both remains unclear.

## 5. DIVERSIFICATION OF CARTILAGINOUS TISSUES

A major challenge has been the classification of different cartilage types at the molecular and biochemical levels, and understanding the interrelationships among this diverse family of tissues. Depending on relative amounts of cells and extracellular matrix, there are generally four kinds of cartilage in vertebrates and invertebrates: matrix-rich cartilage, cell-rich cartilage, vesicular cartilage, and acellular cartilage, although skeletal tissues with an intermediate or mosaic composition have been identified in some vertebrates, such as the cartilage-like chondroid tissues, which possess characters of both bone and cartilage (Cole and Hall, 2004a). Whether these four cartilage types evolved independently or diversified from a single type of ancestral connective tissue is unknown (Fig. 2.2). The similarities in matrix composition, histological properties, gene expression profiles, and cell biology of notochord cells and chondrocytes have led some to propose that vertebrate cartilage may have evolved from the notochord of early chordates (Stemple, 2004; Zhang and Cohn, 2006). Alternatively, vertebrate cartilage may have its origins in the secretion of acellular matrix by ectodermal cells. Acellular cartilage, which lacks chondrocytes, has been found in hemichordates, cephalochordates, and vertebrates (e.g., rays) (Cole and Hall, 2004b; Meulemans and Bronner-Fraser, 2007; Rychel and Swalla, 2007; Rychel *et al.*, 2006; Wright *et al.*, 2001). Rychel *et al.* proposed that ectodermally derived acellular cartilage is an ancestral mode of pharyngeal cartilage development in deuterostomes (Fig. 2.2) (Rychel and Swalla, 2007; Rychel *et al.*, 2006). The conservation of cartilage matrix genes in invertebrates could be interpreted as evidence for an unexpectedly deep origin of cartilage, or may simply reflect the limited number of tools in the genetic toolkit for making cartilaginous tissues. According to the latter idea, the molecular program for chondrogenesis has a single origin, but the tissue itself may have evolved many times. Resolving this question will require comparative studies of the molecular mechanisms of chondrogenesis across

metazoa. In the next two sections, we review the diversity of cartilaginous tissues in vertebrates and invertebrates.

## 5.1. Cartilage variation within vertebrates

### 5.1.1. Tetrapods

Cartilage exists in a variety of forms in vertebrates (Fig. 2.2). In tetrapods, cartilage is broadly divisible into three major subtypes: hyaline cartilage, elastic cartilage, and fibrocartilage (Hall, 2005). *Hyaline cartilage* is the primary component of the endoskeleton and serves as the scaffold for bone that develops by endochondral ossification. Sometimes termed “true cartilage,” hyaline cartilage derives its structural integrity mainly from glycosaminoglycans and type II collagen fibrils. *Elastic cartilage*, such as that found in the mammalian ear pinnae and epiglottis, is also rich in glycosaminoglycans and collagen proteins, but additionally contains thick bundles of elastic fibrils and elastin-rich extracellular matrix (Naumann *et al.*, 2002). This combination of matrix proteins gives elastic cartilage the toughness of hyaline cartilage but with increased elasticity. *Fibrocartilage* is found at the attachment points of tendons and ligaments, in intervertebral disks, and at the pubic symphysis. Fibrocartilage matrix contains large amounts of type I collagen, which makes it both tensile and tough (Benjamin and Evans, 1990; Benjamin and Ralphs, 2004; Eyre and Wu, 1983). Even in tetrapods, some cartilage can demonstrate intermediate tissue properties that do not adhere to this tidy classification scheme. For example, secondary cartilage, which forms from osteoblast precursors at stressed joint regions, is similar to hyaline cartilage, but expresses high amounts of type I collagen (Fang and Hall, 1997; Fukada *et al.*, 1999; Fukuoka *et al.*, 2007; Ishii *et al.*, 1998).

