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Homeostatic Mechanisms in Articular Cartilage and Role of Inflammation in Osteoarthritis

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Abstract

Osteoarthritis (OA) is a whole joint disease, in which thinning and disappearance of cartilage is a critical determinant in OA progression. The rupture of cartilage homeostasis whatever its cause: aging, genetic predisposition, trauma or metabolic disorder, induces profound phenotypic modifications of chondrocytes, which then promote the synthesis of a subset of factors that induce cartilage damage and target other joint tissues. Interestingly, among these factors are numerous components of the inflammatory pathways. Chondrocytes produce cytokines, chemokines, alarmins, prostanoids and adipokines and express numerous cell surface receptors for cytokines and chemokines, as well as toll-like receptors. These receptors activate intracellular signaling pathways involved in inflammatory and stress responses of chondrocytes in OA joints. This review focuses on mechanisms responsible for the maintenance of cartilage homeostasis and highlights the role of inflammatory processes in OA progression.

Keywords

Chondrocytes; Homeostatic mechanisms; Articular; Cartilage; Osteoarthritis; Inflammation; Mechanical stress; Homeostasis; Cartilage matrix degradation; Alarmins; Toll-like receptors; Chemokines; Adipokines; Mechanotransduction

Introduction

Although osteoarthritis (OA) is considered a disease of the whole joint as an organ, the articular cartilage is altered to some extent in all affected joints with OA. In addition to the development of cartilage changes with aging, cartilage degeneration may occur in response to inappropriate mechanical stress and low-grade local or systemic inflammation associated

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with trauma, obesity, metabolic syndrome, and genetic predisposition, which are major risk factors of OA development and progression [1, 2]. However, strong functional interactions among the cartilage, synovium, and subchondral bone impact on cartilage function in such a way that it is difficult to know where and when pathological changes begin. Nevertheless, the knowledge we have gained from studies of cartilage derived from the clinic and from animal models has uncovered many important biological factors that impinge on chondrocytes, the cellular component of cartilage, in a temporal and spatial manner to produce pathological changes.

Structure and organization of the articular cartilage

Cartilage is a connective tissue comprising chondrocytes as the unique cell type, which are embedded within an extracellular matrix. Chondrocytes maintain the matrix components under normal, low-turnover conditions in which the glycosaminoglycans on proteoglycans and other non-collagen molecules can be replaced. In normal adult cartilage in the resting, non-stressed steady state, chondrocytes are quiescent cells and there is very little turnover of the collagen network, as the half-life of type II collagen has been calculated as 120 years, whereas that of aggrecan is 120 days.

In spite of this apparently simple structure, articular cartilage is a complex tissue showing different matrix composition and cellular organization ranging from the superficial zone through subchondral bone (Fig. 1). The thickest part of articular cartilage consists of non-mineralized tissue, whereas the thinnest and deepest layer is calcified cartilage. Within the non-mineralized cartilage can be defined three distinct zones, the superficial, the intermediate, and the radial, each characterized by the distinct extracellular matrix composition and organization, as well as by different phenotypic and the gene expression patterns of the resident chondrocytes [3]. Another level of complexity is revealed by differences in matrix constituents between the interterritorial region containing the collagen network and aggrecan as major components, and the pericellular matrix, containing such proteins as collagen VI, fibromodulin, and matrilin 3, but little or no type II collagen.

The calcified cartilage interfaces the non-mineralized articular cartilage and the subchondral bone, although direct interactions between the non-calcified cartilage and the subchondral bone have also been described [4]. The tidemark, a thin line revealed after hematoxylin staining, marks the mineralization front between the calcified and non-calcified articular cartilage [5]. The tidemark displays a peculiar matrix composition [6] and also comprises matrix vesicles [7]. The calcified cartilage has unique matrix composition with chondrocytes that express markers of hypertrophy. With aging, blood vessels and nerves can be observed in the calcified cartilage arising from the subchondral bone [8], whereas the non-calcified cartilage is normally avascular and aneural (Fig. 1).

Cartilage functions and homeostasis

Cartilage provides a smooth surface with a very low coefficient of friction allowing for an efficient gliding motion during joint movement. This is facilitated by a boundary layer of lubricants on the articular surface provided by lubricin and hyaluronic acid produced by both chondrocytes and synovial cells [9,10]. A main function of cartilage is the absorption and

dissipation of mechanical load. This is allowed by the spatial organization of the matrix components in the superficial layer and by the high content of proteoglycans. Mechanical load is necessary for cartilage homeostasis (Fig. 1). It induces fluid movement between the cartilage and the synovial fluid, playing an important role in the diffusion of molecules across cartilage and thus facilitating its nutrition [11].

