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SOX9 Governs Differentiation Stage-Specific Gene Expression in Growth Plate Chondrocytes via Direct Concomitant Transactivation and Repression

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**Abstract**

Cartilage and endochondral bone development require SOX9 activity to regulate chondrogenesis, chondrocyte proliferation, and transition to a non-mitotic hypertrophic state. The restricted and reciprocal expression of the collagen X gene, Col10a1, in hypertrophic chondrocytes and Sox9 in immature chondrocytes epitomise the precise spatiotemporal control of gene expression as chondrocytes progress through phases of differentiation, but how this is achieved is not clear. Here, we have identified a regulatory element upstream of Col10a1 that enhances its expression in hypertrophic chondrocytes in vivo. In immature chondrocytes, where Col10a1 is not expressed, SOX9 interacts with a conserved sequence within this element that is analogous to that within the intronic enhancer of the collagen II gene Col2a1, the known transactivation target of SOX9. By analysing a series of Col10a1 reporter genes in transgenic mice, we show that the SOX9 binding consensus in this element is required to repress expression of the transgene in non-hypertrophic chondrocytes. Forced ectopic Sox9 expression in hypertrophic chondrocytes in vitro and in mice resulted in down-regulation of Col10a1. Mutation of a binding consensus motif for GLI transcription factors, which are the effectors of Indian hedgehog signaling, close to the SOX9 site in the Col10a1 regulatory element, also derepressed transgene expression in non-hypertrophic chondrocytes. GLI2 and GLI3 bound to the Col10a1 regulatory element but not to the enhancer of Col2a1. In addition to Col10a1, paired SOX9–GLI binding motifs are present in the conserved non-coding regions of several genes that are preferentially expressed in hypertrophic chondrocytes and the occurrence of pairing is unlikely to be by chance. We propose a regulatory paradigm whereby direct concomitant positive and negative transcriptional control by SOX9 ensures differentiation phase-specific gene expression in chondrocytes. Discrimination between these opposing modes of transcriptional control by SOX9 may be mediated by cooperation with different partners such as GLI factors.

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**Introduction**

Chondrogenesis and the formation of bone by endochondral ossification depend on progressive steps of cell differentiation. Mesenchymal cells condense and differentiate into chondrocytes in a pattern that will define the eventual shape of the different skeletal elements. These chondrocytes proliferate, mature, exit the cell cycle and become prehypertrophic. The differentiation program culminates in the terminal differentiation and apoptosis of post-mitotic hypertrophic chondrocytes [1]. This differentiation program is controlled by members of the SOX and RUNX families of transcription factors and the integration of multiple signaling pathways mediated by Indian hedgehog (Ihh), parathyroid hormone-related protein (PTHrP), Wnts, BMPs, and Notch (reviewed in [2]). PTHrP and Ihh are two important players which interact to form a feedback loop that controls the pace of the differentiation program [3].

Sox9 is essential for chondrogenesis and chondrocyte differentiation [4–6]. It is essential for mesenchymal condensation prior to chondrogenesis, and in its absence chondrocyte differentiation fails. Inactivation of Sox9 in chondrocytes at different stages of differentiation suggests that its expression is essential for the survival of chondrocytes so that they can progress to hypertrophy [5–7]. Mutations in Sox9 are associated with the human skeletal malformation syndrome, campomelic dysplasia, in which skeletal abnormalities can be attributed to the disruption of the chondrogenic differentiation program due to failure to express SOX9 target genes. Upon hypertrophy, chondrocytes down-regulate Sox9 expression [8,9], which is believed to mark the end of SOX9 control in the growth plate.

Despite the wealth of information about spatial and temporal gene expression patterns in the developing growth plate, it is not clear how transcriptional controls achieve appropriate and specific
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Author Summary

Chondrogenic differentiation is a key process in the formation of endochondral bone. Despite the wealth of information about gene expression patterns and signaling pathways important for this process, it is not clear how differentiation state-specificity of transcription is controlled. The transcription factor SOX9 regulates chondrocyte differentiation, proliferation, and entry into hypertrophy and is highly expressed in immature/proliferating chondrocytes. It directly transactivates Col2a1, enhancing this gene’s expression in immature/proliferating chondrocytes. The Col10a1 gene is specifically expressed in hypertrophic chondrocytes in which Sox9 is downregulated. How is differentiation phase-specific transcription of genes controlled in chondrocytes, particularly during hypertrophy? We found that SOX9 directly represses Col10a1 expression in immature/proliferating chondrocytes of the growth plate, so that its expression is restricted to hypertrophic chondrocytes. Discrimination of this concomitant opposing transcriptional control may involve cooperation between SOX9 and different partners such as GLI factors (effectors of hedgehog signaling). SOX9 control of chondrocyte maturation therefore may be integrated with hedgehog signaling. Mutations in human SOX9 cause the skeletal malformation syndrome campomelic dysplasia, which is attributed to the disruption of the chondrogenic differentiation program because of failure to express SOX9 target genes. This interpretation should be revised to include inappropriate expression of genes normally repressed by SOX9.

gene expression during chondrocyte differentiation. SOX9 activates many genes expressed in proliferating chondrocytes, including the extracellular matrix (ECM) genes Col2a1, Col9a1, Col11a2, Acan (aggrecan) and Cd274/Mat2 [10–15]. For the Col2a1 gene, which is expressed most strongly in proliferating chondrocytes, SOX9 directly transactivates the gene in vivo via a conserved enhancer sequence within the first intron [10,11].

