



Lessons from joint development for cartilage repair in the clinic

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Abstract

More than 250 years ago William Hunter stated that when cartilage is destroyed it never recovers¹. In the last 20 years, the understanding of the mechanisms that lead to joint formation and the knowledge that some of these mechanisms are reactivated in the homeostatic responses of cartilage to injury has offered an unprecedented therapeutic opportunity to achieve cartilage regeneration. Very large investments in ambitious clinical trials is finally revealing that, although we do not have perfect medicines yet, disease modification is a feasible possibility for human osteoarthritis.

Developmental morphogenesis and homeostatic responses to injury share basic mechanisms

During embryonic development, mesenchymal cells deriving from the lateral plate mesoderm (LPM), condense within the limb bud to form a cartilage anlage. The chondrocytes in the centre (diaphysis) of the skeletal elements undergo hypertrophic differentiation, expressing collagen type X, VEGF, MMP13 and alkaline phosphatase. Hypertrophic differentiation, in turn, triggers mineralization and ultimately replacement by bone^{2,3}. Endochondral ossification proceeds from the diaphysis towards the epiphysis sparing the joint interzones, which separate the future skeletal elements and will give rise to the joints. The joint interzones are composed of a distinct population of chondrogenic precursors expressing GDF5, WNT9A, WNT16 and other markers. Sox9⁺ cells from the limb

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mesenchyme are recruited to the joint interzone where they transiently express *Gdf5*⁷. Cavitation through the middle of the joint interzone completes the separation of the skeletal elements. The first cells recruited to the *Gdf5*+ interzone lineage contribute largely to the epiphyses; cells recruited at later stages contribute to the articular cartilage and finally to the other soft tissues of the joints, including menisci, synovial membrane, ligaments and tendons³⁻⁶. WNT signaling is required and sufficient for joint formation. While the deletion of individual genes results in minor phenotypes – for instance, deletion of *Wnt9a* results in synovial chondromatosis⁸, possibly because of compensation - complete suppression of WNT signalling resulted in joint fusion^{9,10}. Misexpression of WNT9A was sufficient to induce interzone markers including *Gdf5*, but not the formation of ectopic joints¹⁰. *Gdf5*-null mice lack some distal skeletal elements in the autopod, and also have anomalies in the proximal joints: for instance, the knees are missing the menisci and the cruciate ligaments^{6,11}. The more severe phenotype in the distal skeletal elements is possibly due to the proximo-distal expression gradient of *Gdf5* compared to other BMPs which may partially compensate in the proximal joints. Deletion of *c-Jun*, which is upstream of *Wnt9a* in the joint interzones, also resulted in lack of joint cavitation¹², however, morphologically, joint interzones were still present both after WNT blockade and *c-Jun* deletion^{9,12}. Therefore, while substantial progress has been made in the understanding of joint morphogenesis and maturation, the prime mechanisms determining joint specification remain elusive.

As opposed to the epiphyseal cartilage, the articular cartilage is stable throughout life, resistant to hypertrophic differentiation and endochondral ossification. Once the skeleton is mature, in adult life, the articular cartilage enters a status of extremely low turnover¹³. However, shortly after injury the articular cartilage deploys an impressively rapid homeostatic response that, in many cases, restores integrity and function¹⁴. This repair response is triggered by the re-activation of several of those molecules which during development mark the joint interzone and are not normally expressed in quiescent uninjured adult cartilage¹⁵. These responses contribute to healing¹⁶ and to re-establishing homeostasis^{17,18}. Spontaneous healing is most likely to be successful for small isolated lesions in otherwise healthy and young patients. With age, joint instability and other comorbidities including obesity, the likelihood of successful repair decreases¹⁴.

If repair is unsuccessful, or if injury persists, the excessive or prolonged molecular responses to injury may become a pathogenic factor leading to ectopic activation of hypertrophic differentiation and mineralization within the articular cartilage. This, in turn, drives further cartilage loss and development of osteoarthritis¹⁹⁻²¹.

Osteoarthritis is the most common cause of disability for which we have no cure²². Targeting basic mechanisms shared by developmental morphogenesis and injury responses has allowed researchers to aim for cartilage regeneration for disease modification (Fig 1). One key example of this is ectopic chondrocyte hypertrophy: while hypertrophic differentiation is essential for normal development of the appendicular skeleton, adult articular chondrocytes should not undergo hypertrophy. When homeostasis is disrupted, a series of events requiring the transcription factor HIF-2 α induce ectopic hypertrophy within the articular cartilage; the articular cartilage becomes mineralized and further cartilage loss

ensues^{19–21} (Fig 2). Indeed, genetic deletion of *Hif-2α* in adult cartilage protected chondrocytes from ectopic hypertrophic differentiation and resulted in decreased cartilage degradation in murine models of osteoarthritis^{20,21}. Additional mechanisms shared between developmental morphogenesis and homeostatic responses to injury are shown in Fig 1 and summarized in table 1.

Table 1. Processes with roles in both skeletal development and osteoarthritis.

Process	Function in development	Effect in osteoarthritis	Molecular player(s)	Key references
Chondrocyte hypertrophy and mineralization	Initiate endochondral bone formation	Cartilage mineralization and breakdown	WNTs, BMPs, PTH/PTHrP, HIF-2α, RUNX2	19–21,23–25,25–29
Apoptosis	Joint cavitation; replacement of cartilage by bone	Cartilage loss	BMPs, mTOR, inflammatory cytokines (e.g. CXCL12, GCP2)	18,30–33,33–36
Mobilization of stem cells	Growth and morphogenesis	Repair and homeostasis	HMGB1, BMPs; WNT16	37–39
Proliferation and extracellular matrix synthesis	Growth and morphogenesis	Repair and homeostasis	TGF-β, BMPs	5,40

At this point the main questions were: how can we utilize such mechanisms to support cartilage repair? What are the molecules that, in injured adult cartilage, become reactivated and regulate these processes? What initiates production of stable cartilage, which doesn't result in bone formation? A transcriptomic analysis of adult articular cartilage, 24 hours after injury, revealed the re-expression of morphogenetic signals that play important roles during joint development but are otherwise inactive in the adult cartilage including the WNT, TGF-β/BMP, Hedgehog, and FGF signalling pathways^{15,16,41}.

