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## Growth Factor Signalling in Osteoarthritis

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### Abstract

Osteoarthritis (OA) is one of the most common diseases, affecting more than 10% of populations and thus creating immense socioeconomic burden. The pathological changes of OA involve the entire joint, which is composed of multiple types of tissues and cells, exemplified by cartilage degradation, subchondral bone thickening, osteophyte formation, synovium inflammation and hypertrophy, and ligament degeneration. As joint homeostasis requires a complex network of growth factors to regulate anabolic and catabolic events, the dysregulation of growth factor signaling would have negative impacts on structure and function of multiple joint tissues and eventually lead to the onset and progression of OA. In this review, we will discuss TGF- $\beta$ , NGF, Hedgehog and Wnt, the four growth factors which have received extensive attention in the field of OA and clinical/translational interrogation about their application in OA therapies.

### Keywords

Osteoarthritis; TGF- $\beta$ ; NGF; Hedgehog; Wnt

Among synovial joint disorders, osteoarthritis (OA) is the most common form and causes pain and disability in 13.9% of adults aged 25 years and older in the United States (Lawrence et al., 2008). OA affects the entire joint and causes complex pathological changes, such as joint space narrowing, articular cartilage (AC) destruction, synovial inflammation and hyperplasia, osteophyte formation, and subchondral bone sclerosis. It is now recognized that OA is a highly heterogeneous joint disorder, therefore it is necessary to develop personalized therapeutics to treat OA (Tonge et al., 2014). As growth factors are essential regulators in the development, homeostasis and pathogenesis of the joint, the studies of growth factors in OA have accumulated and provided sophisticated understandings. In this review, we will focus on four growth factors, TGF- $\beta$ , NGF, Hedgehog and Wnt, which have important functions in joint homeostasis and OA pathogenesis and could be used as potent medicine or promising drug targets for the treatment of OA. For quick reference, we also summarize in Table 1 in vivo findings for the roles of these growth factors in OA pathogenesis or treatment.

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## TGF- $\beta$ superfamily

The TGF- $\beta$  superfamily has attracted great attention regarding their pleiotropic roles in joint pathophysiology, including healthy joint homeostasis and OA pathogenesis. This family embodies 42 growth factors in humans (International Human Genome Sequencing 2001), which can be classified into two subfamilies: the TGF- $\beta$ /Activin/Nodal subfamily, and the bone morphogenetic protein (BMP)/growth and differentiation factor (GDF)/Muellerian inhibiting substance (MIS) subfamily (Shi and Massague, 2003). For canonical activation of the TGF- $\beta$  signaling pathway, a ligand of the TGF- $\beta$  superfamily, e.g. TGF- $\beta$ 1, BMP-2, or other TGF- $\beta$  family members, form dimers that bind to two type I and two type II receptors on cell membranes to constitute a heteromeric complexes, inside which the type II receptors phosphorylate the type I receptors, significantly enhancing the recruitment and phosphorylation of receptor-regulated Smads (R-Smads) transcription factors. Upon phosphorylation, two R-Smads and one Smad4 form heteromeric complexes and translocate into the nucleus, where they interact with additional transcription factors to control gene transcription. The differences of the two subfamilies of TGF- $\beta$  ligands reside not only in their sequences, but also in the R-Smads that they activate, such as Smad2/3 activated by TGF- $\beta$ /Activin/Nodal, or Smad1/5/8 activated by BMP/GDF/MIS. As Smad2/3 and Smad1/5/8 regulate different sets of gene expression, the two TGF- $\beta$  subfamilies elicit contrasting cellular responses in joint homeostasis and OA pathogenesis. Thus, the two subfamilies will be separately discussed in terms of their roles in OA.