The collagen X gene, Col10a1, is a hypertrophic chondrocyte specific marker. The specificity and reciprocity of Sox9 and Col10a1 expression epitomise the strict control of temporal and differentiation phase-specific gene expression in the growth plate. Col10a1 is ideal for studying transcriptional regulation because as well as its highly specific expression pattern, over-expression or loss-of-function does not disrupt chondrocyte differentiation. These properties simplify interpretation of changes in gene expression resulting from perturbing transcriptional control [16–18]. Here, we examined the transcriptional controls that restrict Col10a1 expression to hypertrophic chondrocytes. We found that SOX9 coordinates gene expression during chondrocyte differentiation through both transcriptional activation and repression. Discrimination between these opposing actions is probably achieved by cooperation between SOX9 and different partners such as GLI factors.

Results

Proliferating and hypertrophic chondrocytes show overlapping and different protein binding domains in the Col10a1 enhancer

Previous cell transfection studies identified an enhancer element upstream of human COL10A1 [19]. This element is highly conserved in mammals and corresponds to a 640 bp region between –4.3 and –3.6 kb of the mouse Col10a1 gene (designated element A) (Figure 1A and 1B). We used DNase I footprinting assays to test the configurations in which the element A sequences could be directly bound by nuclear factors derived from chondrocytes at different differentiation states (Figure 2A). Extracts from hypertrophic chondrocytes MCTs, but not fibroblasts COS-1 or osteoblasts MC3T3-E1, protected six blocks of sequence (H1–H6). Noticeably, four different blocks (P1–P4) that partially overlap H1–H4 were protected by extracts from the proliferating chondrocyte/chondrosarcoma cell line CCL (Figure 1C and Figure 2A). Since proliferating chondrocyte/chondrosarcoma cells do not express Col10a1 (Figure S1A), these results suggest that in these cells, the proteins that bind to element A may contribute to the repression of Col10a1.

SOX9 binds to Col10a1 element A in proliferating chondrocytes

We and others previously showed that SOX9 regulates COL2A1/Col2a1 gene via a functional in vivo binding site in the intron 1 enhancer element [10,11]. We identified the same SOX9-binding sequence within the Col10a1 element A (Figure 1C and Figure 2B). This site, COL2A1, lies on a region in block P3 that is not protected in hypertrophic chondrocytes, and is adjacent to a stretch of thymidine/guanine-rich (TG-rich) sequence. Electromobility shift assays revealed that SOX9 bound to this SOX9/TG-rich motif with a similar affinity as to the COL2A1 enhancer element (Figure S1C, S1E, S1F) [10] and the interaction involved dimeric binding (Figure 2C, cf. lane 3–4). SOX9 also interacted with the TG-rich motif but with a lower affinity than with the consensus SOX9 site. Mutation of the TG-rich motif reduced the overall SOX9 binding to the P3 element (Figure 2C, cf. lanes 6–10). The TG-rich motif resembles a RUNX binding consensus sequence, but we found that RUNX2 did not interact with this motif effectively compared with its binding to the RUNX site in the Bglap (osteocalcin) enhancer (Figure 2D). Chromatin immunoprecipitation (ChIP) assays using extracts from E13.5 mouse limb, a stage at which the cartilage anlagen is largely composed of immature chondrocytes, confirmed specific SOX9 binding to the Col10a1 element A and the Col2a1 enhancer in vivo (Figure 2E).

SOX9/TG-rich motif is required for appropriate Col10a1 expression

The paired SOX9 binding sequences in element A are separated by 4 bp, a distance similar to that between the paired SOX-like consensus sequences in Col2a1, Col9a1, and Acan that mediate transactivation of expression [15]. We tested the in vivo role of element A and the effects of SOX9/TG-rich motif mutations on the expression of Col10a1 mini-genes (Figure 3A) in transgenic mice. We have previously shown that a Flag-tagged Col10a1 vector Col10Flag [formerly known as FColX] is expressed in P10 hypertrophic chondrocytes [18]. Here, we show that in E15.5 humeri, the Col10Flag transgene was expressed in islands in prehypertrophic and hypertrophic chondrocytes in the upper hypertrophic zone (Figure 3B, c). In two independent mouse lines, a transgene comprising element A fused to the Col10Flag (Col10Flag-E) was expressed in a similar pattern as Col10Flag, but was significantly more strongly expressed than Col10Flag in all hypertrophic chondrocytes (Figure 3B, g), reflecting the enhancer activity of element A (see also Figure S2). However, mutation of the SOX9 site in element A (Col10Flag-EA1) resulted in marked expansion of the expression domain of the transgene, extending from the hypertrophic zone to the proliferating zone in the majority of transgenic fetuses (71.4%) (compare Figure 4, a with...
Figure 1. Conserved non-coding regions in COL10A1. (A) Global alignment of COL10A1 loci was performed using mammalian genomes. The translated regions in exons 2 and 3 of COL10A1 are highly conserved (deep blue). Element A of mouse Col10a1, which corresponds to the human enhancer, is located in the nearest conserved upstream non-coding region (pink). The untranslated regions (light blue) are poorly conserved in opossum. The mouse genome serves as the base sequence for alignment. Op: opossum; Ca: canine; Bo: bovine; Hu: human. (B) The 640 bp element A is located between −4286 and −3646 bp of mouse Col10a1. (C) Conserved non-coding regions in mammalian COL10A1. Alignment showed that the functional SOX9 binding site (COL2C1) is conserved in the mammalian COL10A1 enhancers together with the adjacent TG-rich sequence. The
Figure 3B, e and in almost all the Sox9-expressing chondrocytes in the rest (Figure 4, e). Expansion of transgene expression in proliferating chondrocytes was also noted but was less marked when the TG-rich motif in element A was mutated (Col10^Flag-E, EA2) (compare Figure 4, m and i with a and e). Mutation of either SOX9 or the TG-rich motif did not abrogate transgene expression in hypertrophic chondrocytes. Together, these observations suggest that element A contains both positive and negative regulatory sequences, and that mutations in the SOX9/TG-rich motif in element A might disrupt SOX9-mediated repression in immature chondrocytes.

