SMAD3 and SMAD4 have a more dominant role than SMAD2 in TGFβ-induced chondrogenic differentiation of bone marrow-derived mesenchymal stem cells

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To improve cartilage formation by bone marrow-derived mesenchymal stem cells (BMSCs), the signaling mechanism governing chondrogenic differentiation requires better understanding. We previously showed that the transforming growth factor-β (TGFβ) receptor ALK5 is crucial for chondrogenesis induced by TGFβ. ALK5 phosphorylates SMAD2 and SMAD3 proteins, which then form complexes with SMAD4 to regulate gene transcription. By modulating the expression of SMAD2, SMAD3 and SMAD4 in human BMSCs, we investigated their role in TGFβ-induced chondrogenesis.

Activation of TGFβ signaling, represented by SMAD2 phosphorylation, was decreased by SMAD2 knockdown and highly increased by SMAD2 overexpression. Moreover, TGFβ signaling via the alternative SMAD1/5/9 pathway was strongly decreased by SMAD4 knockdown. TGFβ-induced chondrogenesis of human BMSCs was strongly inhibited by SMAD4 knockdown and only mildly inhibited by SMAD2 knockdown. Remarkably, both knockdown and overexpression of SMAD3 blocked chondrogenic differentiation. Chondrogenesis appears to rely on a delicate balance in the amount of SMAD3 and SMAD4 as it was not enhanced by SMAD4 overexpression and was inhibited by SMAD3 overexpression. Furthermore, this study reveals that TGFβ-activated phosphorylation of SMAD2 and SMAD1/5/9 depends on the abundance of SMAD4. Overall, our findings suggest a more dominant role for SMAD3 and SMAD4 than SMAD2 in TGFβ3-induced chondrogenesis of human BMSCs.

Joint injuries frequently cause articular cartilage lesions that do not heal well in adults as articular cartilage has poor regenerative capacity. Since bone marrow-derived mesenchymal stem cells (BMSCs) can chondrogenically differentiate, they are promising for cell-based regeneration of damaged articular cartilage. Chondrogenic differentiation is potently induced by transforming growth factor-β (TGFβ)1–3. However, cartilage tissue formed by BMSC-derived chondrocytes does not completely resemble native articular cartilage as these cells tend to lose the chondrogenic phenotype due to hypertrophic differentiation4–8. Therefore, understanding how mediators of TGFβ signal transduction govern chondrogenesis will be crucial to improve cartilage regeneration by BMSCs.

Binding of TGFβ to its type II serine/threonine receptor TGFBR2 activates the type I receptor TGFBR1, also termed activin receptor-like kinase 5 (ALK5), to intracellularly phosphorylate receptor-regulated SMAD proteins (R-SMADs). Activated R-SMADs form complexes with co-factor SMAD4 and these complexes translocate to the nucleus where they regulate gene transcription9. Previously, we demonstrated that either blocking the kinase activity or downregulating the expression of ALK5 in human BMSCs inhibits chondrogenesis6,10, indicating an important role for TGFβ signaling via ALK5 in chondrogenic differentiation of BMSCs.

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ALK5 can activate two R-SMADs, SMAD2 and SMAD3, which share similar structures including a Mad-Homology 1 (MH1) domain, linker region and MH2 domain. Despite their similarities, SMAD2 and SMAD3 have a differential role in TGFβ signal transduction. Whereas Smad2 knockout mice die during gastrulation, Smad3 knockout mice develop cartilage and survive for several months after birth. Moreover, SMAD3, but not SMAD2, is involved in enhanced transcriptional activity of SRY (Sex Determining Region Y)-Box 9 (SOX9); a master regulator of chondrogenesis, in human mesenchymal stem cells. In contrast to SMAD3, SMAD2 lacks the MH1 domain. Therefore, SMAD2 cannot bind DNA without complex formation with SMAD4, which may explain the differential effects of SMAD2 and SMAD3. However, whether SMAD2 and SMAD3 have a different function during TGFβ3-induced chondrogenic differentiation of human BMSCs remains largely unknown. Also the specific role of SMAD4 in chondrogenesis of human BMSCs has not been investigated. In mice, deletion of Smad4 causes early embryonic death. Therefore, tissue-specific Smad4 knockout mice have been generated. Conditional deletion of Smad4 in the limb bud mesenchyme of mice leads to an absence of cartilage elements prefiguring the limb skeleton, indicating that SMAD4 is required for cartilage formation. Furthermore, chondrocyte-specific Smad4 knockout mice exhibit dwarfism and impaired growth plate organization. Similarly, Smad3 knockout mice have forelimb malformations, are smaller than wild-type mice and they develop spontaneous joint degeneration resembling the degenerative joint disease osteoarthritis in humans. In humans, mutations in SMAD3 lead to skeletal anomalies and early-onset of osteoarthritis. Moreover, SMAD3 is required for TGFβ-mediated suppression of hypertrophic differentiation of human articular chondrocytes. Although SMAD3 does not appear directly required for embryonic cartilage and joint development, SMAD3 seems to be important for maintaining a stable cartilage phenotype by preventing cartilage degeneration.