The TGF- $\beta$  subfamily has been demonstrated to play instrumental functions in maintaining the integrity of articular cartilage. *In vitro* treatment of articular chondrocytes or articular cartilage organ culture with TGF- $\beta$  stimulated the biosynthesis of both collagen and proteoglycan, two major cartilage matrix macromolecules contributing to the mechanical strength of articular cartilage (Redini et al., 1988; Morales and Roberts, 1988). In addition, TGF- $\beta$ 1 can block the catabolic effects of IL-1 $\beta$  on articular chondrocytes by dramatically inhibiting protease production (Chandrasekhar and Harvey, 1988) and also down-regulate IL-1 receptor expression (Réadini et al., 1993). Notably, TGF- $\beta$ 3 and phosphorylated Smad2 were evidently expressed in normal cartilage, whereas they were not detected in severe osteoarthritic cartilage (Blaney Davidson et al., 2006), suggesting that TGF- $\beta$  signaling plays an important role in maintaining cartilage homeostasis that protects cartilage from destruction. Besides ample TGF- $\beta$  production by chondrocytes, large amounts of TGF- $\beta$  ligands are secreted in a latent form and stored in the extracellular matrix of cartilage (Morales et al., 1991). Thus, TGF- $\beta$  in reservoir could serve as a device quickly responding to matrix perturbation due to cartilage wear and tear, as cartilage lesions induce protease production that acts on latent TGF- $\beta$  activation, which provides protective effects to cartilage by antagonizing catabolic factors and stimulating matrix synthesis. Importantly, TGF- $\beta$  represses terminal hypertrophic differentiation of chondrocytes (Ballock et al., 1993; Yang et al., 2001), which otherwise leads to higher expression of matrix metalloproteinase 13 (MMP13) and type X collagen, chondrocyte hypertrophy and apoptosis, and cartilage calcification. Together, TGF- $\beta$  regulates a diverse array of joint pathophysiology, including cartilage metabolism and chondrocyte differentiation.

Studies using genetically modified mice with mutations within the TGF- $\beta$  signaling pathway offer a great opportunity to study how TGF- $\beta$  regulates OA pathogenesis *in vivo*. Homozygous Smad3 loss-of-function in mice caused comprehensive degenerative changes in joints resembling human osteoarthritis, including progressive degradation of articular cartilage, outgrowth of large osteophytes, reduced production of proteoglycans, and an aberrant increase of hypertrophic chondrocytes in synovial joints (Yang et al., 2001), suggesting that TGF- $\beta$ /Smad3 signaling is vital for repressing chondrocyte differentiation and OA pathogenesis. Also, loss of responsiveness to TGF- $\beta$  can be achieved by overexpression of a truncated type II TGF- $\beta$  receptor, which retains the ability to bind to TGF- $\beta$  but cannot phosphorylate Smad2/3 due to the deletion of its cytoplasmic domains, in order to generate a dominant-negative effect. Markedly, both OA-like phenotype and enhanced terminal differentiation of articular chondrocytes were observed in the mice expressing dominant-negative type II receptors (Serra et al., 1997). To further characterize if the loss of TGF- $\beta$  signaling in chondrocytes contributes to OA pathogenesis, TGF $\beta$  receptor type II was deleted specifically in chondrocytes by *Col2-CreER* (Chen et al. 2007; Zhu, Chen, Lichtler, et al. 2008) and found that the decrease of TGF- $\beta$  signaling in chondrocytes caused severe OA-like pathological changes in mice, concomitantly with a significant upregulation of genes encoding for cartilage degrading enzymes, including *Mmp13*, *Adamts5* and *Adamts4* (Shen et al., 2013).

Both *in vitro* data and mouse genetics studies indicated that TGF- $\beta$  could be an effective agent to restore or prevent cartilage damage, a central histologic feature of OA. However, intra-articular injection or adenoviral overexpression of TGF- $\beta$  appeared to have profound negative effects on the entire joint, including extensive osteophyte formation, synovial inflammation and hyperplasia (van Beuningen et al., 2000; Bakker et al., 2001). On the other hand, inhibition of TGF- $\beta$  signaling in animal OA models reduced osteophyte formation and synovial thickening (Scharstuhl et al., 2003), and systemic administration of a TGF- $\beta$  receptor I inhibitor or subchondral application of a TGF- $\beta$  antibody alleviated subchondral sclerosis and cartilage degeneration (Zhen et al., 2013), substantiating the notion that TGF- $\beta$  administration could cause deleterious effects in OA-inflicted joints, especially in terms of synovial hyperplasia and osteophyte formation. There are also studies describing that introduction of extra TGF- $\beta$  may benefits OA treatment (Lee et al., 2001; Guo et al., 2006; Ivkovic et al., 2010), which administer fibroblasts, cultured mesenchymal stem cells or bone marrow aspirates with high level expression of TGF- $\beta$  into the joints. Thus, the seemingly contradiction between different studies poses a significant difficulty on further developing TGF- $\beta$ -based OA therapy, especially in terms of its safety and efficacy. Importantly, the heterogeneous nature of OA and the involvement of multiple tissue/cell types in a joint as a complex organ need to be thoroughly understood, in order to facilitate the evaluation and optimization of TGF- $\beta$ -based therapeutic strategies.