SOX9 is a negative regulator of Col10a1

To test whether SOX9 negatively regulates Col10a1, we established a cell line from hypertrophic chondrocytes MCTs which expressed the Col10^Flag-E transgene at the non-permissive (growth-arrest) temperature (Figure 5A). Similar to previous findings for dedifferentiated chondrocytic cells MC615, over-expression of SOX9 in MCTs did not transactivate endogenous Col2a1 [20]. However, SOX9 over-expression significantly down-regulated expression of both endogenous Col10a1 and the exogenous Col10^Flag-E reporter (Figure 5B) supporting the notion that SOX9 is a negative regulator of Col10a1. To study the regulation in vivo, Sox9 was ectopically expressed in hypertrophic chondrocytes in mice. Mice expressing Cre recombinase inserted into the endogenous Col10a1 gene (Col10a1-Cre) [21] were crossed with transgenic mice carrying a single copy of a Cre-inducible Sox9-IRES-EF1 expression construct (Z/Sox9) [22] (Figure 5C). In Col10a1-Cre; Sox9 mice, Sox9 and the linked Eefp reporter gene were activated in the hypertrophic chondrocytes at E17.5 in the anterior ribs (Figure 5D, h, i). These mice displayed an expanded hypertrophic zone and reduced Col10a1 expression (Figure 5D, e, k). Interestingly, we also found that transcription of Cre from the Col10a1 locus was reduced in Col10a1-Cre;Z/Sox9 mice (Figure 5D, a, g). Col2a1 expression in Col10a1-Cre;Z/Sox9 mice hypertrophic chondrocytes was not up-regulated suggesting the reduction of Col10a1 expression in these cells was not because of a reversion to a more immature state (Figure 5D, d, j). In the ribs Runx2 was expressed predominantly in osteoblasts, the perichondrium flanking the hypertrophic chondrocytes, and in prehypertrophic chondrocytes (Figure 5D, f). Expression was low in hypertrophic chondrocytes. There was no significant change in Runx2 expression in prehypertrophic and hypertrophic chondrocytes in Col10a1-Cre;Z/Sox9 mice (Figure 5D, f). Collectively, these data suggest that SOX9 negatively regulates Col10a1 gene expression independent of Runx2.

GLI factors bind and regulate Col10a1 in proliferating chondrocytes

The specificity of SOX protein action is known to be achieved through interaction with cell-specific partners [23,24]. We questioned whether concomitant transactivation of Col2a1 and repression of Col10a1 by SOX9 in proliferating chondrocytes could be mediated by different combinations of cofactors. ChiP assays in E13.5 mouse limb chondrocytes or CCL cells revealed similar interactions of TRAP230/MED12, a mediator of SOX9 activity [25], and of TRPS1, a GLI3-interacting repressor [26,27], with both the Col10a1 element A and the Col2a1 enhancer (Figure 6A, upper panel). On the other hand, the transcriptional co-repressor, histone deacetylase HDAC4 [28] immunoprecipitated neither element. GLI1, GLI2 and GLI3 are effectors of Hh signaling which controls chondrocyte proliferation and maturation [29]. GLI1 is a transactivator expressed in proliferating chondrocytes and perichondrial tissue flanking the prehypertrophic and hypertrophic zones [30] whereas GLI2 and GLI3 can act as repressors and are predominantly expressed in non-hypertrophic chondrocytes and are down-regulated in hypertrophic chondrocytes [29,31]. Since there is a conserved GLI-binding site near the SOX9/TG-rich motif in the same footprint block P3 (Figure 1C), we examined whether GLI1, GLI2 and GLI3 can interact with the element A. Strikingly, while SOX9 bound to both the Col10a1 element A and Col2a1 enhancer, GLI2 and GLI3 associated with only Col10a1 element A (Figure 6A, lower panel). GLI3 interacted the most with element A, while GLI1 interaction was much less. Quantitative ChiP assays confirmed the preferential interaction (Figure 6B). From these results we hypothesized that GLI proteins may repress Col10a1 expression. To test this in vivo, we examined the impact on transgene expression of mutating the GLI-binding site in element A (Col10^Flag-EA3). Consistent with our hypothesis, the majority of fetuses (7 out of 10) expressing Col10^Flag-EA3 showed distinct islands of transgene misexpression in non-hypertrophic chondrocytes (Figure 6C, e, f). Mutating all three sites (GLI, SOX9, TG-rich) in the transgene (Col10^Flag-EA4) did not restrict the expansion of the expression domain to proliferating chondrocytes in all the expressing transgenic fetuses obtained (Figure 6C, i, j). Indeed in the majority of these expressing fetuses (3 out of 5), transgene expression extended throughout the entire cartilage zones. Thus mutation of the GLI site alone had a similar derepressing effect as mutating the SOX9/TG-rich motif and mutating all the motifs did not restrict expression but resulted in more extensive mis-expression. This is consistent with a model whereby SOX9 and GLI act cooperatively to repress Col10a1 transcription.