The re-activation of such molecules in the acute-injury phase have long-term consequences on the outcome of repair. The focus on early morphogenetic events is a complete change of perspective compared to the previous emphasis, in osteoarthritis research, which targets late, downstream events such as extracellular matrix production and degradation. Two examples are the re-activation of WNT16 and PTHR1/PTHrP in adult cartilage after injury.

The case of WNT16

Wnt16 is one of the earliest markers of the joint interzone^{9,10}, but is undetectable in adult cartilage^{15,17}. We showed that 1 day after injury, *WNT16* became abundantly re-expressed in cartilage and canonical WNT signalling became activated¹⁵. The re-expression of WNT16 after injury was transient, however adult mice lacking *Wnt16* developed more severe cartilage loss and osteoarthritis 8 weeks following joint destabilization¹⁷. During its injury-induced expression, WNT16 supported the maintenance and activity of a *Prg4+* stem cell population within the superficial layer of the articular cartilage^{42,43}, while at the same time preventing more potent WNT agonists from uncontrollably activating the β -catenin-dependent pathway, which would lead to ectopic cartilage hypertrophy and ultimately loss of cartilage¹⁷. Tong et al. showed that *Wnt16* overexpression protected cartilage in a model of osteoarthritis⁴⁴. *Wnt16* delayed cartilage breakdown by activating JNK and the WNT planar cell polarity pathway, thereby ultimately upregulating *PTHrP* expression⁴⁴.

PTHrP/PTHR1 signalling

In the periarticular cartilage of the developing skeleton, activation of parathyroid hormone receptor 1 (PTHR1) by parathyroid hormone-related protein (PTHrP) increases proliferation and inhibits ectopic hypertrophic differentiation^{25,26,29,45}. This mechanism allows elongation of the bones. PTHR1 is not normally expressed in adult articular cartilage. After chronic injury, such as in osteoarthritis, PTHR1 was re-expressed and, when stimulated by exogenous recombinant human parathyroid hormone, it protected cartilage from breakdown⁴⁶.

The pathway towards disease modification and clinical application

Manipulation of the molecules driving the homeostatic responses to cartilage injury have led to remarkable results in animal models, with a seemingly endless list of potential targets. In practice, however, several factors limit clinical applicability. Some molecules play important roles in several tissues and targeting these could possibly lead to undesired effects. For instance, this is the case of mTOR, which is a central regulator of metabolism. The mTOR inhibitor rapamycin improved the outcome of osteoarthritis in mice^{47,48}, but it has severe side effects on overall health. Accessibility is also a limiting factor. Intracellular molecules and transcription factors are often difficult to target in humans (RUNX2²⁷ or HIF-2 α ^{20,21}). The route of delivery and pharmacokinetics also present limitations: for instance, intra-articular injections may limit systemic toxicity, but they are painful and would not be tolerated by patients if required too frequently.

Hereafter we review, using three examples, the path that has led to clinical experimentation and, in some cases, successful clinical trials.

Blockade of WNT signalling

WNTs are a family of secreted morphogens originally discovered for their role in oncogenesis and subsequently well studied for their role in embryonic morphogenesis ⁴⁹. In the absence of WNTs, β -catenin is constitutively degraded. When so-called “canonical” WNTs such as WNT1 or WNT3A bind to frizzled (FZD) receptors and to their co-receptors LRP5 and LRP6, the molecular complex responsible for β -catenin degradation is disrupted. This causes β -catenin to accumulate in the cytoplasm, translocate to the nucleus where it binds to TCF/LEF transcription factors and contributes to the activation of target genes ⁴⁹. Other WNTs activate pathways collectively denominated “non-canonical”, mediated by different co-receptors including ROR1 and ROR2 ^{50,51}.

Early cell and developmental biology experiments showed that the canonical WNT pathway regulates skeletogenesis ^{24,52–54} and joint morphogenesis ^{9,10,24}. In broad terms, these studies suggested that activation of canonical WNT signalling inhibited chondrogenesis in progenitor cells and initiated hypertrophic differentiation in mature chondrocytes ²⁴.

Wnt4, *Wnt9A* and *Wnt16* are the earliest markers of joint interzones ^{9,10}. Although WNT signalling is essential for joint formation ^{9,10,55–57}, the specific functions of individual ligands and receptors are largely redundant. Their function in development and adulthood are summarized in table 2.