Numerous *in vivo* studies show that immobilization leads to joint damage [12]. Notably, a loss of proteoglycan content associated with increased MMP-3 (matrix metalloproteinase 3) and ADAMTS-5 (A Disintegrin and Metalloproteinase with Thrombospondin Motifs 5) is observed in rodents after hind limb immobilization, whereas joint movement prevents protease increase and proteoglycan loss [13]. Moreover, mechanical stimulation has opposite effects on anabolism and catabolism, increasing aggrecan and decreasing MMP-3 expression in human chondrocytes [14]. In addition, *in vitro* low-intensity cyclic mechanical loading of chondrocytes inhibits interleukin 1 (IL-1)- and tumor necrosis factor α (TNF- α)-induced inflammatory and catabolic responses [12]. Mechanical sensors in chondrocytes include integrin, syndecan, and ion channels. The primary cilium is a non-motile organelle that projects from cells in almost all vertebrate cells and acts as a mechanical sensor [15]. In Tg737^{orpk} mutant chondrocytes, which do not express the protein polaris required for ciliary assembly, compression-induced Ca²⁺ signaling is lost [16]. Mechanical sensors, including calcium channels and integrins, are found in the primary cilium [15, 17], especially in chondrocytes [18]. In the load-bearing area of horse cartilage, the primary cilium is aligned in different orientations in the superficial and radial zones, whereas this organization is lost in the non-load-bearing areas [19].

The primary cilium has roles in cartilage homeostasis that exceed its involvement solely as a mechanical sensor, as suggested by observations of skeletal defects in mutant mice without primary cilia (Fig. 1) [20]. In the absence of primary cilia, marked changes in the cellular organization and defects in matrix component deposition are observed in the growth plate and the articular cartilage of mice [21-23]. Hedgehog (Hh) signaling plays an important role in chondrogenesis, hind limb formation and growth plate organization. Recent studies have shown that the primary cilium is a crucial component of Hh signaling [24]. Moreover, in the Col2aCre;Ift88^{fl/fl} mouse strain, in which the polaris protein is specifically deleted in chondrocytes, the defect in articular cartilage structure is associated with increased Hh signaling [21]. A recent study proposed that increased Hh signaling due to the loss of primary cilia is involved in chondrosarcoma development [25]. In addition to mechanotransduction and Hh signaling, the primary cilium can also be a partner in inflammatory pathways. The induction of prostaglandin (PG) E₂ and nitric oxide (NO) release by IL-1 β in chondrocytes is indeed prevented in Tg737^{orpk}-derived chondrocytes [16].

Since cartilage is an avascular tissue, chondrocytes live in a hypoxic environment (Fig. 1). Oxygen and nutrients come from the vascular supply in the joint capsule, synovium and subchondral bone. Hypoxia is therefore the normal environment for chondrocytes, which synthesize and accumulate higher amounts of type II collagen and aggrecan when cultured under hypoxia rather than normoxia [26]. In addition, hypoxia displays a protective effect on cartilage, since the basal synthesis and release of MMP-1 and MMP-13, as well as

generation of type II collagen cleavage fragments, are lower under hypoxia than in normoxia [26]. Similarly, the production of PGE₂ and NO by porcine chondrocytes in response to IL-1 α and TNF- α is decreased when cells are cultured in hypoxia [27]. Hypoxia inducible factor 1 (HIF-1) is a heterodimeric (α/β) transcription factor, whose protein levels are regulated by oxygen. Under normoxia, the cell content of HIF-1 is low due to the hydroxylation of the α -subunit on specific proline residues by prolyl-hydroxylases. The proline-hydroxylated form of HIF-1 α promotes interaction with the von Hippel-Landau tumor suppressor protein, an E3 ubiquitin ligase, and proteolytic inactivation by the proteasome. In contrast, under hypoxia, prolyl-hydroxylase activity is reduced and sustained amounts of HIF-1 α can be measured. The gene encoding HIF-1 α , *Epas1*, is expressed in cartilage. Several studies have provided evidence that HIF-1 α is an important factor promoting chondrocyte function and survival [28-30]. The specific deletion of the *Epas1* gene in the cartilaginous growth plate is associated with chondrocyte apoptosis [30]. The intraarticular injection of 2-methoxyestradiol, an inhibitor of HIF-1, in Balb/C mice promotes OA lesions with cartilage degradation and osteophyte formation [31].