Since SMAD2, SMAD3 and SMAD4 have been shown to differentially regulate TGFβ signaling and to have distinct functions during in vivo cartilage differentiation, we investigated their role in TGFβ-induced signaling and chondrogenesis of human BMSCs. We knocked down and overexpressed either Smad2 or Smad4 in human fetal BMSCs and determined the effects on TGFβ3-activated SMAD phosphorylation and induction of chondrogenic differentiation.

**Results**

**Efficient knockdown and overexpression of SMAD2, SMAD3 and SMAD4.** To study the role of Smad2, Smad3 and Smad4 in TGFβ3-induced SMAD phosphorylation and chondrogenesis of human BMSCs, their expression was modulated in human fetal BMSCs using short hairpin RNA (shRNA)-mediated knockdown and adenoviral (ad)-mediated overexpression.

We confirmed efficient shRNA-mediated knockdown of Smad2 (Fig. 1a,b), Smad3 (Fig. 1c,d) and Smad4 (Fig. 1e,f) at the mRNA and protein level. In addition, we observed that Smad2 (Fig. 1a) and Smad3 (Fig. 1c) mRNA levels, but not their protein levels (Fig. 1b,d), were increased in Smad4-shRNA compared to Ctrl-shRNA. Although gene expression of Smad3 (Fig. 1c) and Smad4 (Fig. 1e) was similar between Smad2-shRNA and Ctrl-shRNA, their protein expression (Fig. 1d,f) was decreased in Smad2-shRNA. Next, we verified adenoviral overexpression of Smad2 (Fig. 2a,b), Smad3 (Fig. 2c,d) and Smad4 (Fig. 2e,f) at gene and protein level. Notably, only Smad4 protein (Fig. 2f) was slightly reduced in ad-Smad2 compared to ad-LacZ. Thus, these data confirm efficient knockdown and overexpression of Smad2, Smad3 and Smad4.

**TGFβ3-activated phosphorylation of R-SMADs is altered by knockdown and overexpression of SMAD2, SMAD3 or SMAD4.** TGFβ3 signaling appears to be a straightforward cascade in which the ALK5 receptor phosphorylates Smad2 and Smad3, which upon binding to Smad4 translocate to the nucleus where they regulate gene transcription. However, this system is more complex as multiple mechanisms have been discovered that control TGFβ signal transduction. Since it remained unknown whether R-SMAD phosphorylation depends on the amount of Smad2 and Smad3 present, we investigated whether modulating the expression of Smad2 and Smad3 affected TGFβ3-activated phosphorylation of R-SMADs. We only show the effects on phosphorylated Smad2 (pSmad2) due to difficult detection of pSmad3. First, we verified that TGFβ3 induced pSmad2 in Ctrl-shRNA cells (Fig. 3a) and in ad-LacZ cells compared to no stimulation (Fig. 3b). TGFβ3-activated Smad2 phosphorylation was reduced in the Smad2-shRNA condition (Fig. 3a) and it was enhanced in ad-Smad2 (Fig. 3b). No effect on pSmad2 was observed with Smad3-shRNA (Fig. 3a) or ad-Smad3 (Fig. 3b). Moreover, to determine if co-factor Smad4 is involved in TGFβ3-activated R-SMAD phosphorylation, the expression of Smad4 was modulated. We found that pSmad2 was lower in Smad4-shRNA than in Ctrl-shRNA (Fig. 3a) and was similar between ad-Smad2 and ad-LacZ (Fig. 3b).

Next to Smad2/3, TGFβ3 can activate Smad1/5/9, and both these R-SMAD signaling pathways are important for chondrogenic induction. Moreover, the TGFβ3 receptor ALK5 is required for TGFβ3-activated phosphorylation of Smad2/3 and Smad1/5/9. Hence, we hypothesized there could be competition between Smad2/3 and Smad1/5/9 for phosphorylation by ALK5. We confirmed Smad1/5/9 phosphorylation (pSmad1/5/9) in response to TGFβ3 stimulation compared to no stimulation in Ctrl-shRNA (Fig. 3c) and ad-LacZ (Fig. 3d). TGFβ3-induced pSmad1/5/9 was higher in Smad2-shRNA and Smad3-shRNA than in Ctrl-shRNA (Fig. 3c). Although Smad1/5/9 phosphorylation was similar between ad-Smad2 and ad-LacZ, it was slightly reduced in ad-Smad3 (Fig. 3d). Next, we studied the involvement of Smad4 in TGFβ3-activated Smad1/5/9 phosphorylation. We observed that in the Smad4-shRNA condition TGFβ3 stimulation did not lead to induction of pSmad1/5/9 (Fig. 3c), whereas TGFβ3-induced pSmad1/5/9 was comparable between ad-Smad4 and ad-LacZ (Fig. 3d).