Table 2. Roles of WNTs in cartilage development and adulthood

Molecule	Development	Adult cartilage
WNT3A	Maintains mesenchymal stem cells in an immature state in the developing limb bud, in chicks induces expression of FGF8 in the apical ectodermal ridge, promoting its formation ^{58–60}	Dose-dependent activation of β -catenin pathway, increasing chondrocyte proliferation; and non-canonical Ca ²⁺ -CaMKII dependent pathways leading to dedifferentiation of chondrocytes ⁶¹ .
WNT4	Expressed at site of future joint formation ¹⁰ . Promotes chondrocyte differentiation and hypertrophy ¹⁰ , regulating the transition from pre-hypertrophy to hypertrophy ⁸ , but is also not strictly required for normal joint formation ⁵⁸ .	Synergises with WNT9A in preventing ectopic chondrogenic differentiation of synovial MSCs ⁸
WNT5A	Expressed in the perichondrium ⁶² and regulates limb outgrowth through the planar cell polarity pathway, by activating ROR2 and Vangl2 ^{63,64} . Inhibits chondrocyte transition from	Reduces <i>COL2A1</i> and <i>Aggrecan</i> , and induces MMP1 and MMP13 expression in osteoarthritic chondrocytes ⁶⁷ .

	a resting state to proliferative. It is required for the transition from proliferative to pre-hypertrophic state, but blocks hypertrophy. Knockout and overexpression of WNT5A show similar phenotypes <i>in vivo</i> ^{10,64–66} .	
WNT8	Expressed in the perichondrium. Promotes chondrocyte hypertrophy and calcification ²⁴ .	
WNT9A	Expressed at site of future joint formation ¹⁰ . Blocks and can reverse chondrocyte differentiation ^{8–10} . Ectopic expression in chick limbs induces ectopic joint interzone formation ^{9,10} - but not required for joint formation ⁸ .	Wnt9A deficient mice develop synovial chondromatosis ⁸
WNT16	Early marker of joint interzone ⁹ . Prevents chondrocyte hypertrophy ⁴⁴ .	Buffers activation of β -catenin pathway by stronger canonical WNT ligands. Promotes cartilage homeostasis by maintaining Prg4+ expression ¹⁷ , and prevents hypertrophy through regulating mTORC1-PTHrP ⁴⁴ .
Inactivation of β -catenin	Joint fusion and delayed endochondral ossification ^{9,24,55,68} . Reduced lubricin and COL2A1 expression ⁴ .	Increased proteoglycan content and reduction in endochondral ossification <i>in vitro</i> ²⁴ . Increased chondrocyte apoptosis and articular cartilage destruction <i>in vivo</i> ^{57,69,70} .
Over-activation of β -catenin signalling	Blocks and can reverse chondrocyte differentiation ^{4,8–10,71} . Ectopic expression of constitutively active β -catenin in chick limbs induced ectopic joint interzone formation ^{9,10} .	Promotes chondrocyte differentiation, hypertrophy and cartilage calcification ^{9,24,37,55–57,62} ; Catabolism of cartilage extracellular matrix and chondrocyte apoptosis ^{54,57,72} .

		Worse outcomes in rodent OA models with cartilage loss and osteophyte formation ^{54,73} .
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In adult cartilage, both inhibition ⁷⁰ and forced activation of β -catenin signalling ⁷³ led to cartilage destruction in mice. This is because a population of cartilage-specific chondroprogenitors expressing *Prg4* ⁴² are dependent on β -catenin signalling ⁴³ whereas excessive WNT activation inhibits chondrogenesis and drives hypertrophy in already differentiated chondrocytes ^{9,24,37,56}.

Consequently, a “Goldilocks” theory took hold whereby WNT activation needs to be above a certain level in order to maintain progenitor cell populations, but below levels which drive hypertrophic differentiation in mature chondrocytes. Further complexity was added by the understanding that while a short burst of WNT activation supports articular cartilage formation and homeostasis ^{17,57}, excessively prolonged activation resulted in cartilage breakdown. Interestingly, WNT16 is both required and sufficient for cartilage homeostasis following cartilage injury ^{17,44}, and it is a partial activator of the canonical WNT pathway, maintaining “homeostatic levels” and preventing excessive activation from other more potent ligands ^{17,44}.

The relevance of these findings to human osteoarthritis was confirmed by the association of allelic variants of WNT inhibitory molecules such as *FRZB* ⁷⁴ and *DOT1L* ⁷⁵ with osteoarthritis. These data were replicated in animal models ^{28,54}.

These exciting data triggered the search for WNT inhibitors which could be used to treat osteoarthritis. Given the high level of redundancy of WNT ligands and receptors, it was unlikely that WNT inhibition outside or at the level of the cell membrane would be successful. Inhibition of WNT signalling through upregulating FRZB, by Verapamil ⁷⁶, or with a small molecule XAV-939 ⁷⁷ led to improved outcomes of osteoarthritis in animal models.

Deshmukh et al. identified a small compound (SM04690, now commercialized by SAMUMED as Lorecivivint) which, by inhibiting the intracellular kinases CLK2 and DYRK1A, inhibited WNT signalling downstream of β -catenin ^{78,79}. SM04690 proved to have a remarkable pharmacokinetic profile: after intra-articular administration in rats it could not be detected in plasma, it was detected just above therapeutic levels in bone, but it accumulated in cartilage for at least 180 days ⁷⁹. A single intra-articular administration of SM04690 improved structural outcomes in an instability-induced osteoarthritis model and improved structural outcomes, pain and weight-bearing in the monosodium iodoacetate model in rats ⁷⁹. In a phase I clinical trial, a single intra-articular injection of SM04690 proved to be safe after one year follow-up in patients with osteoarthritis (Kellgren-Lawrence score 2-3). Although the study was not designed for, and was vastly underpowered to test efficacy (61 patients in total followed up for one year), pain parameters were improved at all doses and joint space width was improved in the intermediate dose ⁸⁰. A phase II study, although it did not meet its primary endpoint, confirmed pain relief and some evidence of improvement of joint space width in patients with unilateral osteoarthritis at an intermediate dose ⁸¹.

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Interestingly, and in keeping with the notion of a “Goldilocks zone” of WNT activation, the intermediate dose yielded the best results. Whether the long-term efficacy of this compound after a single injection is due to its long-term accumulation in cartilage⁷⁹ or that perhaps the initial delivery is sufficient to trigger a self-maintaining homeostatic cascade is unknown. Although these results are promising, phase III studies are required to demonstrate efficacy.