Cartilage changes in osteoarthritis

In OA, early changes in cartilage appear at the joint surface in areas where mechanical forces such as shear stress are greatest [32]. The normally quiescent chondrocytes undergo a phenotypic shift and become “activated”, characterized by cell proliferation, cluster formation, and increased production of both matrix proteins and matrix-degrading enzymes (Fig. 2) [33]. Disruption of the normal resting state of chondrocytes may be viewed as an injury response involving the recapitulation of developmental programs, leading to matrix remodeling, inappropriate hypertrophy-like maturation, and cartilage calcification [10, 33, 34]. This increased cartilage calcification is associated with tidemark advancement, or duplication, and vascular penetration from the subchondral bone. Whether these events precede, or not, the early changes appearing at the surface remains controversial [35].

Hypertrophic chondrocytes express the genes encoding Runx2, MMP-13, and type X collagen, which can all be detected in OA cartilage. Interestingly, increased mRNA expression of these markers is observed in the articular cartilage of Col2a-Cre;Ift88^{fl/fl} mice, whose chondrocytes are devoid of primary cilium [21], suggesting that disruption of cartilage development due to loss of primary cilia may play a role in OA development in adult mice. Paradoxically, the number of primary cilia observed on chondrocytes in bovine OA tissues seems to increase with OA progression [36], suggesting that any disruption of the normal pattern of primary cilia in cartilage results in loss of homeostasis.

At the osteochondral junction, vessels are found in structures called vascular channels [37], which also contain osteoblasts and osteoclasts (Fig. 2) [38]. Interestingly, soluble mediators secreted by these bone cells could cross the osteochondral junction inducing deleterious phenomenon in cartilage (Fig. 2) [39]. Osteoclast-derived TGF- β 1 is activated in subchondral bone in response to altered mechanical loading in an anterior cruciate ligament transection (ACLT) mouse model of osteoarthritis [40]. Osteoblast-derived 14-3-3 ϵ dose-dependently induces the release of catabolic factors by chondrocytes [41]. These vascular channels also contain sensory nerve terminations [42]. The presence of sensory nerve

terminations within vascular channels and the positive association between the number of vascular channels and the clinical disease activity [42] suggest a link between the remodeling of the osteochondral junction and OA pain [42]. Moreover, the application of a specific angiogenesis inhibitor PPI-2458 in a rat OA model limits joint damage and pain, in addition to osteochondral angiogenesis [43].

Consequences of cartilage matrix degradation

The main cartilage matrix degrading enzymes are zinc-dependent metalloproteinases belonging to MMP and ADAMTS families. MMPs include the collagenases MMP-1 and MMP-13, the latter being highly efficient against type II collagen as a substrate, and MMP-3, which is a potent aggrecanase and MMP activator. The other major aggrecanases in cartilage are ADAMTS-4 and ADAMTS-5. In addition, several serine and cysteine proteases are found in OA joint, including cathepsins K [44].

Chondrocytes sense mechanical stress and changes in the pericellular matrix largely through receptors for extracellular matrix (ECM) components. The patterns of integrin receptors, for example, change in response to mechanical or inflammatory stimuli, resulting in upregulation of aggrecanases and collagenases. However, the receptors on the resting chondrocyte are protected from interacting with certain matrix components by the unique composition of the pericellular matrix. The type II collagen-containing network in the interterritorial region is normally not accessible to degradation because it is coated with proteoglycans. The importance of proteoglycan depletion in cartilage erosion was demonstrated in *Adamts5* knockout mice, which are protected against progression in the surgical OA model [45]. However, aggrecan depletion, by itself, does not drive OA progression, as suggested by studies in *Mmp13* knockout mice showing that MMP-13 deficiency inhibits cartilage erosion, but does not prevent aggrecan depletion [46]. Once the collagen network begins to degrade, this marks progression to irreversible cartilage degradation.

Mechanical stimulation induces the expression of MMPs by chondrocytes (Fig. 2) [47]. In addition, recent studies suggest that biomechanical stress may initiate the disruption of the pericellular matrix through the serine proteinase, High Temperature Requirement A1 (HTRA1) [48]. The receptor tyrosine kinase, discoidin domain receptor 2 (DDR2) is then exposed to its ligand, native type II collagen, becomes activated, and preferentially induces and activates MMP-13 [49]. Syndecan-4, a trans-membrane heparan sulfate proteoglycan involved in the maintenance of homeostasis, is a positive effector of ADAMTS-5 activation through controlling the synthesis of the MMP-3 [50].