In addition to the TGF- $\beta$  subfamily, the BMP subfamily also represents potent regulators in osteogenesis and chondrogenesis. In addition, key factors in the BMP signaling, including BMP-2/4, pSmad1/5/8, and two BMP antagonists, Noggin and Gremlin1, are evidently expressed in articular cartilage (Yu et al., 2017). Thus, it is conceivable that BMPs are also critical modulators in OA pathogenesis. Similar to TGF- $\beta$ , BMP-2 also promoted proteoglycan synthesis (Chubinskaya et al., 2008), which is positive for maintaining

cartilage integrity. Moreover, combination of BMP-2 and TGF- $\beta$ 1 under hypoxia has a synergistically strong effect in inducing chondrogenesis of human mesenchymal stem cells (Legendre et al., 2017). However, BMP-2 expression is increased in severely damaged cartilage whereas TGF- $\beta$  is not detected, suggesting that BMP-2 has functions different from TGF- $\beta$  (Blaney Davidson et al., 2006). Indeed, BMP-2 injection into osteoarthritic joints aggravated osteophyte formation (van Beuningen et al., 1998), although the sites of osteophyte growth were mostly close to the growth plate, different from the osteophyte formation site induced by TGF- $\beta$ . Contrary to TGF- $\beta$  that inhibits chondrocyte hypertrophy, BMP-2 induced chondrocytes into terminal differentiation through Smad1 and Smad5 (Kobayashi et al., 2005; Retting et al., 2009), which underlies the observation that BMP treatment increases MMP13 expression in sternal chondrocytes, since MMP13 is induced in hypertrophic chondrocytes (D'Angelo et al., 2000). However, inducible chondrocyte-specific BMP-2 overexpression does not induce structural alterations of articular cartilage in either healthy or osteoarthritic murine joints, while it causes severe osteophyte formation in the experimental OA models (Blaney Davidson et al., 2015), suggesting that elevated expression of BMP-2 at the postnatal stage may not have considerably deleterious effects in articular cartilage. Interestingly, a recent study demonstrated that BMP-2 deletion in joint tissues (as targeted by Gdf5-Cre) results in defective development and maturation of both the meniscus and articular cartilage, which could be an critical risk factor for the ageing-related OA pathogenesis in the BMP-2 deficient mice (Gamer et al., 2018). This confirms a previous study that mice with loss of BMP signaling, achieved by targeting BMP receptor type-1A with Gdf5-Cre, display a failure in maintaining postnatal articular cartilage (Rountree et al., 2004). Thus, BMP signaling is thought to be essential for proper development and maintenance of joint tissues including articular cartilage and meniscus, which is a key to prevention of OA pathogenesis. Together, detailed characterization of the TGF- $\beta$  superfamily, including the TGF- $\beta$  or BMP subfamily, would be helpful to design safe, effective therapies based on these potent growth factors to treat OA, a complex degenerative joint disease.

## Nerve Growth Factor

Musculoskeletal pain is a primary symptom of OA and the major reason for the disability of OA patients. Thus, pain alleviation is a prime goal of OA treatment, which would greatly improve quality of life for OA patients. As radiographic features are poorly associated with pain symptoms in OA patients, the aetiology of pain may involve additional factors than structural deterioration of the joint (Hannan et al., 2000). Specifically, aberrant neuronal activities are believed to be essential to the generation and chronicity of pain. Particularly, nerve growth factor (NGF), a member of the neurotrophin family, is required by nociceptive neurons for their survival and function, and has been demonstrated to undergo significant upregulation in the joints of OA patients (Iannone et al., 2002). NGF binds to two transmembrane receptors, of which trkA is a tyrosine receptor kinase with a high affinity with NGF and p75<sup>NTR</sup> is a member of the tumour necrosis factor receptor superfamily with a low NGF-binding capacity (Shu and Mendell, 1999), resulting in the activation of a multitude of signalling pathways that sensitize neurons and stimulate growth of axons and dendrites. Specifically, the binding of NGF to its receptors promotes the formation of trkA

homodimers and trkA-p75<sup>NTR</sup> heterodimers and the autophosphorylation of the receptors, which then activate downstream signalling cascades such as mitogen-activated protein kinases (MAPK), also known as extracellular signal-regulated kinases (ERKs), and phosphatidylinositol-4,5-bisphosphate 3-kinase (PI3K)-protein kinase B (PKB, also known as AKT), resulting in enhanced neuronal survival and growth (Kaplan et al., 1991; Verdi et al., 1994).