Taken together, these data demonstrate that activation of the Smad2/3 and Smad1/5/9 signaling pathways by TGFβ3 is affected by modulating Smad2, Smad3 or Smad4 expression, indicating that the levels of TGFβ3-induced phosphorylated R-SMADs depend on the amount of R-SMAD2/3 and co-SMAD4.
Knocking down either SMAD3 or SMAD4 strongly inhibits chondrogenesis. We determined the contribution of SMAD2, SMAD3 and SMAD4 during TGFβ-induced chondrogenic differentiation by knocking down the expression of these SMADs and culturing the BMSCs in chondrogenic medium containing TGFβ. After 1, 7 and 14 days we evaluated expression of chondrogenesis-specific genes ACAN, COL2A1 and SOX9, formation of cartilage matrix and the macroscopic appearance of the BMSC pellets.

In 1, 7 and 14 days-cultured BMSC pellets, ACAN (Fig. 4a), COL2A1 (Fig. 4b) and SOX9 (Fig. 4c) were similarly expressed in the SMAD2-shRNA and Ctrl-shRNA condition, except for a significant decrease in COL2A1 expression at day 1 in SMAD2-shRNA (p = 0.007). Although ACAN and SOX9 expression were mildly affected by SMAD3-shRNA, transcription of COL2A1 was significantly inhibited by SMAD3-shRNA at day 1 (p = 0.007), day 7 (p < 0.001) and day 14 (p = 0.029). Furthermore, a strong and significant inhibition of ACAN, COL2A1 and SOX9 expression was observed in SMAD4-shRNA at all time points (p < 0.01 for all genes and time points).

Next, we analyzed cartilage matrix deposition by determining the presence of glycosaminoglycans (GAGs) and collagen type II protein. In 14 days-cultured pellets, ACAN (Fig. 4a), COL2A1 (Fig. 4b) and SOX9 (Fig. 4c) were similarly expressed in the SMAD2-shRNA and Ctrl-shRNA condition, except for a significant decrease in COL2A1 expression at day 1 in SMAD2-shRNA (p = 0.007). Although ACAN and SOX9 expression were mildly affected by SMAD3-shRNA, transcription of COL2A1 was significantly inhibited by SMAD3-shRNA at day 1 (p = 0.007), day 7 (p < 0.001) and day 14 (p = 0.029). Furthermore, a strong and significant inhibition of ACAN, COL2A1 and SOX9 expression was observed in SMAD4-shRNA at all time points (p < 0.01 for all genes and time points).

Once BMSCs have differentiated into chondrocytes, they undergo hypertrophic maturation, which is characterized by enhanced expression of collagen type X α1 (COL10A1) and runt-related transcription factor.
We observed that COL10A1 and RUNX2 mRNA levels were similar between SMAD2-shRNA, SMAD3-shRNA and Ctrl-shRNA in 7 and 14 days-cultured pellets (Supplementary Fig. S2a,b). In contrast, compared to Ctrl-shRNA, COL10A1 expression was lower in the SMAD4-shRNA than in the Ctrl-shRNA condition (Supplementary Fig. S2a), while SMAD4-shRNA had no significant effect on RUNX2 expression (Supplementary Fig. S2b).

Altogether, these results indicate that shRNA-mediated knockdown of SMAD2 had a minor inhibitory effect on TGFβ-induced chondrogenic differentiation of human BMSCs. However, SMAD3 knockdown strongly reduced cartilage deposition, and SMAD4 knockdown completely blocked chondrogenesis.

Since knockdown of SMAD2, SMAD3 and SMAD4 inhibited chondrogenesis, we investigated whether overexpression of these SMADs might enhance TGFβ-induced chondrogenic differentiation of human BMSCs. However, SMAD3 knockdown strongly reduced cartilage deposition, and SMAD4 knockdown completely blocked chondrogenesis.