One important contribution of this paper was the improvement of the clinical trial technology in osteoarthritis. In particular, the finding that selecting patients with unilateral symptoms and without widespread pain allows a higher level of sensitivity, especially in terms of pain, will greatly facilitate future studies with this or other compounds.

TGF- β and bone morphogenetic proteins

In 1965 Urist and Daly published the seminal paper “Bone: formation by autoinduction” in which they described that ectopic implantation of demineralised bone matrix triggered ectopic endochondral bone formation, ultimately leading to the formation of an ossicle made by cells originating from the host organism⁸². They also correctly hypothesised that some substance contained in the acellular bone matrix would be responsible for initiating the morphogenetic events leading to bone formation. In the years that followed, several groups went on to identify a family of molecules, named Bone Morphogenetic Proteins (BMPs), which, when implanted in an appropriate matrix, resulted in ectopic cartilage and bone formation^{83–85}. It became apparent that, far from being specific cartilage/bone growth factors, BMPs had a broad array of functions in different cells, stages of development and adult life. Regulation of the BMP pathway is essential for gastrulation, the formation of mesenchyme in early development, establishing the dorso/ventral patterning and the morphogenesis of virtually all organs^{86,87}.

In spite of relatively stereotypical, shared signalling mechanisms and similar *in vitro* effects on skeletal cells, the expression pattern and the biological activity of different BMPs *in vivo* varies enormously. This is exemplified by the elegant studies in the chick model in the Hurler laboratory in the mid 1990s⁸⁸. Macias et al. showed that *BMP7* is expressed in the diaphyseal perichondrium, skipping the joint interzone, and when delivered next to a joint interzone, it inhibited joint formation. Conversely, *BMP2* was expressed in the joint interzone and its ectopic delivery resulted in ectopic joint-like structures⁸⁸.

Because of the capacity of BMPs to induce cartilage and bone formation, several products were generated and tested for the repair of critical size defects, non-unions and spinal fusions^{89–92}, however, over forty years after the discovery of BMPs, the results of clinical testing in osteoarthritis and chondral defects are underwhelming⁹³. This could be due to several factors, but the stability of these molecules in inflammatory sites, their pleomorphic function in different settings and different cells, and especially their propensity to induce ectopic cartilage and bone represent serious issues^{92,94}. Overexpression of *BMP2* in adult joints resulted in ectopic cartilage and bone formation within the joint soft tissues⁹⁵ and additional cartilage degradation through upregulation of matrix metalloproteinases⁹⁶.

To circumvent this problem, investigators have tested the use of transforming growth factor (TGF)- β . TGF- β is a potent inducer of chondrocyte differentiation in a variety of stem cells, promoting *SOX9* expression, extracellular matrix production⁹⁷⁻⁹⁹.

In humans, a genetic association of alleles of *TGF- β* and downstream molecules with osteoarthritis was identified¹⁰⁰. In keeping with this, transgenic expression of a dominant negative Tgf- β receptor 2 (*Tgf- β 2*) led to formation of hypertrophic cartilage and an osteoarthritis-like phenotype¹⁰¹. However, *in vivo*, TGF- β overexpression exacerbated osteoarthritis, whereas its inhibition was beneficial in murine models¹⁰². This was true when using the TGF- β inhibitor halofuginone¹⁰³, an antibody against TGF- β 1, systemic delivery of a TGF- β 1 inhibitor or by knocking out *Tgf- β 2* in nestin-positive MSCs¹⁰².

The discrepancy between the requirement of TGF- β signalling in joint homeostasis and its negative effect when overexpressed in osteoarthritis remains enigmatic. One explanation was offered by Blaney-Davidson et al. who demonstrated that upregulation of ALK1 receptor switches TGF- β signalling from SMAD2/3 which inhibits chondrocyte hypertrophy to SMAD1/5/8 downstream, which induces chondrocyte hypertrophy^{104,105}.

The disappointing results of the use of TGF- β and BMPs in cartilage repair can be attributed to the fact that although BMP and TGF- β signalling are essential for cartilage morphogenesis and homeostasis, their function is tightly regulated both spatially and temporally, and inappropriate or excessive activation are detrimental.

FGF18

Fibroblast growth factor (FGF) signalling was one of the first pathways discovered to be activated by cartilage injury. It contributes to repair responses through release of FGF2 from the injured articular cartilage^{106,107}. However, FGF2 activates both FGF receptor-1 (FGFR1) and FGFR3, the former associated with prevalently catabolic effects on articular cartilage and the latter promoting anabolic events^{108,109}.

Mutations of FGF receptors result in a variety of skeletal defects¹¹⁰. With few exceptions, mutations of *FGFR1* and *FGFR2* result in defects of skeletal elements that form through intramembranous bone formation (craniosynostoses and similar syndromes); whereas mutations in *FGFR3* result in dwarfisms caused by defects of the bones that form through endochondral bone formation. For all these reasons, FGFR3 signalling was considered a suitable target for articular cartilage homeostasis. Dominant activating mutations in *FGFR3* resulted in hypochondroplasia, achondroplasia¹¹¹ and thanatophoric dysplasia¹¹². Recessive loss-of-function mutations of *FGFR3* resulted in camptodactyly, tall stature, scoliosis, and hearing loss syndrome (CATSHL syndrome)¹¹³. Mice lacking *Fgfr3*^{114,115} had features resembling CATSHL syndrome, whereas mice with activating mutations of *Fgfr3* had features similar to achondroplasia¹¹⁶. The skeletal defects were due to a delay in chondrocyte hypertrophy and endochondral bone formation. Given the pathogenic role of ectopic chondrocyte hypertrophy in the adult articular cartilage, this property of FGFR3 signalling supported its activation to prevent osteoarthritis progression.