### 5.1.2. Teleosts

Teleost fishes exhibit an even richer diversity of cartilage types (Fig. 2.2). According to one classification scheme, there are five “cell-rich” cartilages and three “matrix-rich” cartilages (Benjamin, 1989, 1990). The “cell-rich” cartilages, which are defined by cells or lacunae making up >50% of a cartilage tissue’s volume, include (1) hyaline-cell cartilage, (2) cell-rich hyaline cartilage, (3) fibrocell cartilage, (4) elastic/cell-rich cartilage, and (5) Schaffer’s Zellknorpel. *Hyaline-cell cartilage*, which is found in the lips, rostral folds, and other cranial cartilages, is characterized by compact chromophobic chondrocytes and hyaline cytoplasm with little matrix (Benjamin, 1989). Hyaline-cell cartilage is divisible into three subtypes; fibro/hyaline has greater quantities of collagen than elastin, elastic/hyaline contains more elastin in the matrix, and lipo/hyaline contains adipocytes as well as chondrocytes. *Cell-rich hyaline cartilage* is more cellular than hyaline-cell cartilage, with lacunae occupying more than half of the total volume. Parts of neurocranium and Meckel’s cartilage belong in this category

(Benjamin, 1990). *Fibrocell cartilage* is a highly cellular (nonhyaline) fibrocartilage that is rich in collagen, lacks a perichondrium, and is commonly found on articular surfaces. *Elastic/cell-rich cartilage*, which is usually found in the barbels and maxillary oral valves, is dense with elastin, the cells are not hyaline, and these elements are surrounded by a thick fibrous perichondrium (Benjamin, 1990). The fifth type of “cell-rich” cartilage is known as Schaffer’s Zellknorpel and occurs in teleost gill filament rays and the basal plate. Zellknorpel chondrocytes are more chromophilic than those of hyaline-cell cartilage and are shrunken within large lacunae (Benjamin, 1990).

The “matrix-rich cartilages” of teleosts are defined by cells or lacunae making up <50% total volume. In teleosts, like tetrapods, the “matrix-rich cartilages” are divisible into three subtypes (1) matrix-rich hyaline cartilage, (2) fibrocartilage, and (3) elastic cartilage. Each of these cell-rich and matrix-rich cartilages can be found in the cranial and postcranial skeletons, with the exception of the cranially restricted Zellknorpel (Benjamin *et al.*, 1992). Scleral cartilage is particularly interesting, as it has been described as a composite structure, in which a central zone of cell-rich hyaline cartilage is surrounded by a cortex of matrix-rich hyaline cartilage (Benjamin and Ralphs, 1991; Franz-Odenaal *et al.*, 2007). This classification system is based on histological/structural characters, and little is known about their molecular composition or development. The observation that teleosts have a broader variety of cartilage tissue types than do tetrapods may relate to the larger number of matrix (and other skeletogenic) genes that resulted from the teleost genome duplication event. Accordingly, the increased number of gene expression combinations that are possible in teleosts may underlie the diversity of cartilage types. Alternatively, similar patterns of gene expression in chondrogenic tissues may yield different structural and histological patterns due to differences in the local environment during chondrogenesis. Molecular characterization of the different cartilaginous tissues of teleosts is needed to uncover the developmental basis of their diversity.

### 5.1.3. Chondrichthyans

Chondrichthyan skeletons are almost entirely cartilaginous; however, their cartilage undergoes extensive mineralization (Dean and Summers, 2006; Eames *et al.*, 2007; Hall, 2005). The majority of the shark skeleton appears to be true hyaline cartilage, staining strongly for sulfated proteoglycans and type II collagen (Eames *et al.*, 2007). The cartilaginous nature of chondrichthyan skeletons is likely a derived condition that followed an evolutionary loss of bone (Fig. 2.2). Catsharks, for example, retain true bone in their neural arches, and the fossil record of sharks shows evidence of both exoskeletal and endochondral bones (Coates *et al.*, 1998; Kemp and Westrin, 1979; Moss, 1970, 1977; Peignoux-Deville *et al.*, 1982). Biochemical studies showed that shark and skate cartilage may contain type I collagen in addition to type II collagen (Mizuta *et al.*, 2003; Moss, 1977;

Rama and Chandrakasan, 1984); however, antibodies to type I collagen did not react to shark cartilage immunohistochemically (Eames *et al.*, 2007). It has been suggested that biochemical identification of type I collagen in shark cartilage may have resulted from contamination from shark bone (Eames *et al.*, 2007). Cartilage development within chondrichthyans has not received the level of scrutiny provided to teleost skeletal tissues, and a comprehensive and comparative analysis of gene expression, regulation and function is needed.