Deposition of GAGs (Fig. 5d) was significantly decreased in pellets of BMSCs transduced with ad-SMAD2 compared to control after 7 days (p = 0.009) and 14 days (p = 0.003). However, this significant reduction was not observed when the GAG content was corrected for the DNA content (Fig. 5e; Supplementary Fig. S3). Pellets of ad-SMAD3-transduced BMSCs had a significantly lower amount of GAGs per pellet (Fig. 5d; p < 0.001 at day 7; p = 0.006 at day 14) and per μg DNA (Fig. 5e; Supplementary Fig. S3; p = 0.007 at day 7; p < 0.001 at day 14) than the control condition. At all time points, GAG deposition (Fig. 5d,e) was similar between ad-SMAD4 and ad-LacZ. Histological analysis of 14 days-cultured pellets revealed that the abundance of GAGs and collagen type II protein (Fig. 5f) was similar between ad-SMAD2, ad-SMAD4 and ad-LacZ, whereas their abundance was strongly reduced in the ad-SMAD3 condition. In line with these observations, pellets of ad-SMAD2-transduced

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**SMAD3 overexpression results in a strong inhibition of chondrogenesis.** Since knockdown of SMAD2, SMAD3 and SMAD4 inhibited chondrogenesis, we investigated whether overexpression of these SMADs might enhance TGFβ-induced chondrogenic differentiation of human BMSCs.

Expression of ACAN (Fig. 5a), COL2A1 (Fig. 5b) and SOX9 (Fig. 5c) was comparable between the control condition (ad-LacZ) and ad-SMAD2, ad-SMAD3 and ad-SMAD4 after 1 day of pellet culturing. In 7 days-cultured pellets ACAN, COL2A1 and SOX9 were slightly lower expressed in ad-SMAD2 than in ad-LacZ (ACAN: p = 0.016; COL2A1: p < 0.001; SOX9: p = 0.047). However, after 14 days only ACAN expression was significantly decreased in ad-SMAD2 compared to ad-LacZ (p = 0.038). At all time points expression of ACAN, COL2A1 and SOX9 was significantly reduced by ad-SMAD3 (p < 0.05 for all genes), whereas their expression was not affected by ad-SMAD4.

Deposition of GAGs (Fig. 5d) was significantly decreased in pellets of BMSCs transduced with ad-SMAD2 compared to control after 7 days (p = 0.009) and 14 days (p = 0.003). However, this significant reduction was not observed when the GAG content was corrected for the DNA content (Fig. 5e; Supplementary Fig. S3). Pellets of ad-SMAD3-transduced BMSCs had a significantly lower amount of GAGs per pellet (Fig. 5d; p < 0.001 at day 7; p = 0.006 at day 14) and per μg DNA (Fig. 5e; Supplementary Fig. S3; p = 0.007 at day 7; p < 0.001 at day 14) than the control condition. At all time points, GAG deposition (Fig. 5d,e) was similar between ad-SMAD4 and ad-LacZ. Histological analysis of 14 days-cultured pellets revealed that the abundance of GAGs and collagen type II protein (Fig. 5f) was similar between ad-SMAD2, ad-SMAD4 and ad-LacZ, whereas their abundance was strongly reduced in the ad-SMAD3 condition. In line with these observations, pellets of ad-SMAD2-transduced
BMSCs were slightly smaller than control pellets, whereas pellets of ad-SMAD3-transduced BMSCs were much smaller (Fig. 5g). The pellet size was comparable between the ad-SMAD4 and ad-LacZ condition (Fig. 5g).

In addition, we found that chondrocyte hypertrophy markers, \( \text{COL10A1} \) and \( \text{RUNX2} \), were similarly expressed between ad-LacZ and ad-SMAD4 after 7 and 14 days (Supplementary Fig. S4a,b). Although \( \text{COL10A1} \) expression was lower in ad-SMAD2 than in ad-LacZ at day 7, the two conditions were comparable at day 14 (Supplementary Fig. S4a). At both time points, \( \text{RUNX2} \) mRNA levels were similar between ad-SMAD2 and ad-LacZ (Supplementary Fig. S4b). Strikingly, in the ad-SMAD3 condition \( \text{COL10A1} \) mRNA was lower (Supplementary Fig. S4a), whereas \( \text{RUNX2} \) mRNA was higher than in the ad-LacZ condition (Supplementary Fig. S4b).

Our data demonstrate that TGF\( \beta \)-induced chondrogenesis was slightly inhibited by SMAD2 overexpression and not affected by SMAD4 overexpression, whereas it was strongly inhibited by SMAD3 overexpression.

Discussion

The pro-chondrogenic effect of TGF\( \beta \) on human BMSCs is well-known, however, the contribution of the downstream signaling molecules SMAD2, SMAD3 and SMAD4 during chondrogenesis has been less well investigated. By using human fetal BMSCs as a model for TGF\( \beta \)-induced chondrogenic differentiation, we demonstrate here that modulating SMAD2 expression had a minor effect on chondrogenesis. In contrast, knockdown as well as overexpression of SMAD3 strongly inhibited cartilage formation and SMAD4 knockdown completely blocked chondrogenesis.