To assess whether the cooperation of SOX9 and GLI2/3 is a potential common mechanism for restricted or preferential gene expression in hypertrophic chondrocytes, we searched in silico for this configuration of binding sites in genes, other than Col10a1, that have strong and specific up-regulation in hypertrophic chondrocytes (HC genes) in the growth plate. Six of 11 HC genes analyzed, namely Col11a1, Bmp2, Htap4, Mef2c, Runx2, and Sox4, possess the linked SOX9 and GLI sites (<100 nt spacing) in the inter- or intragenic conserved non-coding regions (Figure 7A and Figure S3). In contrast, these sites were absent from most of the genes tested (12 out of 14) that were expressed in proliferating but not (or down-regulated) in hypertrophic chondrocytes (PC genes). These include known SOX9 targets: Col2a1, Col9a1, Col11a2, Acan, and Mait (see Figure 7A legend for all negative genes). The exceptions were Sox3 and Sox6 (Figure 7A and Figure S3). To investigate whether the over-representation of linked SOX9-GLI sites in the HC genes but not the PC genes occurs by chance, we performed a hypergeometric test to calculate the probability of finding 6 or more SOX9-GLI site-containing genes out of 11 genes randomly sampled from the mouse genome. For the HC genes, the results showed that the occurrence of 6 or more genes with associated conserved SOX9-GLI sites is unlikely to occur by
chance ($p = 0.0000201$) (Figure 7B). For the PC genes, the $p$-value was 0.17, which is comparable to random occurrence. Furthermore the frequency of the presence of SOX9-GLI sites for HC genes (6/11) was significantly higher than that for PC genes (2/14) (Fisher’s test $p = 0.043$, one tailed). This suggests that the linked SOX9-GLI sites are preferentially associated with the HC genes.
Discussion

The positive and negative mechanisms mediating the stage-specific transcription of genes within the growth plate are not well defined, partly because of the difficulty in distinguishing direct effects on transcription from the consequences of abnormal differentiation. In this study we have exploited the specificity of Col10a1 expression in hypertrophic chondrocytes and the fact that manipulating its expression in vivo has no overt effect on differentiation, to dissect these transcriptional controls. We provide new insight into how differentiation stage-specific gene expression is achieved in the growth plate, presenting in vitro and in vivo evidence that SOX9, in addition to its known role as a transactivator of many genes preferentially expressed in non-hypertrophic chondrocytes, such as Col2a1, directly represses expression of Col10a1 at a stage prior to the onset of hypertrophy and subsequently in proliferating chondrocytes. This discovery extends our understanding of the mecha-

Figure 3. Element A enhances Col10a1 transgene expression in the growth plate. (A) Diagram showing the Flag-tagged Col10a1 mini-genes for transgenesis. The constructs included all introns and a 5' flanking region up to -2.07 kb (green). At the 5' end, the constructs were combined with the 640 bp element A (orange) containing wild-type sequence (E). (B) The expression pattern of the Flag-tagged Col10a1 mini-genes (a,e,i) was compared with that of endogenous Col10a1 (b,f), Runx2 (c,g,k), and Sox9 (d,h,l) by in situ hybridization of proximal humerus in E15.5 expressing fetuses. (a–d) Tissue-specific Col10a1 expression in hypertrophic zone of non-transgenic littermate (NT) was shown. (e–h) In the absence of element A, patchy expression of the mini-gene was observed in prehypertrophic and upper hypertrophic chondrocytes. (i–l) Addition of element A resulted in marked up-regulation of mini-gene expression in the whole hypertrophic zone (*). Since expression of Col10a1 was used as readout of derepression, Runx2 was used as an alternative marker of hypertrophic chondrocytes. In addition to hypertrophic chondrocytes, expression of Runx2 was noted in the trabecular bone and in the prehypertrophic chondrocytes. The prehypertrophic and hypertrophic zones (encircled) were identified based on Runx2 expression. PC, proliferating chondrocytes; PHC, prehypertrophic chondrocytes; HC, hypertrophic chondrocytes.

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Figure 4. Mutation of SOX9 binding consensus results in derepression of Col10a1 transgene expression in vivo. The expression pattern of mutant Flag-tagged Col10a1 mini-genes, in which the SOX9 site (Col10Flg-EΔ1) or the TG-rich motif (Col10*Flg-EΔ2) within the element A was mutated, was examined by in-situ hybridization of proximal humeri in E15.5 expressing fetuses. In a major (5/7) portion of Col10Flg-EΔ1 fetuses (a–d), the expression in the proliferating zone (*) was relatively higher than in the hypertrophic zone. In a minor (2/7) portion (e–h), the expression was predominant in nearly all immature chondrocytes (*). For Col10*Flg-EΔ2, a minor (2/6) portion of fetuses (m–p) showed up-regulated expression in the non-hypertrophic zone (*), while a major (4/6) portion showed relatively slight mis-expression (i–l). The prehypertrophic and hypertrophic zones are encircled. PC, proliferating chondrocytes; PHC, prehypertrophic chondrocytes; HC, hypertrophic chondrocytes.

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Figure 5. SOX9 directly represses Col10a1 in hypertrophic chondrocytes. (A) Clonal cell line MCTs-F expressing the Col10Flag-E was established from MCTs. (a) Immunohistochemistry indicated up-regulated Flag-tagged collagen X in growth arrested MCTs-F cells. (b) Flag signal in the cytosolic vesicles. (B) MCTs-F cells transfected with SOX9 expression vector (pSG-Sox9), or empty vector (pSG5). Expression of Col10a1 and Col10a1-Flag (36 bp longer in amplicon) was significantly reduced upon exogenous Sox9 expression (*, p<0.02). No RNA (−) or RNA from E16.5 Col10Flag-E expressing fetus (+) was used as control. (C) Strategy for activating ectopic Sox9 expression in hypertrophic chondrocytes. The pZ/Sox9
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isoforms by which SOX9 controls chondrocyte differentiation phase-specific gene expression.