NGF is a major mediator of pain in mammals, as injection of NGF induced pain and hyperalgesia in animals (Lewin et al., 1993) and humans (Petty et al., 1994) in a dose-dependent manner. Moreover, it has been reported that articular chondrocytes isolated from OA patients have upregulated levels of NGF and trkA (Iannone et al., 2002) and NGF is present in the synovial fluid of some OA patients but not detectable in the synovial fluids from normal subjects (Aloe et al., 1992). Thus, antagonism of NGF has been proposed as a promising strategy to reduce OA pain. To date, clinical trials using monoclonal antibodies against NGF, tanezumab or fasinumab, have demonstrated that NGF inhibition significantly reduced musculoskeletal pain associated with OA, compared with placebo or non-steroidal anti-inflammatory drugs (NSAIDs) (Brown et al., 2013; Tiseo et al., 2014; Lane et al., 2010). However, an adverse event, i.e. rapidly progressive OA, was confirmed to occur frequently in the patients receiving anti-NGF therapy (Hochberg et al., 2016; Lane et al., 2010), prompting the US FDA to place a hold on all clinical trials of anti-NGF therapy. Thus, NGF antagonism displays both beneficial and adverse effects strikingly in treating OA. An explanation for this unexpected result could be that significant pain palliation may encourage the patients to use their joints more than they can endure. Nevertheless, it may also implicate that NGF signalling regulates a plethora of biological activities not confined to the nervous system, or that a proper interaction with NGF-directed neural activity is essential to the wellbeing of non-neural tissues inside a synovial joint. Thus, more extensive, in-depth studies about the function of NGF in OA pathophysiology and anti-NGF therapeutics to manage OA pain would help to stratify the patients and identify those who can receive significant pain mitigation with minimal adverse effects from NGF antagonism.

## Hedgehog

Expression of dominant negative type II TGF- $\beta$  receptor results in an OA-like phenotype and points to increased indian hedgehog (IHH) expression that could be responsible for hypertrophic differentiation of articular chondrocytes observed in OA (Serra et al., 1997). IHH, sonic hedgehog (SHH) and desert hedgehog (DHH), are three members of the mammalian Hedgehog family (Ingham and McMahon, 2001). As secreted peptide ligands, Hedgehog (Hh) proteins act both locally and remotely in a dose- and duration-dependent manner as important morphogens in development and key players in tissue homeostasis. For Hh ligands, the primary receptor is Patched 1 (PTCH1), a transmembrane protein that inhibits activities of the Hh pathway if unbound to the Hh ligands. The repression of Hh pathway by PTCH1 is mediated by its inhibition of Smoothened (SMO), a member of the G protein-coupled receptor (GPCR) superfamily. Thus, upon Hh binding, SMO is relieved from PTCH1 suppression and activates transcriptional factors named Gli (Gli1, Gli2, and Gli3 in vertebrates) to conduct specific sets of gene expression. Among three ligands, Ihh has been demonstrated to play multiple important functions in the development of bone and

cartilage, including its regulatory role in proliferation and hypertrophic differentiation of chondrocytes (Vortkamp et al., 1996; St-Jacques et al., 1999; Kobayashi et al., 2002; Long et al., 2001), as well as in osteoblast differentiation (St-Jacques et al., 1999; Chung et al., 2001). Predominantly produced by prehypertrophic chondrocytes, *Ihh* promotes the expression of parathyroid hormone-related protein (PTHrP) in periarticular chondrocytes, and keeps these chondrocyte proliferating without differentiating (Vortkamp et al., 1996; St-Jacques et al., 1999). *Ihh* also induces the differentiation of periarticular chondrocytes into columnar chondrocytes independently of PTHrP (Kobayashi et al., 2005). Moreover, *Ihh* is also required for the osteoblast differentiation of perichondrial cells that is essential to bone collar formation (Long et al., 2004). Because of its proliferation-stimulating effects on chondrocytes, *Ihh* was tested for its cartilage repairing potential, by delivering bone marrow coagulates with adenoviral expression of *Ihh* to osteochondral defects in the rabbit knees. The result was promising, suggesting the capability of *Ihh* in cartilage repair (Sieker et al., 2015).