To the best of our knowledge, the specific role of SMAD2 and SMAD3 during chondrogenic differentiation of human BMSCs has been studied in one study so far, which demonstrated that modulating SMAD2 expression does not affect chondrogenesis\(^\text{22}\). In contrast, we observed a slight reduction in cartilage formation when SMAD2 was knocked down or overexpressed. We also found that SMAD2 knockdown led to reduced protein levels of SMAD3 and SMAD4, whereas Furumatsu et al.\(^{\text{22}}\) did not report an effect of SMAD2 knockdown on SMAD3 and SMAD4 expression. Since knockdown of either SMAD3 or SMAD4 inhibited chondrogenesis, reduced SMAD3 and SMAD4 abundance might explain why chondrogenesis was slightly inhibited by SMAD2 knockdown. Our
Figure 4. Chondrogenesis is mildly inhibited by SMAD2-shRNA, is strongly inhibited by SMAD3-shRNA and completely blocked by SMAD4-shRNA. Human fetal BMSCs were transduced (lentivirus) either with SMAD2-shRNA, SMAD3-shRNA, SMAD4-shRNA or Ctrl-shRNA and subsequently pellet-cultured for 1, 7 or 14 days in chondrogenic medium with TGFβ. The effect of shRNA-mediated knockdown of SMAD2, SMAD3 and SMAD4 on chondrogenesis was determined by RT-qPCR analysis of the chondrogenesis-specific genes; ACAN, COL2A1 and SOX9, deposition of glycosaminoglycans (GAGs) per pellet and per μg DNA, histological examination of GAGs by Safranin O (Saf.O) staining and collagen type II by immunohistochemistry in sections of 14 days-cultured pellets, and macroscopic evaluation of 14 days-cultured pellets. In (f) representative images of consecutive pellet sections per condition are shown and the scale bar represents 500 μm. Gene expression data are presented as −ΔC_T compared to the mean C_T value of RPS27a and TBP. Bars represent mean ± S.D. of triplicate pellets from 2 experiments. *p < 0.05; **p < 0.01; ***p < 0.001 compared to Ctrl-shRNA.
Figure 5. Chondrogenesis is strongly inhibited by SMAD3 overexpression, whereas it is mildly inhibited by SMAD2 overexpression and unaffected by SMAD4 overexpression. Human fetal BMSCs transduced either with adenoviral SMAD2 (ad-SMAD2), ad-SMAD3, ad-SMAD4 or ad-LacZ as control were pellet-cultured for 1, 7 or 14 days in chondrogenic medium with TGFβ3. The effect of SMAD overexpression on chondrogenesis was determined by RT-qPCR analysis of the chondrogenesis-specific genes; ACAN (a), COL2A1 (b) and SOX9 (c), deposition of glycosaminoglycans (GAGs) per pellet (d) and per μg DNA (e), histological examination of GAGs by Safranin O (Saf.O) staining and collagen type II by immunohistochemistry in sections of 14 days-cultured pellets (f), and macroscopic evaluation of 14 days-cultured pellets (g). In (f) representative images of consecutive pellet sections per condition are shown and the scale bar represents 500 μm. Gene expression data are presented as −ΔCt compared to the mean Ct value of RPS27a and TBP. Bars represent mean ± S.D. of triplicate pellets from 2 experiments. *p < 0.05; **p < 0.01; ***p < 0.001 compared to ad-LacZ.
finding that TGFβ-induced chondrogenic differentiation of human BMSCs is more strongly inhibited by SMAD3 knockdown than by SMAD2 knockdown is in line with the aforementioned study22. While we employed continuous knockdown by viral transduction with shRNA, Furumatsu and co-workers employed transient knockdown by transfection with siRNA22. We, thus, verified that continuous knockdown of SMAD2 and SMAD3 had effects on chondrogenesis similar to transient knockdown.

Whereas the previous study has shown that SMAD3 overexpression accelerated chondrogenesis22, in our study SMAD3 overexpression blocked chondrogenic differentiation of human BMSCs. This discrepancy might be caused by a difference in chondrogenic media composition (details of medium components were not reported), cell source (fetal or adult origin, bone marrow or other tissue derived) or amount of overexpression (western blots of overexpressed SMAD3 were not shown). In addition, we found that the DNA content per pellet decreased over time in cells overexpressing SMAD3 (Supplementary Fig. S3). In multiple cell types, it has been shown that overexpression of SMAD3 leads to an inhibition of proliferation41–43. Importantly, proliferation of BMSCs early during chondrogenic differentiation is required for chondrogenesis44. Therefore, SMAD3 overexpression might have inhibited chondrogenesis, because it blocked proliferation. Overall, this indicates that constantly high levels of SMAD3 in BMSCs do not accelerate cartilage matrix formation. Since both knockdown and overexpression of SMAD3 inhibited chondrogenic differentiation, chondrogenesis seems to rely on well-balanced levels of SMAD3.