In addition to halting chondrocyte hypertrophy and endochondral bone formation, FGFR3 is essential for the differentiation of mesenchymal cells into chondrocytes, as limb bud mesenchymal cells from *Fgfr3* knockout mice failed to undergo chondrogenesis in 3D culture and to proliferate in monolayer¹¹⁷. Finally, the expression of *FGFR3* is associated with the capacity of adult articular chondrocytes to form stable articular-like cartilage *in vivo*¹⁰⁸ and to repair cartilage defects in goats¹¹⁸ and humans^{119,120}.

Activating FGF receptors only in cartilage is difficult because FGFs are ubiquitous, pleiotropic and several FGF ligands can signal through multiple FGFRs. Fortunately, FGFR3 is mostly expressed in cartilage, its mutations result almost exclusively in skeletal phenotypes. FGF18, a selective ligand for FGFR3, promoted chondrocyte proliferation and differentiation^{121 117}. Alleles of *FGF18* were genetically associated with osteoarthritis in humans¹⁰⁰. Therefore, recombinant FGF18 was tested as a therapeutic for osteoarthritis. Moore et al. showed that intra-articular injections of recombinant FGF18 induced chondrocyte proliferation and cartilage repair when delivered in a therapeutic regime in rats subjected to a severe model of instability-induced osteoarthritis¹²².

Two large clinical trials provided evidence that treatment with intra-articular recombinant FGF18 (developed by Merck and Nordic Bioscience as Sprifermin) resulted in some degree of improvement of cartilage integrity in osteoarthritis^{123,124}. However, symptomatic improvement which was suggested in the first trial (phase I)¹²⁴ was not replicated in the subsequent larger trial (phase II)¹²³. Clearly, pain is a fundamental outcome for patients. We do not know whether the failure to detect pain improvement with FGF18 was due to trial design, for instance by not excluding patients with widespread chronic pain, or whether FGF18 treatment does not result in pain relief. Published pre-clinical data in animal models did not include pain measurements¹²². A corollary is that, in the absence of pain relief, it is difficult to judge the clinical relevance of the small degree of improvement in joint space narrowing reported by the authors.

Taken together, data on inhibition of WNT signalling and using FGF18 suggest that targeting homeostatic pathways has led us to turn the corner in developing pharmacological approaches for treating osteoarthritis. It is likely that improvements in clinical trial design and patient stratification will be key to measure efficacy.

From cell-based therapeutics to stem cell niches

In the mid-1990s Brittberg et al. successfully repaired full thickness cartilage defects by implanting autologous chondrocytes that had been briefly expanded *in vitro*¹²⁵. Since then, autologous chondrocyte implantation (ACI) has been tested in multiple clinical trials and has resulted in good and persistent clinical and structural benefits^{126,127}. Unfortunately, due to the autologous nature of the cells, these technologies are extremely laborious, costly, are not easily upscalable and therefore have not reached routine clinical application.

Transplantation of mesenchymal stem cells (MSCs) of various origins into cartilage defects have also shown some degree of efficacy, although the clinical trials so far have been much smaller than those with chondrocytes¹²⁸. Stem cells are clonogenic cells that

have two remarkable features: the ability to differentiate into multiple lineages (multipotency) and the ability to simultaneously replenish the stem cell pool (self-renewal)¹²⁹. Bone marrow mesenchymal cells, the first adult MSCs identified, were originally discovered as plastic adherent, non haematopoietic clonogenic cells that can differentiate into multiple skeletal lineages including adipogenic, osteogenic and chondrogenic^{130–132}.

The subsequent discovery that multiple stem cell populations persist within adult skeletal tissues^{37,38,97,98,118,131} opened up the possibility of harnessing the regenerative machinery of the adult joint by recruiting local resident stem cells to the site of damage. Stem cells originating from different tissues - such as the synovial membrane⁹⁷, the periosteum⁹⁸, the bone marrow¹³³ and the cartilage itself^{42,118,134} have distinct “default” differentiation pathways^{135–137}. The development of lineage tracking technologies enabled a much more sophisticated understanding of the nature and function of different progenitor lineages in development and in post-natal repair.

The pressing questions in order to pursue this opportunity are: why are there so many different stem cell types? Do they differ in their repair capacity? What are the molecules that govern their niches?

Progenitor lineages within the developing limb bud persist and contribute to healing in the adult skeleton

The development of the appendicular skeletal elements requires the proliferation and migration of mesenchymal cells from the LPM to form the limb bud^{138–141}. The MSCs at the periphery of the limb bud are maintained in an undifferentiated state by molecular signals (specifically FGF8 and WNT3A) which are released from the apical ectodermal ridge (AER) and surrounding ectoderm respectively^{58,142–146}. However, in the centre of the limb bud, away from the control of these signals, MSCs aggregate into the mesenchymal condensations to form the skeletal anlage. From the early stages of limb development, the anlage appears to be composed of distinct cell populations which give rise to specific cell lineages and sub-lineages, and ultimately to different skeletal structures (Fig 3)^{2,60,140,147}.

PRX1+ progenitors

Paired Mesoderm Homeobox 1 (*PRX1*) is one of the first progenitor cell markers that appears in the limb bud. *Prx1* is expressed as early as 9.5 days post coitum (dpc), stemming directly from the LPM, and by 10dpc it can be detected in almost all the skeletal mesenchyme in the limb, including the condensing mesenchyme, chondrocytes, periosteum and tendons^{148–150}. By 15dpc however, the expression of *Prx1* becomes restricted to the periosteum and tendons¹⁵⁰. The *Prx1*-expressing periosteal cells are maintained after birth and retain their capacity to differentiate into chondrocytes *in vitro*, suggesting that these periosteum-*Prx1*+ cells are both chondro- and osteo-progenitor cells^{91,150,151}.