As articular cartilage matrix proteins are degraded, activation of certain receptors stimulates the production of matrix-degrading proteinases and inflammatory cytokines and chemokines, either as initiating or feedback amplification events. Fragments of matrix proteins are produced which can interact with integrin receptors and stimulate or feedback amplify further matrix destruction (Fig. 2). Fragments found in OA cartilage include fibronectin [51, 52], small leucine-rich proteoglycans [53], and collagen [54]. Fibronectin

and collagen fragments, in turn, can stimulate the production of inflammatory cytokines, chemokines, and MMPs [10,51, 55, 56].

Cartilage matrix degradation products may activate innate immune responses. Members of the small leucine-rich proteoglycan (SLRP) family such as fibromodulin and decorin may target the classic complement pathway and enhance or inhibit its activation [57]. COMP, on the other hand, is a potent activator of the alternative complement pathway and complexes of COMP and C3b may be found in OA synovial fluids [58]. Interestingly, expression levels of inflammatory and degradative molecules are lower in chondrocytes from destabilized joints from C5-deficient mice than C5-sufficient mice, and the membrane attack complex induces production of these molecules in cultured chondrocyte [59]. Many of the receptors discussed above may be present in synovial cells accounting for amplification of their downstream responses and perpetuation of the “vicious” cycle.

Pro-inflammatory signals and mechanotransduction

Although overt inflammatory processes are not present except locally in OA joints, abnormal mechanical and oxidative stresses are probably involved in the induction of inflammatory mediators, including cytokines, chemokines, cyclooxygenase (COX)-2, microsomal PGE synthase-1 (mPGES-1), soluble phospholipase A2 (sPLA2), and inducible nitric oxide synthase (NOS2), which contribute to the dysregulation of the chondrocyte function and the exacerbation of the cartilage erosion and loss of function (Fig. 2). Chondrocytes in OA cartilage, especially those in clonal clusters, express receptors that may respond to cytokines and chemokines produced in the synovium and other periarticular joint tissues and detected in OA synovial fluid [60]. Although IL-1 β mRNA may be induced in chondrocytes, and the inflammasome complex, including NALP-3 and the IL-1 β activator caspase-1, is expressed in OA cartilage, active IL-1 β is not produced and secreted by OA chondrocytes suggesting that cartilage may be degraded independently of inflammasome activity [61]. Many studies have shown that inflammatory cytokines stimulate expression of MMP-3, -9, and -13, which co-localize with type II collagen cleavage epitopes in regions of matrix depletion in OA cartilage. The regulation of ADAMTS-4 and -5 by inflammatory stimuli in cartilage may be species-specific [62-64].

High magnitude, injurious mechanical stress, which results in the subsequent release of cartilage matrix degradation products, is a major risk factor for OA onset and progression, in part because it triggers the same signaling pathways as those induced by inflammatory cytokines. Along with NF- κ B activation and translocation [65-67], the activation of cell surface mechano-receptors by mechanical forces also induces mitogen activated protein kinase (MAPK) signaling [68, 69], thus controlling the expression of downstream target genes such as *MMP13*, *NOS2*, *COX2*, *ADAMTS*, and *IL1B* genes. Since these pathways are also known to both induce and amplify the expression of cytokine and chemokine genes, it therefore remains controversial whether inflammatory mediators are primary or secondary regulators of cartilage damage and defective repair mechanisms in OA (for review, see [33, 70]). Activation of the extracellular-regulated kinase (ERK), c-Jun N-terminal kinase (JNK) and p38 MAPK signaling cascades coordinates phosphorylation events that result in the activation of transcription factors such as AP-1 (cFos/cJun), ETS, Runx2, HIF-2 α , and C/

EBP β , which together with NF- κ B, regulate expression of genes involved in catabolic and inflammatory events [60, 62, 71-76].

During mechanical loading and the development of OA, there is evidence for the loss of cells starting in the superficial zone of cartilage [77], which is associated with an age-related decrease in HMGB2 [78]. Increased production of ROS mediated by mechanical injury or in response to cytokines and matrix fragments may also contribute to cell death [77]. Caspase inhibitors block cell death and result in decreased severity of cartilage lesions in a rabbit model of post-traumatic OA [79]. Autophagy, which serves as a protective mechanism used by cells under stress, also declines with increasing OA severity [80], and rapamycin acting through the mTOR signaling pathway activates autophagy and reduces the severity of experimental murine osteoarthritis [10,81-83].