We have identified a conserved regulatory sequence, element A, that acts as an enhancer of Col10a1 expression in both cultured cells and in vivo. This element contains a SOX9 binding sequence that, when bound by SOX9, represses Col10a1 expression in immature and proliferating chondrocytes. Since Sox9 is expressed in non-hypertrophic chondrocytes but not in hypertrophic chondrocytes, this repressive action of SOX9 restricts Col10a1 expression to hypertrophic chondrocytes.

SOX9 has been proposed to direct chondrogenic fate in osteochondroprogenitor cells in part by interacting with RUNX2 [32,33]. SOX9 may inhibit chondrocyte hypertrophy in part via activation of Bapts1 which represses Runx2 [34,35]. Previous in vitro and in vivo studies suggest that Col10a1 expression is regulated positively by Meis2, Runx2/Chp1a, and AP-1 members, which are expressed in hypertrophic chondrocytes [19,36–38]. RUNX2 has been shown to directly regulate the expression of Col10a1 [37].

The element A that we identified contains no conserved consensus RUNX site. The RUNX2 site revealed by Zheng et al. [37] is located within a poorly conserved region outside the element. Our data showed that the ectopic expression of Col10a1 in transgenic mice [38] can down-regulate Col10a1 expression in primary costal chondrocyte culture, and that over-expression of Sox9 can down-regulate it [35]. These contradictory results may be related to the incomplete elimination of SOX9 protein and the known dosage dependent requirement of SOX9 action. A role for SOX9 as transcriptional repressor of Col10a1 in non-hypertrophic chondrocytes is consistent with the observation that Col10a1 expression was up-regulated in cartilage isolated from Sox9 haploinsufficient campomelic dysplasia patients [33].

How may SOX9 act both as a transactivator and a repressor in non-hypertrophic chondrocytes? It has been proposed that interactions between specific partner factors stabilize SOX protein binding to DNA and hence regulate target selection [24], thereby determining cell specification, as exemplified by Sox9 in embryonic stem cells and other systems [45]. Such selective cooperation of protein binding partners may mediate the concomitant positive and negative regulation of SOX9 target genes in the same cell that contributes to specification of the differentiation state (Figure 8). As illustrated in the schematic (Figure 8), we propose that SOX9 mediates repression of Col10a1 in proliferating chondrocytes by selective cooperation with GLI factors. Together with its role in activating Col2a1 and other matrix genes, SOX9 therefore plays an important role in maintaining chondrocytes in an immature non-hypertrophic state.

RUNX2 by contrast promotes chondrocyte hypertrophy.

SOX9 cannot regulate chondrocyte differentiation appropriately without sonic hedgehog (Shh), which mediates the generation of chondrogenic precursor cells [46], and Indian hedgehog (Ihh), which regulates their proliferation and maturation [47]. GLI proteins are the effectors of Hh signaling. Double knockout mutants indicate that GLI2 has overlapping functions with GLI1 and GLI3 in skeletal and CNS development [48,49]. Binding of Hh to its receptor, Patched, blocks the proteolytic processing of the GLI transcription factors from active (GLIA) to repressive (GLIR) forms, and the balance between these forms modulates hedgehog target gene expression [50]. In the growth plate, GLI2A can positively regulate chondrocyte hypertrophy and control vascularization of the hypertrophic cartilage in endochondral ossification [29,51]. GLI3, which acts mainly as a repressor, has been suggested to inhibit chondrocyte hypertrophy [29,52] and it is interesting that the highest interaction of element A was with GLI3. Mau et al. reported that GlI2/3 null mutations altered the expression domain of collagen X, but it was not possible to distinguish whether this was due to a direct effect on Col10a1 transcription or more general perturbation of hypertrophy [29].

How the GLI factors interact with other regulatory factors or genes in the chondrocyte differentiation program is not clear. Our results are consistent with cooperation between SOX9 and the Hh signaling pathway and suggest that SOX9 acts in synergy with GLI2 and GLI3, probably their repressive forms GLIR, to repress transcription in chondrocytes. Thus, reduced synergy between GLIR and SOX9 may explain the accelerated chondrocyte hypertrophy seen when Ptk1 is inactivated [53].

Over-representation of the SOX9-GLI paired consensus in a number of genes that are preferentially expressed in hypertrophic chondrocytes and
Figure 6. GLI as SOX9 partner in Col10a1 repression. (A) ChIP assays with CCL cells (upper panel) and E13.5 mouse limbs (lower panel) using various antibodies. The products were amplified with primers for element A of Col10a1 or enhancer element of Col2a1 in intron 1. Extract was immunoprecipitated with rabbit IgG or without antibody (−) as negative reference. Extract was directly used in PCR as positive control (input). (B) The
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specific interaction of GLI with Col10a1 element A was validated in CCL cells by quantitative ChIP assay with real-time PCR. The degree of enrichment was calculated by normalization of readouts to that of IgG control. (C) The expression of Col10a1 mini-genes with mutation in the GLI site was examined by in-situ hybridization of proximal humeri in E15.5 fetuses. Islands of misexpression (Flag and Col10a1, arrows) were detected in the non-hypertrophic chondrocytes in most (7/10) expressing fetuses (e–h), while the rest showed milder mis-expression (not shown). For the transgene with a mutation in both the GLI site and the SOX9/TGF-rich motif (Col10a1SRE.EA4), the majority of expressing fetuses (3/5) showed strong and extensive mis-expression (*) (i–l), while the rest showed relatively little mis-expression. Non-transgenic littermate (NT) is shown as control (a–d). The prehypertrophic and hypertrophic zones are encircled. PC, proliferating chondrocytes; PHC, prehypertrophic chondrocytes; HC, hypertrophic chondrocytes.