The present study, for the first time, investigated the role of SMAD4 during chondrogenic differentiation of human BMSCs. Previous studies in mice have demonstrated that mesenchyme-specific deletion of Smad4 leads to an absence of the limb skeleton as a result of impaired mesenchymal condensation10–15; a process required for initiating chondrogenesis45. In our study, SMAD4 knockdown did not interfere with pellet formation, implying that human BMSCs can form pellets even with a low amount of SMAD4. Although BMSCs transduced with SMAD4-shRNA formed pellets, they did not undergo chondrogenic differentiation. This observation is in line with a previous study demonstrating that BMSCs isolated from Smad4 knockout mice show reduced expression of Sox946. In murine chondrogenic progenitor cells, complex formation between Smad4 and phosphorylated Smad1/5 proteins is required for transactivation of the Col2a1 promoter47. This might explain why chondrogenesis did not occur when we knocked down SMAD4. Furthermore, we previously demonstrated that the SMAD2/3 as well as the SMAD1/5/9 pathways are required for TGFβ-induced chondrogenesis of human BMSCs6,10. In the present study activation of both pathways was reduced by SMAD4 knockdown, thereby possibly explaining the absence of cartilage formation. Altogether, these findings underline the importance of SMAD4 during TGFβ-induced chondrogenic differentiation of human BMSCs.

Following chondrogenesis, BMSC-derived chondrocytes display signs of hypertrophic differentiation. This is undesired for the formation of articular cartilage, as hypertrophic chondrocytes produce cartilage that will mineralize and ossify when implanted in vivo5. We found that modulating SMAD2 expression did not have an effect on expression of hypertrophic differentiation markers, neither did SMAD4 overexpression. SMAD3 overexpression and SMAD4 knockdown did result in lower COL2A1 expression. In these conditions, however, next to hypertrophy markers, the markers of chondrogenesis were also much lower expressed than in the control condition, following the principle that reduced chondrogenesis leads to reduced hypertrophic differentiation. Whereas COL2A1 expression was lower by SMAD3 overexpression, RUNX2 expression was slightly, but significantly, higher. This was surprising, because SMAD3 is required for repression of RUNX2 expression and chondrocyte hypertrophy38,48–51. Possibly, as a result of decreased chondrogenesis RUNX2 expression failed to go down during the early phase of chondrogenesis or RUNX2 expression levels might depend on the abundance of SMAD3, but this requires further investigation. Overall, our results failed to show effects specifically on hypertrophic differentiation of BMSC-derived chondrocytes without effects on the induction of chondrogenesis.

Besides the effects on chondrogenic and hypertrophic differentiation, this study investigated the effect of modulating SMAD2, SMAD3 and SMAD4 expression on TGFβ signal transduction. After activation by TGFβ, the ALK5 receptor phosphorylates SMAD2/3 proteins5. We show that SMAD2 phosphorylation was reduced by knockdown of SMAD2, while it highly increased by SMAD2 overexpression. These findings suggest that TGFβ-activated phosphorylation depends on the number of R-SMADs present in the cytoplasm rather than, for instance, on the kinase activity or number of ALK5 receptors.

We previously showed that TGFβ does not only induce phosphorylation of SMAD2/3, but also of SMAD1/5/9 in BMSCs6,10,52. Although SMAD1/5/9 cannot be directly phosphorylated by the TGFβ receptor ALK5, TGFβ-activated SMAD1/5/9 phosphorylation requires the intracellular kinase domains of ALK552. Moreover, ALK5 is the only receptor through which TGFβ can induce phosphorylation of SMAD2/353,54. Consistent with a study showing enhanced pSMAD1/5/9 in SMAD3 knockout chondrocytes55, we demonstrate increased pSMAD1/5/9 when SMAD3 or SMAD2 were knocked down. This supports the idea that TGFβ-induced phosphorylation of SMAD1/5/9 requires the ALK5 receptor and is independent of other receptors that can activate SMAD1/5/953,56.