As an aside, the widely held belief that sharks do not develop tumors is false (neoplasias in sharks have been known for over 150 years) and there is no scientific basis to support the notion that consumption of crude shark cartilage affects tumor development in cancer patients (reviewed in Ostrander *et al.*, 2004). Some general features of cartilage (not restricted to sharks) that may contribute to the rarity of tumor invasion into cartilaginous tissues are that it is hypoxic, has poor vascularity, produces collagenase inhibitors, and may contain antiangiogenic factors.

#### 5.1.4. Cyclostomes

Cartilaginous skeletons are also present in both extant groups of jawless (agnathan) vertebrates, lampreys and hagfishes. Lamprey and hagfish have mucocartilage (Fig. 2.2) and were described as lacking collagen (Wright *et al.*, 2001). Instead, their matrix was reported to contain the elastin-like molecules *lamprin* and *myxinin*, respectively (Wright *et al.*, 2001). Recent molecular developmental studies have overturned the idea that agnathans lack collagenous cartilage by demonstrating that both lampreys and hagfishes do indeed have type II collagen-based cartilage (Ohtani *et al.*, 2008; Zhang and Cohn, 2006; Zhang *et al.*, 2006). Lamprey cartilages are found mainly in the cranial region. The postcranial skeleton is limited to paired axial cartilage nodules (termed arcualia) and caudal fin rays (Morrison *et al.*, 2000). In the head of larval lamprey, the proteoglycan-rich mucocartilage occurs as a transient, avascular cartilage that is surrounded by perichondrium (Hall, 2005). During metamorphosis, mucocartilage is transformed into the pial and tongue cartilages (Hall, 2005). In the nineteenth century, two kinds of cartilages, “soft” and “hard,” were identified in lampreys (Parker, 1883). The hard cartilage is similar structurally to mammalian hyaline cartilage. In hagfishes, cartilage is also present in the cranium and median fin rays, although they lack the paired arcualia found along the trunks of lampreys. Like lampreys, hagfish were reported to contain soft and hard cartilages (Cole, 1905). Cole (1905) described hagfish “soft” cartilage as containing large hypertrophic chondrocytes that stain with hematoxylin (blue) and are surrounded by a thin extracellular matrix, whereas “hard” cartilage contains smaller chondrocytes that are surrounded by an abundance of extracellular matrix. Biochemical analysis also supported the two types of hagfish cartilage, designated type I and

type II cartilage, with only type I containing myxinin and type II being more similar to adult lamprey cartilage (Wright *et al.*, 1984). Neither lamprey nor hagfish cartilage is mineralized, but lamprey cartilage can be calcified *in vitro* (Langille and Hall, 1988). Interestingly, calcified cartilage was reported in the fossil lamprey *Euphanerops*, suggesting that mineralized cartilage in this group persisted at least to the Devonian (Janvier and Arsenault, 2002). These recent analyses of extant and extinct agnathans suggest that cartilage containing high amounts of type II collagen and sulfated proteoglycans was present in the common ancestor of jawed and jawless vertebrates (Fig. 2.2).

## 5.2. Invertebrate cartilage

Cartilaginous tissues are not restricted to the vertebrates; examples of cellular and/or acellular cartilage exist in such diverse taxa as cephalochordates, hemichordates, annelids, mollusks, brachiopods, arthropods, and cnidaria (see Cole and Hall, 2004a for a detailed review). Some of these tissues bear striking similarities to vertebrate cartilage at the structural, morphological, and histological levels. In general, there are three kinds of cartilages found in invertebrates: central cell-rich cartilage, vesicular cartilage with large vesicles or vacuoles, and acellular cartilage. Within deuterostomes, fibrillar collagens are expressed in the developing acellular cartilage of hemichordates and cephalochordates, in the cellular cartilage and the notochord of cephalochordates, and in the notochordal sheath of urochordates (Rychel *et al.*, 2006; Wada *et al.*, 2006; Zhang *et al.*, 2006). Vesicular cartilage has been identified in polychaete worms, horseshoe crabs, and mollusks (Cole and Hall, 2004b). To some degree, the vertebrate notochord can be considered a vesicular cell-rich cartilage, since notochordal cells are vacuolated and surrounded by cartilage-like extracellular matrix containing type II collagen, type I collagen, type X collagen, aggrecan, and polysaccharides (Domowicz *et al.*, 1995; Eikenberry *et al.*, 1984; Linsenmayer *et al.*, 1986; Welsch *et al.*, 1991). How similar or different are the developmental processes and molecular mechanisms involved in chondrogenesis in invertebrates and vertebrates? The paucity of molecular and even embryological data on invertebrate cartilage development makes it difficult to answer this question. The structural similarities are striking, and given the conservatism of developmental evolution and the limited number of “toolkit genes,” it would be surprising if entirely different mechanisms were utilized to build this tissue type in different lineages. Nonetheless, the possibility of convergence using different mechanisms remains, and comparative analyses of chondrogenesis will be required to resolve this evolutionary mystery.