A different mode by which SOX9 may repress gene expression in chondrocytes has been proposed by Huang et al. [55]. In their model, SOX9 negatively regulates Ccn2 expression in non-hypertrophic chondrocytes via binding to overlapping binding sites for SOX and TCF/LEF, thereby interfering with binding of a TCF/LEF/β-catenin transactivation complex. Reduction of SOX9 upon hypertrophy allows this TCF/LEF/β-catenin complex to activate Ccn2 expression [55]. However, Ccn2 is also expressed in resting zone chondrocytes in the epiphyses of the growth plate and it is not clear why SOX9 does not repress the gene in these cells. We identified a conserved TCF consensus site in Col10a1 element A, but this is unlikely to interfere with SOX9 binding since it is located 59 bp downstream of the functional SOX9-GLI motif, unlike in Ccn2 where the SOX and TCF/LEF sites overlap (Figure 1C). This suggests that the model proposed by Huang et al. does not apply to Col10a1 element A-mediated repression of transcription.

It is also possible that SOX9 and GLI cooperate to activate or repress transcription depending on context. While our data implicate a cooperation of SOX9 with GLI factors in transcriptional repression, this association between SOX9 and GLI may not be restricted to negative regulation. Amano et al. have recently shown that SOX9可以直接 represses Vegf in cultured primary chondrocytes [44] by interacting with the 5′ untranslated region of the gene. This agrees with our findings of a repressive role of SOX9, however, we found no linked SOX9-GLI binding sites near the Vegf gene and a recent SOX9-ChIP-on-chip study reported no in vivo interaction in Vegf exon 1 [54].

Validation of these different modes of cooperative regulation by SOX9 and GLI factors in vivo would require the generation and analyses of compound null or conditional knockout mutants; however, the consequent dysregulation of chondrogenesis and impact on cell survival would make it impossible to distinguish changes in transcriptional control from effects on differentiation. For example, Sox9 is essential for chondrogenesis and Sox9 conditional null chondrocytes undergo apoptosis and as a consequence, hypertrophy with the characteristic activation of Col10a1 expression, fails to occur [4,7,59]. Because inactivation of Col10a1 does not disrupt the chondrogenic program, it provides an ideal system and tools to interrogate the transcriptional controls governing specificity of gene expression within the growth plate, independent of changes in chondrocyte differentiation. Important questions to be addressed in future are the identities and diversity of SOX9 partnerships and how the activity of SOX9 and its partners is modulated. In early myogenic differentiation, Sox9 and Smad3 have been reported to prevent premature expression of σ-sarcoglycan gene expression by synergistic repression in a transforming growth factor β dependent manner [60] suggesting negative transcriptional regulation by SOX9 and its partners may be more common. The transactivation of Mital1 in chondrocytes by SOX9 can be modulated by combined action of L-SOX5, SOX6 and NFI factors [61]. Whether control of transcription by the SOX9-GLI partnership can be modulated by additional factors is an important question to be addressed in future.

In summary, our study implicates a complex regulatory function for SOX9 whereby it acts with different partners to orchestrate activation and repression of transcription in the chondrogenic differentiation pathway. Mutations in human SOX9 cause the skeletal malformation syndrome campomelic dysplasia which is attributed to the disruption of the chondrogenic differentiation program because of failure to express SOX9 target genes. This interpretation may need to be revised to include inappropriate expression of genes normally repressed by SOX9.

Materials and Methods

Bioinformatics analysis

Col10a1 sequences were aligned using LAGAN and PipMaker. The conserved SOX9 binding sites (COL2C1 and COL2C2) [10] were identified by rVISTA. The UCSC Mouse 30-Way Multiz Alignment data and a custom Perl script were used to identify human-mouse perfectly conserved SOX9, GLI, and TCF sites with a maximum spacing of 100 bp in the inter- and intra-genic non-coding regions. Conservation percentage of sequence span-
Figure 7. Differential presence of SOX9-GLI sites in proliferating and hypertrophic phase-specific genes. (A) Position, orientation, and spacing of the conserved linked SOX9 (COL2C1 and COL2C2) and GLI binding sites within the inter- and intra-genic regions of genes preferentially expressed in proliferating (PC) or hypertrophic (HC) chondrocytes. Numbers between the sites indicate the length of nucleotide spacing. Conservation indicates the percentage of nucleotides and species conserved in the alignments spanning the SOX9 and GLI sites. The alignments were based on multiz30way in UCSC genome browser and were simplified to only include sequences from mouse (M), human (H), chimpanzee (P), canine (D), bovine (C), and opossum (O) genome. Genes tested but found negative include HC genes Bmp6, Cdkn1c, Loxl4, Spp1, and Vegfa as well as PC genes Acan, Bmp7, Col2a1, Col9a1, Col9a2, Col9a3, Col11a1, Col11a2, Fgfr3, Fos, Mia1, and Sox9. (B) Left panel: Venn diagram showing frequency of genes in the genome that contain perfectly conserved SOX9, GLI, or linked SOX9-GLI sites within the inter- and intra-genic regions. SOX9 and GLI sites co-exist but are not linked in the majority of genes. Right panel: Number of HC, PC and all genes in the mouse genome with conserved SOX9-GLI sites and p-values from hypergeometric test (HT, for the over-representation of positive HC and PC genes compared to the genome) and one-tailed Fisher’s exact test (FET, for the difference in number of positive genes between HC and PC group). The test was based on all genes in the mouse genome (32,120 genes). See also Figure S3 for alignment data of the linked sites.