The pathological features such as hypertrophy and apoptosis of articular chondrocytes and bony growth including osteophytes and subchondral sclerosis suggested that *Ihh* signalling, an important pathway in cartilage and bone development, may undergo aberrant changes during OA pathogenesis. An examination of gene expression in human cartilage samples with early focal OA-like lesions revealed that chondrocyte differentiation associated genes, such as *Col10a1*, *Mmp9*, *PTHrP* and *Ihh*, are upregulated in OA cartilage compared with normal healthy cartilage (Tchetina et al., 2005). Further investigations on human OA samples and a mouse model with surgically-induced OA demonstrated that the expression of the genes targeted by the Hh family, including *GLI1*, *PTCH1* and *HHIP*, significantly increased in OA cartilage (Lin et al., 2009). Moreover, studies of multiple genetically modified mice showed that the levels of Hh signalling in chondrocytes are closely associated with the severity of OA, suggesting a causal effect of Hh signalling upregulation in the development of OA (Lin et al., 2009). Administration of a small molecule inhibitor for Smo, an indispensable factor for Hh activation, blocked Hh signalling in a mouse arthritis model and thus significantly reduced osteophyte formation (Ruiz-Heiland et al., 2012). Similarly, specific *Ihh* deletion in chondrocytes reduced the progression of surgically-induced OA in mice, as shown by a relatively intact cartilage surface and decreased expression of OA marker genes such as *Col10a1* and *Mmp13* (Zhou et al., 2014). In summary, aberrant activation of Hh signalling may underlie the pathogenesis of OA and inhibition of the Hh pathway could provide a therapeutic strategy for the OA treatment.

## Wnt

Canonical Wnt signalling could be regarded as the most important pathway in bone biology if we focus on human genetic studies to identify the pivotal genes in bone diseases. A prominent example is that loss-of-function mutations in *LRP5* cause reduced bone mass in patients with the autosomal recessive disorder osteoporosis-pseudoglioma syndrome (Gong et al., 2001). Mechanistic studies confirmed the role of *LRP5* as a co-receptor in the canonical Wnt signalling, of which its crucial role in bone formation was substantiated by numerous additional human and mouse genetic studies. Like the TGF- $\beta$  superfamily and Hh proteins, the members of the Wnt family are also secreted proteins playing fundamental



functions in a variety of processes in animal development. The central event in the Wnt signalling regarding its activation or deactivation is the stabilization or degradation of  $\beta$ -catenin, a transcriptional regulator. In the absence of Wnt,  $\beta$ -catenin would undergo phosphorylation by the destruction complex comprised of Axin, APC, and GSK3 and then degradation by the ubiquitin-proteasome system. Upon the physical interaction between Wnt and its receptors Frizzled and LRP5/6, the destruction complex is recruited by the receptors to the cell membrane and the ubiquitination of  $\beta$ -catenin is blocked, resulting in the stabilization and accumulation of  $\beta$ -catenin proteins, which translocate to the nucleus and activate transcription of its target genes (Nusse and Clevers, 2017). It is notable that Wnts also bind to some subfamilies of tyrosine kinase receptors, including those from the related to tyrosine kinase (RYK) and RTK-like orphan receptor (ROR) subfamilies, regulating canonical Wnt signalling and other pathways (Roy et al., 2018). However, their functional roles in OA pathogenesis remain to be identified.