The generation of *Prx1-cre* mice and their crossing to suitable reporters have demonstrated that *Prx1*-lineage progenitor cells give rise to all the cell sub-lineages that contribute to the formation of the bony elements, the articular cartilage, tendons and ligaments^{91,150}. *Prx1*⁺ cells also persist as MSCs postnatally within the periosteum where they contribute to callus formation after bone fracture¹⁵².

The *Prx1* lineage arises from a still earlier mesenchymal lineage expressing platelet-derived growth factor receptor α (*Pdgfra*)^{153–155} which appear as early as 6.5 dpc. Interestingly, *Pdgfra* is also a marker of progenitor cells which persist within the adult synovial membrane, and that contribute to cartilage repair³⁸.

Within the *Prx1*⁺ population, two distinct MSC populations emerge. *Osterix*⁺ cells give rise to calcified tissues including bone^{156,157} and the calcified layer of the articular cartilage⁴²; and *Gdf5*⁺ cells which give rise to the articular cartilage and other soft tissues of the joints including ligaments and tendons^{4–6}.

Osterix⁺ progenitors

During embryonic development *Osterix* (*Osx*) is expressed by both the epiphyseal chondrocytes where it promotes hypertrophic differentiation¹⁵⁷ and by an MSC population residing around the vessels of the perichondrium¹⁵⁶. Subsequently, the *Osx*⁺ periosteal precursors enter the hypertrophic cartilage accompanying the ingrowing vessels and give rise to osteoblasts to form the bone replacing the hypertrophic cartilage¹⁵⁶.

Multiple separate cell lineages were detected within developing epiphyses including *Gremlin*⁺¹⁵⁸, *Nestin*⁺¹⁵⁹ and *LeptinR*⁺^{156,160,161} progenitor cells. Whereas their identity, marker profile, and differentiation potential has been well-studied in embryonic development, their persistence as distinct progenitor populations in adulthood and particularly their contribution to tissue repair is unclear. For instance, *Nestin*⁺ cells persist in the perivascular spaces of the periosteum¹⁶² and in the adult synovial cells³⁸, however, in the absence of proper lineage tracking, their respective contribution to fracture and cartilage repair remains unconfirmed^{38,162}.

Scx+SOX9⁺ progenitors

Progenitor cells which contribute to the formation of tendons and their attachment to bones (entheses) express *Scleraxis* (*Scx*) and *Sox9*^{163–166}. *Scx* was required for the formation of tendon-to-bone attachment sites¹⁶⁷. TGF- β and BMP4 signalling were essential for the specification and differentiation of *Scx*⁺*Sox9*⁺ progenitors, respectively¹⁶⁷. Further analysis was able to dissect another distinct subset of progenitors from this pool, those which are *Scx*⁺*Sox9*⁻; both *Scx*⁺*Sox9*⁺ and *Scx*⁺*Sox9*⁻ progenitors can differentiate into tenocytes, however, those closest to the cartilaginous primordium are mostly derived from

the Sox9+ population¹⁶⁶. The Scx+Sox9+ lineage persists in the adult enthesis and periosteum¹⁶⁴ and contribute to tendon and fracture healing^{164,168–170}.

Joint progenitors

The cells that form the adult articular cartilage derive from two main lineages: the superficial and intermediate zone are contributed from progenitor cells deriving from *Prg4*+ progenitors^{4,42,43}, whereas the deep layer, which is calcified, is contributed and renewed by *Osx*+ progenitors⁴² and therefore can be considered a remnant of the epiphyseal growth plate.

GDF5+ progenitors

During embryonic development, *Gdf5/Cdmp1* is expressed within the portion of the cartilage anlage that forms the embryonic skeleton and is destined to give rise to the permanent articular cartilage. Lineage tracking experiments showed that all soft tissues (such as the articular cartilage, meniscus, synovial lining, and joint capsule) within the joint are composed of cells that, within the interzone, derive from the *Gdf5*+ progenitors^{4–6}. Until recently, *Gdf5* lineage cells were thought to be determined early during embryonic development and represented a stable population. Challenging this hypothesis, Shwartz et al. elegantly demonstrated that there is a constant inflow of *Gdf5*-lineage cells recruited to the joint interzone throughout development from the surrounding *Sox9*+ mesenchyme and, depending on the time when such recruitment occurs, they contribute to different joint structures: the first cells to be recruited contribute to the epiphyses, then to the articular cartilage and the last ones to menisci and cruciate ligaments⁶. In addition, these studies demonstrated that far from being a “stable marker”, *Gdf5* expression in the interzone cells is transient.

Gdf5-lineage cells have recently been shown to persist in the adult joint in the perivascular spaces of the synovial membrane and to contribute to the repair of cartilage injuries^{37,38}.

LGR5+ progenitors

A subpopulation of *Gdf5* lineage progenitors acquire the expression of *Lgr5* and *Col22a1* and give rise specifically to cruciate ligaments, synovial membrane, and articular chondrocytes¹⁷¹. LGR5 is a receptor that amplifies the effect of β -catenin dependent WNT signalling through binding R-spondins¹⁷², a signalling pathway that the progenitor cells of the superficial cartilage layer are strictly dependent on⁴³. Implantation of embryonic *Lgr5*+ cells into an adult murine cartilage defect resulted in cartilage repair¹⁷¹, however it is not known if *Lgr5*+ cells persist in the adult joint and, if so, whether they contribute to cartilage healing.