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ning the SOX9 and GLI sites was calculated based on the number of perfectly matched nucleotides among all the aligned species (mouse, human, chimpanzee, canine, bovine, and opossum). From the 32,120 genes in the mouse genome, the number of genes containing conserved linked SOX9-GLI sites was found and used as the reference frequency of such genes in the genome. Whether the frequency of the presence of conserved SOX9-GLI sites in HC or PC genes exceeded this reference frequency was assessed by the hypergeometric distribution. The difference in the frequency of the presence of SOX9-GLI sites in the HC and PC genes was assessed by the Fisher's exact test.

Cell culture and transfection

Hypertrophic chondrocyte cell line MCTs (gift of Ve´ronique Lefebvre [62]) was transfected with pCol10Flag-E, pSG-Sox9 (gift of Peter Koopman), or pSG5 expression vector using Fugene 6 (Roche). Expression of the exogenous collagen X from pCol10Flag-E in MCTs cells was examined by immunohistochemistry using anti-Flag M2 antibody (Sigma). CCL (gift of James Kimura [63]), MCT3T3-E1, and COS-1 cells were cultured in DMEM (Invitrogen) containing 10% FCS (Wisent) at 37°C. MCTs cells were normally cultured at 32°C for expansion. Prior to assays, MCTs cells were cultured at 37°C for 1 day to induce growth arrest [62].

DNase I footprinting

A 300 bp DNA fragment within element A, corresponding to −4240 to −3935 bp of the mouse Col10a1, was used as probe. [γ-32P]ATP-labeled probes were incubated with nuclear extracts from CCL, MCTs, MCT3T3-E1, or COS-1 cells in the presence of

Figure 8. A model for SOX9 control of differentiation phase–specific gene expression in growth plate chondrocytes. As chondrocytes mature during endochondral bone formation, the concomitant transactivation and repression of transcription of differentiation stage-specific genes by SOX9 is exemplified in Col10a1 and Col2a1. Sox9, its transactivation target Col2a1, as well as GLI2 and GLI3 are preferentially expressed by non-hypertrophic chondrocytes. GLI3 is down-regulated when chondrocytes become prehypertrophic, while Sox9 and GLI expression is down-regulated when chondrocytes reach hypertrophy [8,9,29]. Regulation of both Col10a1 and Col2a1 involves dimeric binding of SOX9. The GLI factors, and possibly others, depending on the spatial context of their binding sites, are involved in the differential transcriptional control. MED12 and TRPS1 [25–27] act as common mediators of transcriptional control. In proliferating chondrocytes, Col10a1 is repressed through binding of SOX9 and GLI2/3. SOX9 negatively regulates Runx2 expression via Bapx1 in proliferating chondrocytes [34,35]. When chondrocytes mature and become prehypertrophic, RUNX2 binding to SOX9 may reduce the amount available for Col10a1 [33] and, as GLI3 levels reduce, Col10a1 is partially released from repression. Col2a1 transcription may be maintained due to stabilization of SOX9 binding by SOX5/6 [15]. In hypertrophic chondrocytes, as SOX9-associated machinery diminishes, Col10a1 is completely de-repressed and is highly transactivated by factors such as RUNX2, MEF2C, AP-1. Concomitantly Col2a1 expression is markedly decreased. SOX9 therefore controls differentiation-phase specific gene expression in chondrocytes through direct and indirect mechanisms. PC, proliferating chondrocytes; PHC, prehypertrophic chondrocytes; HC, hypertrophic chondrocytes.

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of poly(dA-dT) at room temperature, followed by DNase I digestion and denaturing PAGE.

Electromobility shift assays
COS-1 nuclear extracts over-expressing SOX9 and RUNX2 were pre-incubated with poly(dI-dC) or poly(dG-dC) at room temperature, followed by reaction with \( [\gamma-\text{P}] \text{ATP} \) labeled probes with or without the presence of nucleotide competitors, or antibodies for SOX9 (gift of Peter Koopman [64]) and OSF2/RUNX2 (gift of Gerard Karsenty [65]), then subjected to non-denaturing PAGE at room temperature. The sequences of oligonucleotide COL2C1 and OSE2 were as previously described [10,65].

Col10\textsuperscript{Flag} transgenic mice
The mouse Col10\textit{a1} element A, a 640 bp fragment located between \(-4.2\) and \(-3.6\) kb, was cloned at the 5' end of the pCol10\textsuperscript{Flag} previously known as pCoxA [15] consisting of \(-2070\) to \(+7176\) bp mouse Col10\textit{a1} genomic sequence to generate pCol10\textsuperscript{PosE}. The SOX9, TG-rich motif, and GLI binding sites in pCol10\textsuperscript{PosE} were mutated to generate the single site mutants – respectively pCol10\textsuperscript{PosE-EA1}, pCol10\textsuperscript{PosE-EA2}, and pCol10\textsuperscript{PosE-EA3}. All of these 3 motifs in pCol10\textsuperscript{PosE} were mutated to generate pCol10\textsuperscript{PosE-EA4}.