As the Wnt signalling plays key roles in bone biology, it also receives great attention in the field of OA. It was reported that mechanical injury to cartilage explants induces expression of the canonical Wnt target genes *Axin2* and *c-Jun* (Dell'Accio et al., 2006). By inhibiting Dickkopf-1 (DKK-1), a Wnt signalling antagonist, in a mouse model of rheumatoid arthritis (RA), Diarra et al. observed osteophyte formation, which is frequently observed in OA, but not bone erosion, a histologic change associated with RA. This result suggested that the enhancement of Wnt signalling overrides bone-eroding pathways in RA to convert the bone-related phenotype and implicated that Wnt signalling had a dominant, positive regulatory function in osteophyte formation (Diarra et al., 2007). Moreover, elevated serum levels of DKK-1 and Frizzled-related protein (FRP), which is also a Wnt signalling inhibitor, are associated with the reduced risk of hip OA progression in elderly Caucasian women (Lane et al., 2007). Thus, these findings suggest that upregulation of Wnt signalling could be a causal factor in the development and progression of OA. Importantly, deletion of Exon 3 of the  $\beta$ -catenin gene in articular chondrocytes, which generates a mutant of  $\beta$ -catenin resistant to phosphorylation by GSK-3 $\beta$  and therefore causes persistent activation of the canonical Wnt signalling, leads to comprehensive OA-like changes including cartilage damage, osteophyte formation and new subchondral bone formation (Zhu et al., 2009). In addition, OA marker genes including *Mmp9*, *Mmp13*, and *Col10a1* are significantly upregulated in articular chondrocytes derived from the mice with  $\beta$ -catenin activation (Zhu et al., 2009). Thus, this study establishes a causal link between the activation of the Wnt/ $\beta$ -catenin signalling and the pathogenesis of OA, which has been corroborated by additional studies using alternative approaches to perturb the Wnt signalling. For examples, transgenic expression of Dkk-1 in chondrocytes inhibited the Wnt pathway alleviated cartilage destruction in surgically-induced OA knee joints (Oh et al., 2012), and intraarticular injection of a GSK-3 inhibitor GIN induces cartilage surface fibrillation, a decrease in glycosaminoglycan expression and chondrocyte hypocellularity (Miclea et al., 2011). In addition, aberrant increase of the Wnt signalling in non-cartilage joint tissues also has a negative impact on cartilage. Synovial overexpression of Wnt ligands through adenoviral transduction induces the Wnt signalling in the cartilage and leads to enhanced activity of cartilage-degrading enzymes and aggravated cartilage damage (van den Bosch et al., 2015; 2017), suggesting that Wnt signalling in synovium promotes catabolic effects in cartilage through increased production of matrix

metalloproteinases. Nevertheless, downregulation of Wnt signalling also had deleterious effects on articular cartilage as demonstrated by overexpression of ICAT, a small peptide inhibiting  $\beta$ -catenin-TCF binding, in chondrocytes (Zhu et al., 2008). Taken together, the perturbation of the Wnt/ $\beta$ -catenin cascade could be a key molecular mechanism underlying the pathogenesis of OA and therefore study of the Wnt signalling pathway would provide insights into the design of new therapeutics to treat OA.

In conclusion, we have accumulated considerable knowledge of the functions of TGF- $\beta$ , NGF, Hedgehog, and Wnt proteins in joint homeostasis and degeneration, many of which holds promise for the invention of new therapies for OA treatment. Still, further investigations, particularly those on translational or clinical studies, would provide irreplaceable insights into the safety and efficacy of the therapies that are designed to boost or target these growth factors inside the joints.

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**Table 1.**

A summary of *in vivo* evidence for the roles of the growth factors discussed in this review.