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Interestingly, however, *Lgr5* expression is detected in the *Gdf5*-lineage population, prior to the expression of *Prg4*¹⁷¹, an additional chondro-progenitor which largely resides in the surface of the articular cartilage.

Prg4+ progenitors

Prg4 (the gene encoding lubricin) is expressed in the mouse joint interzones starting from 15.5dpc⁴. With time, the expression of *Prg4* increases and *Gdf5* decreases⁴. PRG4 expression persists throughout adult life at the surface of the articular cartilage and within the synovium but is not detectable in the growth plate cartilage¹⁷³. *Prg4*+ progenitor cells within the superficial layer of the articular cartilage contribute to the turnover of chondrocytes of the non-calcified cartilage layers throughout life⁴² but it is likely that it is the synovium-residing *Prg4*+ progenitors that contribute to cartilage healing after injury³⁷. By combining nucleoside labeling, *Prg4* lineage tracking and *Confetti* mice, Decker et al. showed that *Prg4*+ progenitors proliferated within the synovial membrane, migrated and contributed to repair of cartilage defects. *Prg4*+ cells residing within the cartilage adjacent to the defect sites did not proliferate or contribute to repair³⁷. Interestingly, Seol et al showed that the transcription factor *Hmgb-1* released by dying chondrocytes functions as a chemoattractant for *Prg4*+ progenitor cells, thereby possibly supplying a mechanistic explanation of their recruitment to the site of damage¹⁷⁴.

The overlap between the *Gdf5*+ and the *Prg4*+ progenitor populations in mature cartilage is not definitively established, given the absence of dual lineage tracking, however, experiments from the Pacifici laboratory suggest that *Prg4* positivity is a feature of the differentiating *Gdf5*+ cells⁴.

Summary

The identification of different stem cell lineages with unique roles during development, homeostasis or the repair of musculoskeletal tissues is a major step forward in regenerative medicine. The understanding of the molecular control of stem cell niches, their maintenance, proliferation, migration and differentiation is revealing molecular tools to trigger repair by mobilizing progenitor cells. This may enable timely morphogenesis of the repair tissues without the need for expensive and laborious cell manipulations outside of the body. These approaches will generate upscalable, affordable production of effective and safe off-the-shelf therapeutics for the treatment of cartilage defects or osteoarthritis.

Conclusions

As described in this review, several molecular targets are now available to treat cartilage degeneration. Clinical success will depend on our ability to understand the hierarchy of the homeostatic signals and the reason for repair failure in individual patients.

Molecular hierarchy. Interactions between the biological pathways and stem cells that contribute to skeletal homeostasis makes it hard to unpick the role of individual molecules, and the changing landscape of ligand/receptor/signalling molecule expression as cartilage degenerates must be carefully considered. The identification of key players that can initiate the repair cascade, from the recruitment of the stem cells from their niches to establishing morphogenesis of the repair tissues, without affecting the surrounding healthy tissues will be key to achieve affordable, effective and safe therapeutic interventions.

Patient stratification. Failure of repair/homeostasis in different patients may depend on different mechanisms. For instance some patients may fail to repair because of poor stem cell recruitment, while others will progress because of poor tissue patterning or failure of differentiation. The selection of the right treatment for the right patient can be achieved with the identification of downstream targets of the homeostatic signals which can be used to identify the failure mechanism and at the same time as surrogate efficacy markers.

Pharmacokinetics. The timing, duration, delivery method and dosing of the interventions within the appropriate tissues will be critical. For instance, a brief, well-dosed activation of WNT signalling is beneficial for cartilage health under certain conditions⁵⁷, but persistent WNT activation is detrimental and even a burst of activation in patients with already established osteoarthritis, where WNT signalling is already over-activated, may be detrimental. Understanding the pathological processes in individual patients, combined to the availability of controlled delivery systems will be key to success.

The understanding of the developmental mechanisms of joint morphogenesis has enabled the identification of individual targets and, we predict, will continue to be crucial to address some of these key issues.

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Conflicts of interest

Professor Dell'Accio has obtained consultancy fees from Samumed and UCB Pharma.

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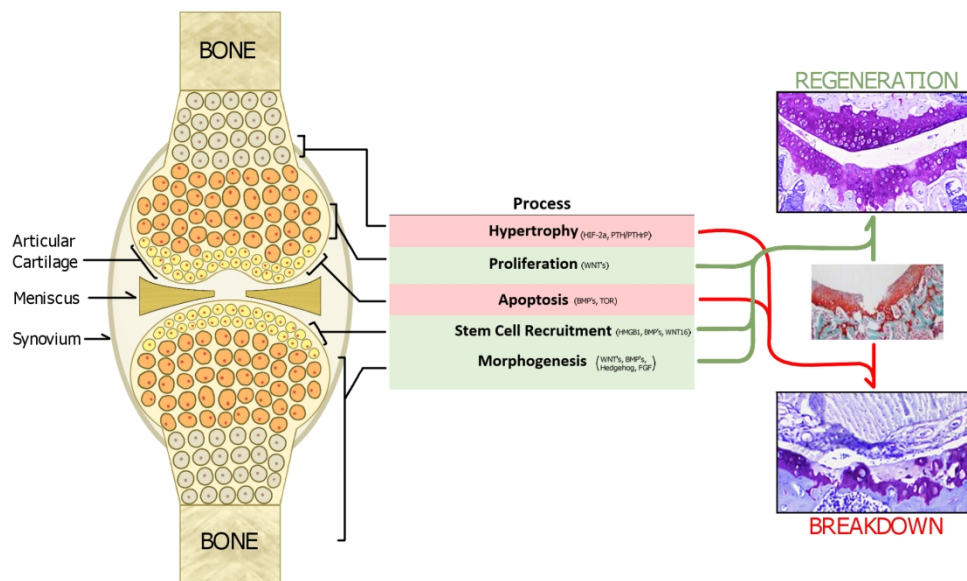


Figure 1. Embryonic morphogenesis and skeletal repair in adulthood share basic processes. Proliferation, hypertrophy, apoptosis, stem cell recruitment and morphogenesis are processes which are initiated during development to create the joint. These processes are re-activated in injured joint tissues. The spatial and temporal regulation of these processes determines the outcome of the injury response, either successful regeneration or breakdown.