Although SMAD4 is an important co-factor for translocation of activated R-SMADs to the nucleus57, it has not been implicated in controlling the phosphorylation of R-SMADs. Patients with Myhre syndrome have mutations in SMAD4 that lead to decreased ubiquitination of SMAD4 protein, resulting in accumulation of SMAD458,61. In skin fibroblasts from these patients, pSMAD2/3 and pSMAD1/5/9 were enhanced compared to healthy controls58,61. Contrary to this, in our study SMAD4 overexpression had no effect on R-SMAD phosphorylation. On the other hand, SMAD4 knockdown reduced TGFβ3-induced phosphorylation of SMAD2 and completely prevented SMAD1/5/9 phosphorylation. Based on these observations, we speculate that SMAD4 is required for R-SMAD phosphorylation, or prevents R-SMADs from de-phosphorylation26,3 or ubiquitination26,46, which adds a regulatory mechanism that controls TGFβ signal transduction.
Lentivirus concentration was determined with the INNOTEST® HIV p24 Antigen assay (Fujirebio Europe, Gent, Belgium). Cells at 80% confluence were incubated for 3 hours with adenovirus (multiplicity of infection of 1 plaque-forming unit (PFU) per cell) or adenovirus (SMAD overexpression) were seeded in chondrogenic medium without TGF-β1 (Biolegend, San Diego, CA, USA). This medium was renewed 3 times per week. At 20% confluence, BMSCs were infected with 1 pfu per cell in MSCGM (Lonza) supplemented with 100 μg/mL protamine sulfate (Sigma-Aldrich) for 1 day. After culture-expanding infected cells for 2 days, pellets were prepared to induce chondrogenesis. 1 day after pellet preparation, the efficiency of shRNA-mediated knockdown of SMAD2, SMAD3 and SMAD4 was determined. Membranes were overnight incubated with an antibody (1:20,000) recognizing pSMAD3 and pSMAD1/5/9 expression. Western blot analysis of (phosphorylated) SMAD proteins. To evaluate the effects of SMAD knockdown and overexpression on activation of TGFβ signaling, cells transduced either with lentivirus (SMAD-shRNA) or adenovirus (SMAD overexpression) were seeded in chondrogenic medium without TGFβ3. After 18 hours, cells were stimulated with 10 ng/mL TGFβ3 (Biologen) for 1 hour and cell lysates were prepared as described below to determine pSMAD2 and pSMAD1/5/9 expression.

To determine protein abundance, cells were lysed (duplicate per condition) using lysis buffer (Cell-Signaling-Technology, Danvers, MA, USA) containing 1% protease inhibitor (Roche, Mannheim, Germany) and lysates were sonicated on ice. Protein concentration was determined using bicinchoninic acid assay. Duplicate samples per condition were pooled and 10 μg protein lysate was subjected to 10% sodium dodecyl sulfate-polyacrylamide gel electrophoresis. Proteins were transferred to nitrocellulose membranes and overnight at 4 °C incubated with an antibody (1:1,000) recognizing SMAD2 (#40855, Abcam), SMAD4 (#AF2097, R&D systems, Minneapolis, MN, USA), pSMAD2 (#3101 L, Cell Signaling Technology) or pSMAD1/5/9 (#9511 L, Cell Signaling Technology). Subsequently, membranes were incubated with HRP-linked antibody (1:1,500) against rabbit-IgG (#P0448, Dako, Glostrup, Denmark) or goat-IgG (#P0449, Dako) for 1 hour at room temperature. To evaluate equal protein loading between conditions, GAPDH expression was determined. Membranes were overnight incubated with an antibody (1:20,000) recognizing SMAD4 was verified at gene (RT-qPCR) and protein (Western blot) level in BMSCs cultured for 1 day in chondrogenic medium.
40 Reader (Bio-Rad). To determine the DNA content, PicoGreen® stock solution (ThermoFisher Scientific) was used to quench samples in cDNA with M-MLV Reverse Transcriptase (Invitrogen). Gene expression was measured by real-time Reverse Transcription Quantitative Polymerase Chain Reaction (RT-qPCR) on a StepOnePlus™ System using SYBR Green Master mix (Applied Biosystems) and the primers listed in Table 1. CT values were determined at a fixed threshold level of fluorescence and efficiency of all primers was between 90% and 110% (Table 1). Data were normalized to the mean Ct value of Ribosomal protein 27a (RPS27A) and TATA-box binding protein (TBP).