Col10\textit{a1-Cre}/Z/Sox9 compound mutants
A 4.8 kb fragment of mouse genomic DNA (from 82 bp upstream of the start of transcription of Sox9 to 1119 bp downstream of the polyadenylation sequences), including the Sox9 coding region, its two introns and 1.1 kb of 3' flanking DNA, together with an IRES2-EGFP (Clontech) sequence inserted between the Sox9 stop codon and the polyadenylation site (at \(+3237\) bp), was cloned downstream of the loxP-flanked \(**bgeo*/3xpA of the pCall2 vector (gift of Andras Nagy [66]) to create the pZ/Sox9 vector. pZ/Sox9 was transfected into 129/SvEv-derived L4 embryonic stem (ES) cells by electroporation and ES clones containing a single copy of the transgene were injected into blastocysts followed by crossing of chimeras with C57BL/6N mice to generate the mouse line Z/Sox9. A mouse line carrying a single copy of pZ/Sox9 was generated which was then crossed with Col10\textit{a1-Cre} mice [21] to obtain compound mutants.

Chromatin immunoprecipitation
CCL cell lysates or 13.5 dpc mouse limb tissue lysates were cross-linked followed by lysis and sonication to yield 200–500 bp DNA fragments then immunoprecipitation with antibodies against acetylated histone H3/H4 (Ac-H3, Ac-H4) (Upstate), HDAC4 (Abcam), GLI1, GLI2, GLI3 (all from Santa Cruz), SOX9 (gift of Robin Lovell-Badge [67]), TRAP230/MED12 (gift of Robert Roeder [25]), or TRPS1 (gift of Yasuteru Muragaki [26]). The target elements in Col10\textit{a1}, Col2\textit{a1}, or C\textit{ygb} genes were amplified by real-time or standard PCR.

Gene expression analysis
\textit{In-situ} hybridization was performed as previously described [9]. The probes used were pRK26 for Col10\textit{a1} [68], pWF21 for the Flag sequence [18], pB8 for full-length Sox9 (gift of Peter Koopman), pBS-Cba1-S for full-length Runx2 (gift of Gerard Karsenty), pWF98 for full-length \( Eg\)g, pBSH-Cre-frag for \( C\)se (gift of Andrew Groves), and pNJ61 for Col2a2 [9]. Gene expression in cell culture was analyzed by RT-PCR.

For additional details of all experiments, see the Text S1.

Supporting Information

Figure S1 Additional gene/protein expression data and EMSA. (A) Expression of Col2\textit{a1} and Col10\textit{a1} in CCL, MCTs, and MC3T3-E1 was analyzed by RT-PCR. Controls were no RNA (−) or RNA from mouse E17.5 embryo (+). Expression of Col10\textit{a1} was found only in MCTs. (B) Western blot analysis showed that both SOX9 and RUNX2 were highly expressed in CCL but weakly in MCTs. (C) Expression of SOX9 in nuclear (lane 3) and cytoplasmic (lane 4) fractions of pcDNA-Sox9 transfected COS-1 cells was compared with CCL (lane 1) and untransfected COS-1 (lane 2) nuclear extracts by Western blotting. (D) Expression of RUNX2 in nuclear (lane 3) and cytoplasmic (lane 4) fractions of pcDNA-Chba1 transfected COS-1 cells was verified by Western blotting. (E) A diagram showing the sequences of oligonucleotides which contained wild-type, mutant SOX9 and/or TG-rich motif for EMSA. Only the mutated nucleotides were shown in the sequence of competitors. (F) Intact DNA-binding property of SOX9 in expressing nuclear extract was tested by its interaction with the COL2A1 enhancer probe (Col2C1) in EMSA, in which the retarded band was challenged with SOX9 antibody (lane 4), unlabeled COL2C1 (lane 5–6), or Col10\textit{a1} element A C10C1 oligonucleotides (lanes 7–8). The triangles represent increasing concentration of competitors from 10× (lane 5,7) to 100× (lane 6,8) excess.

(TIF)

Figure S2 In \textit{vivo} transcriptional activity of Col10\textit{a1} element A. (A) Expression pattern of Col10\textit{PosE} in E15.5 transgenic fetus (mid-sagittal plane) examined by \textit{in-situ} hybridization using digoxigenin-labeled probes. Flag expression was detected in the hypertrophic chondrocytes of cervical pedicle (a) and developing vertebrae (b). Weak expression was detected in the trabecular bone of palate (c). No expression was found in the nucleus pulposus (np) of the intervertebral disc (b), immature costal cartilage (g, cc), brain (b), hair papillae (i), lung (m), aorta (o), or myocardium (o). Expression of Col10\textit{a1} is shown for comparison (d–f, j–l, p–r). No expression was found in erythrocytes or nucleated blood cells (* in n and q). (B) In Col10\textit{PosE} transgenic fetus, strong expression of Flag was found in the ossifying zone of pedicle (a, circled) and the trabecular bone of palate (b, circled). Weak signal was detected in the prehypertrophic zone of the pedicle cartilage (a, arrow). No expression was identified in tissue other than cartilage and bone. Expression of Col10\textit{a1} is shown for comparison (c–d).

(TIF)

Figure S3 Alignment data from SOX9-GLI site analysis. Multispecies alignment of regions spanning the linked SOX9-GLI sites are shown along with chromosomal location (Chr), identical nucleotides (.), insertion or deletion (-), and unaligned positions (=).

(PDF)

Text S1 Additional details of experiments.

(DOC)

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References

Analyzed the data: VYLL BG KHKL IGM SLW TYKA ACYM DC KSEC. Wrote the paper: VYLL KSEC.