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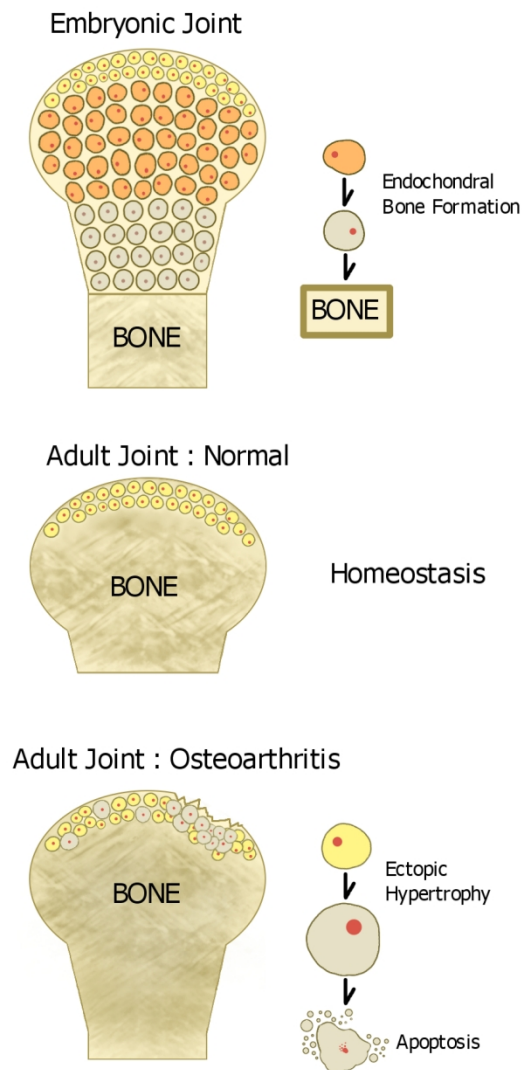


Figure 2. Chondrocyte hypertrophy is required for endochondral bone formation during development but is a pathogenic event in the adult osteoarthritic joint.

During development, epiphyseal chondrocytes undergo hypertrophy and ultimately endochondral bone formation. In a healthy adult joint, chondrocytes remain at the joint surface and reside in the permanent articular cartilage. Throughout the progression of osteoarthritis, however, these articular chondrocytes begin to undergo 'ectopic hypertrophy', resulting in the mineralisation and ultimately, breakdown of the articular cartilage.

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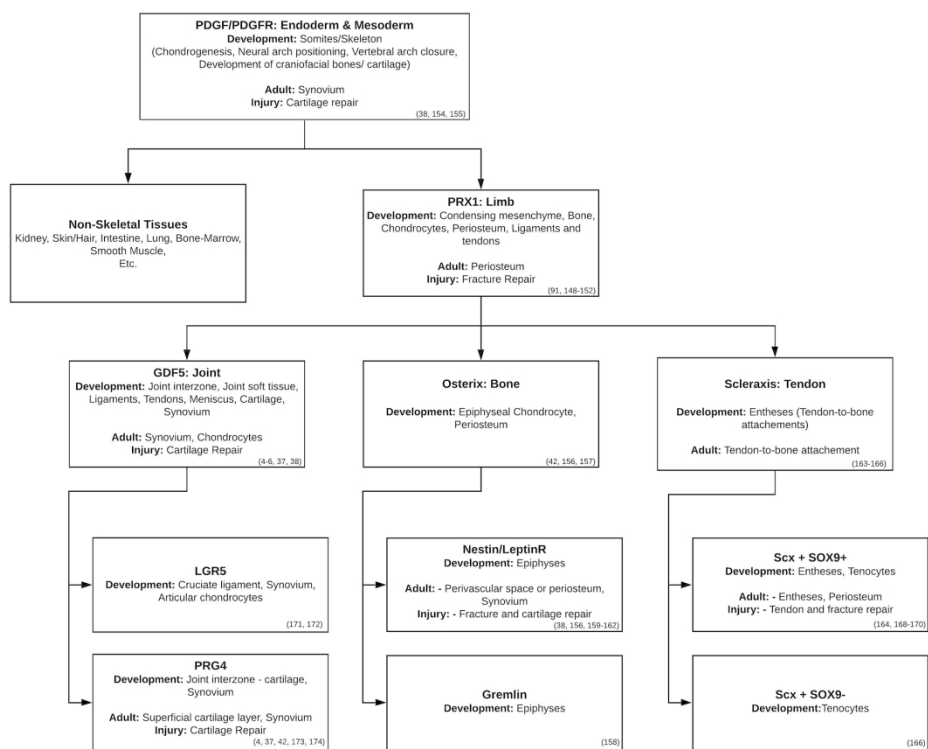


Figure 3. Musculoskeletal stem cell lineage tree. Condensed mesenchymal stem cells expressing PDGFR α differentiate to express PRX1 in the early limb bud. Subsequent differentiation of the PRX1 expressing stem cells recruits them to GDF5, Osterix or the Scleraxis lineage, which are responsible for the development of the tissues in the joint, bone and tendons respectively.

203x161mm (300 x 300 DPI)