Growth factor	Evidence for anti-OA roles	Evidence for pro-OA
TGF- $\beta$	<ul style="list-style-type: none"> <li>Overexpression of dominant negative type II TGF-<math>\beta</math> receptor in mice causes articular cartilage (AC) degeneration, osteophyte growth, and hyperplastic synovium <sup>1</sup>.</li> <li>Smad3<sup>-/-</sup> mice exhibit AC destruction, osteophytes, reduced production of proteoglycans (PG), and an increase of hypertrophic chondrocytes <sup>2</sup>.</li> <li>Chondrocyte-specific deletion of type II TGF-<math>\beta</math> receptor in mice resulted in AC degradation, osteophytes, and increased subchondral bone <sup>3</sup>.</li> <li>TGF-<math>\beta</math>1 injection stimulates PG synthesis in murine joints <sup>4</sup>.</li> <li>Injection of TGF-<math>\beta</math>1-expressing fibroblasts or mesenchymal stem cells into rabbits shows cartilage regeneration <sup>5, 6</sup>.</li> <li>Implantation of TGF-<math>\beta</math>1-transduced bone marrow aspirates repairs cartilage defects in sheep <sup>7</sup>.</li> </ul>	<ul style="list-style-type: none"> <li>Repeated TGF-<math>\beta</math>1 injection induces chondro-osteophyte formation <sup>4</sup>.</li> <li>Injection of TGF-<math>\beta</math> in mice causes cartilage lesion at tide mark and osteophyte formation <sup>8</sup>.</li> <li>Adenoviral expression of TGF-<math>\beta</math>1 in mice results in synovial hyperplasia and chondro-osteophyte formation <sup>9</sup>.</li> <li>Overexpression of TGF-<math>\beta</math> antagonist, such as m LAP-1, Smad6, and Smad7 in mice decreases synovial thickening and/or osteophyte formation <sup>10</sup>.</li> <li>Systemic injection of SB505124, an inhibitor of type I TGF-<math>\beta</math> receptor, or implantation of TGF-<math>\beta</math> antibody in the subchondral bone of rats attenuates subchondral sclerosis and AC degeneration <sup>11</sup>.</li> </ul>
BMP	<ul style="list-style-type: none"> <li>BMP-2 injection stimulates PG synthesis in murine joints <sup>4</sup>.</li> <li>Loss of BMP-2 or BMP receptor type-1A in mice leads to a failure in maturation and maintenance of articular cartilage and meniscus, leading to spontaneous OA <sup>12, 13</sup>.</li> </ul>	<ul style="list-style-type: none"> <li>Repeated BMP-2 injection or inducible chondrocyte-specific overexpression of BMP-2 induces chondro-osteophyte formation <sup>4, 14</sup>.</li> </ul>
NGF	<ul style="list-style-type: none"> <li>Treatment of tanezumab, a monoclonal antibody against NGF, is associated with rapidly progression of OA in the clinical trials of knee and hip OA pain <sup>15</sup>.</li> </ul>	<ul style="list-style-type: none"> <li>Tanezumab and fasinumab, both monoclonal anti-NGF antibodies, have demonstrated efficacy in pain palliation <sup>15, 16, 17</sup>.</li> </ul>
Hedgehog	<ul style="list-style-type: none"> <li>Delivery of bone marrow coagulates with adenoviral expression of Ihh improves cartilage repair in the rabbit knees <sup>18</sup>.</li> </ul>	<ul style="list-style-type: none"> <li>Haploinsufficiency of Ptch1, overexpression of Gli2, or constitutive activation of Smo, which all upregulate Hedgehog signaling, cause OA in mice <sup>19</sup>.</li> <li>Genetic or pharmacological inhibition of Hedgehog signaling by deactivating an allele of Smo, deleting Ihh, or administering small molecule inhibitors, attenuated OA in mice <sup>19, 20, 21</sup>.</li> </ul>
Wnt	<ul style="list-style-type: none"> <li>Inhibition of Wnt signaling in articular chondrocytes by expressing ICAT causes articular cartilage destruction <sup>22</sup>.</li> </ul>	<ul style="list-style-type: none"> <li>Expression of degradation-resistant <math>\beta</math>-catenin in chondrocytes, or induction of Wnt signaling in synovium causes OA in mice <sup>23, 24</sup>.</li> <li>Transgenic expression of Dkk-1, a Wnt antagonist, in chondrocytes alleviated cartilage</li> </ul>

Growth factor	Evidence for anti-OA roles	Evidence for pro-OA
		degradation in knee joints with surgically-induced OA <sup>25</sup> .

- 1) Serra et al., 1997;
- 2) Yang et al., 2001,
- 3) Shen et al., 2013;
- 4) van Beuningen et al., 1998;
- 5) Lee et al., 2001;
- 6) Guo et al., 2006;
- 7) Ivkovic et al., 2010;
- 8) van Beuningen et al., 2000;
- 9) Bakker et al., 2001;
- 10) Scharstuhl et al., 2003;
- 11) Zhen et al., 2013;
- 12) Gamer et al., 2018;
- 13) Rountree et al., 2004;
- 14) Blaney Davidson et al., 2015;
- 15) Lane et al., 2010;
- 16) Brown et al., 2013;
- 17) Tiseo et al., 2014;
- 18) Sieker et al., 2015;
- 19) Lin et al., 2009;
- 20) Ruiz-Heiland et al., 2012;
- 21) Zhou et al., 2014;
- 22) Zhu et al., 2008;
- 23) Zhu et al., 2009;
- 24) van den Bosch et al., 2015;
- 25) Oh et al., 2012.