RNA extraction and gene expression analysis. Pellets (n = 3 per condition at each time point) were collected in TRizol® (Sigma-Aldrich) and disrupted using MagNA Lyser instrument (Roche). After total RNA was isolated according to manufacturer’s protocol (Sigma-Aldrich), RNA samples were treated with DNase (Invitrogen) to remove contaminating genomic DNA. RNA concentration and purity were measured using a NanoDrop® spectrophotometer (Isogen Life Science, Utrecht, the Netherlands). 0.5 μg RNA was reverse transcribed in cDNA with M-MLV Reverse Transcriptase (Invitrogen). Gene expression was measured by real-time Reverse Transcription Quantitative Polymerase Chain Reaction (RT-qPCR) on a StepOnePlus™ System using SYBR Green Master mix (Applied Biosystems) and the primers listed in Table 1. Ct values were determined at a fixed threshold level of fluorescence and efficiency of all primers was between 90% and 110% (Table 1). Data were normalized to the mean Ct value of Ribosomal protein 27a (RPS27A) and TATA-box binding protein (TBP). The following genes were used as markers of chondrogenesis; Aggrecan (ACAN), Collagen type IIα1 (COL2A1) and SRY (Sex Determining Region Y)-Box 9 (SOX9). In addition, markers of chondrocyte hypertrophy; collagen type Iα1 (COL1A1) and runt-related transcription factor 2 (RUNX2), were measured.

Histology. To macroscopically evaluate pellet size of 14-days cultured pellets, pictures were taken using a microscope (Wild M3B, Heerbrugg, Switzerland). Subsequently, pellets were fixed in 4% formalin for 14 hours, embedded in paraffin and sectioned (6 μm). Sections were stained with 0.1% aqueous Safranin O (Brunschwig Chemie, Amsterdam, the Netherlands), resulting in red-staining of negatively-charged GAGs. As counter-staining, 0.1% aqueous Fast Green (Brunschwig Chemie) was used to stain the cytoplasm blue/green.

For immunohistochemical staining of collagen type II, sections were pre-treated with 1 mg/mL pronase and 10 mg/mL hyaluronidase (Sigma-Aldrich), and then incubated with 0.4 μg/mL antibody specific for collagen type II (#II-II6B3, Developmental Studies Hybridoma Bank, Iowa City, IA, USA) or 0.4 μg/mL mouse-IgG (#P0260, Dako). Proteins were visualized by enhanced chemiluminescence using Prime Western Blotting Detection Reagent and a ImageQuant LAS4000 machine (GE Healthcare). Densitometry was performed using ImageJ software (release 1.46r; National Institute of Health, Bethesda, Maryland, USA).

Glycosaminoglycans and DNA content measurements. Pellets cultured for 1, 7 or 14 days were digested overnight at 60°C in 100 μL papain digestion buffer (pH = 6.4) containing 0.1% papain, 10 mM EDTA-disodium salt (both from Merck), 100 mM sodium acetate, and 5 mM L-Cysteine-HCL (both from Sigma-Aldrich). Following digestion, samples were diluted 1:8 in water to measure the GAG content or samples were diluted 1:6 in Tris-EDTA (TE) buffer to measure DNA content. The GAG content was measured by adding 200 μL dimethylmethylen blue (DMB) solution (0.05 mM DMB, 41 mM NaCl, 45 mM glycine and pH = 3.0) to 40 μL papain-digested sample (pre-diluted 1:8 in water) and absorbance was measured at 590 nm using an iMark Reader (Bio-Rad). To determine the DNA content, PicoGreen® stock solution (ThermoFisher Scientific) was diluted 1:200 in TE buffer (10 mM Tris-HCl, 1 mM EDTA and pH = 7.5) and 50 μL of this solution was mixed with 50 μL papain-digested sample (pre-diluted 1:6 in TE buffer). After 5 minutes dark incubation at room temperature, fluorescence was measured at 485/520 nm (excitation/emission) with a CLARIOstar (BMG Labtech, Offenburg, Germany) using DNA obtained from human HEK293T cells to set the standard curve.

Data analysis. Data represent mean ± standard deviation of 6 pellets (from two experiments with triplicate pellets per experiment) per condition per time point. Statistical analyses were performed using SPSS version 22 (IBM, Armonk, NY, USA). Normality and variance were verified with the Shapiro-Wilk test and Levene’s Test, respectively. Statistical differences between control and experimental conditions per time point were determined with two-tailed independent T-tests. Level of significance was set at P < 0.05.

<table>
<thead>
<tr>
<th>Gene</th>
<th>Forward primer</th>
<th>Reverse primer</th>
<th>Product</th>
</tr>
</thead>
<tbody>
<tr>
<td>RPS27A</td>
<td>TGGCTGTCCGTGAAATTTATATAGGT</td>
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<td>COL10A1</td>
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<td>RUNX2</td>
<td>GCAAGGTTCAACGATCTGAGA</td>
<td>TTCGGAGGTTCCATCTACG</td>
<td>141bp</td>
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</table>

Table 1. List of primers used for RT-qPCR.
References


P. M. v. d. K. analyzed the results. All authors reviewed the manuscript.

Author Contributions

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Author Contributions