## 6. ELABORATING THE CHONDROGENETIC TOOLKIT: GENE/GENOME DUPLICATION AND THE ORIGIN OF COLLAGENOUS CARTILAGE

Given the dominant role that fibrillar collagens play in constructing the matrices of a diverse array of vertebrate connective tissues, it seems likely that expansion of this gene family would have been a critical step toward the evolutionary diversification of skeletal tissues. Molecular phylogenetic analyses of deuterostome collagens indicate that a gene ancestral to the vertebrate clade A collagens had arisen in chordates before the origin of vertebrates, but the duplication and divergence of clade A collagens (*Col1 $\alpha$ 1*, *Col1 $\alpha$ 2*, *Col2 $\alpha$ 1*, *Col3 $\alpha$ 1*, and *Col5 $\alpha$ 2*) and clade B collagens (*Col5 $\alpha$ 1*, *Col5 $\alpha$ 3*, *Col11 $\alpha$ 1*, and *Col11 $\alpha$ 2*) occurred within the vertebrate lineage (Boot-Handford and Tuckwell, 2003; Zhang and Cohn, 2006, 2008). A number of findings point to deep conservation of chondrogenic mechanisms, such as the evidence that horseshoe crab cartilage contains chondroitin-6-sulfate (Sugahara *et al.*, 1996) and that squid and cuttlefish cartilages may contain collagen, although these appear to be different than type II collagen (Bairati and Gioria, 2004; Bairati *et al.*, 1999; Kimura and Karasawa, 1985; Kimura and Matsuura, 1974). Fibrillar collagens also have been identified in cartilage-like tissues of protostomes, including sponge, sea urchin, abalone, and hydra. Similarities have been described between the sea urchin  $\alpha$ 1 and vertebrate  $\alpha$ 2(I) chains, and between hydra Hcol1 and vertebrate collagen type I/II (Deutzmann *et al.*, 2000; Exposito *et al.*, 1992). Indeed, some invertebrate cartilage-like tissues crossreact with antibodies against vertebrate types II, V, and X collagen, and proteoglycans (Bairati *et al.*, 1999; Cole and Hall, 2004a,b; Sivakumar and Chandrakasan, 1998), although published phylogenies of the collagen family suggest it unlikely that these vertebrate antibodies are detecting strict orthologs of Col2, Col5, or Col10 in invertebrates (Boot-Handford and Tuckwell, 2003; Rychel *et al.*, 2006; Wada *et al.*, 2006; Zhang *et al.*, 2006, 2007). Nonetheless, the fundamental structure of fibrillar collagens was established early in metazoan evolution (Boot-Handford and Tuckwell, 2003). The phylogenetic distribution of cartilage and cartilage-like tissues suggests that this tissue type evolved independently and multiple times in metazoans (Cole and Hall, 2004a), and while the evidence for convergent evolution precludes structural homologies of invertebrate and vertebrate cartilages, it does not rule out the possibility of homologous developmental mechanisms. The striking structural and molecular similarities between invertebrate and vertebrate cartilages, such as utilization of fibrillar collagens and chondroitin-6-sulfate, suggests that a common suite of developmental tools was used repeatedly by metazoans to generate cartilaginous tissues, much like the deeply conserved

eye development program involving Pax6 has been redeployed time and again to build eyes. The area of invertebrate cartilage biology is ripe for comparative studies using modern molecular developmental approaches.

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