Chemokines

Chondrocytes also express chemokine receptors including CXCR3, CXCR4, CXCR5, CCR1, CCR3, CCR5 and CCR6 and numerous chemokines, including IL-8, MIP-1 α , GRO $\alpha\beta\gamma$, MCP-1, eotaxin-1 and RANTES, which may play important roles in activating catabolic pathways and chondrocyte hypertrophy [56, 84-89]. Chemokines can act as chemoattractants and they play a crucial role in tissue homeostasis, especially in the immune system. Inappropriate activation of the chemokine network is associated with inflammatory arthritis and other autoimmune and inflammatory conditions. Many chemokines are produced in joint tissues of patients with OA and after joint injury [90-92]. The synovia of patients at an early stage OA have a unique synovial chemokine signature, with expression of CCL19 and its receptor CCR7 associated with increased symptoms [92]. Elevated levels of CCL5 and CCL19 have been detected in synovial fluids from patients with both RA and OA [93, 94].

Toll-like receptors and alarmins

Molecules released from the damaged cartilage matrix into the synovial fluid have been implicated in promoting the release of proteolytic enzymes by synovial cells and recruitment of inflammatory cells to the joint (Fig. 2) [95-97]. These secreted damage-associated molecular patterns (DAMPs) or alarmins, act as ligands of Toll-like receptors (TLR) or Receptor for Advanced Glycation Endproducts (RAGE) to activate inflammatory and catabolic events in articular cartilage and other joint tissues [98-100]. Chondrocytes express TLRs, whose expression is increased in OA cartilage and induced by inflammatory stimuli [101-104]. TLR-2 and 4 levels are increased in areas of cartilage near OA lesions. The activation by the TLR-2 and 4 ligands, peptidoglycan and LPS, respectively, leads to increased expression of downstream inflammation-related genes including MMPs and NOS2 via NF- κ B signaling [105]. Plasma proteins present in OA synovial fluid may function as DAMPs and thereby contribute to a low-grade inflammatory state [106].

Both hydroxyapatite crystals and calcium pyrophosphate crystals, associated with calcification of the articular cartilage and meniscus, or chondrocalcinosis, are common in the joints of older adults with knee OA [107, 108]. Calcium pyrophosphate crystals may stimulate TLRs present on chondrocytes and synovial cells to promote production of

inflammatory mediators, including nitric oxide [109]. Activation of the NLRP3 inflammasome by hydroxyapatite crystals may stimulate production of inflammatory mediators, including IL-1 and IL-18 [110].

The alarmins, S100A4, A8, A9, and A11, along with high mobility group box (HMGB) protein 1, also signal through RAGE and TLRs to drive matrix catabolism and increase reactive oxygen species (ROS) through upregulating cytokines and chemokines [71, 111-113]. The RAGE ligand S100A11 can drive inflammation-associated chondrocyte hypertrophy and matrix catabolism [114, 115]. HMGB1 acts on articular chondrocytes [116] and osteoarthritic synoviocytes [116] primarily by potentiating the responses to other alarmins. Together with TLR ligands, HMGB1 acts as a cytokine-like signal of innate immunity to induce a hypertrophy-like phenotypic shift in OA chondrocytes [105]. In addition, S100 proteins, including S100A4, S100A8 and S100A9 have been implicated in enhancing chondrocyte catabolism, indicating that the release of DAMPs by surrounding tissues may contribute to cartilage destruction [112, 118, 119].

Adipokines

Although obesity may result in overloading of joints and subsequent OA, the 'low-grade inflammatory state' of obese subjects is also considered an important risk factor for OA, partly based on the identification of adipokines in white adipose tissue as an endocrine organ that can contribute to immunity and inflammation (for review, see [120, 121]). Adipokines can also be produced by joint cells including chondrocytes and act locally in cartilage homeostasis and destruction (Fig. 2). Although leptin levels are increased in OA cartilage compared to normal articular cartilage, this adipokines has biphasic effects, contributing to degradation at concentrations and promoting anabolism at lower concentrations, whereas adiponectin may have a protective role against OA. Chondrocyte expression of adipokines can be induced by inflammatory stimuli [122], and stimulation of articular chondrocytes with leptin, adiponectin, visfatin/nampt or resistin, alone or in combination with other inflammatory cytokines, can induce and enhance the expression of, MMPs, NOS2, and cytokines themselves [123-127]. Whether the different adipokines are protective, possibly induced as a feedback mechanism, or detrimental *in vivo* is unclear, as there is limited information from *in vivo* models [128-130].

Conclusions

Cartilage is a highly specialized connective tissue, whose damage is the main feature of OA. Whatever the primary determinant of OA: aging, genetic predisposition, metabolic syndrome or trauma, an activation of the inflammatory pathways occurs in cartilage [131]. Chondrocytes express numerous cytokine and chemokine receptors as well as TLRs. Chondrocytes produce inflammatory mediators able to drive cartilage damage and adjacent joint tissue alterations, thus establishing a vicious cycle leading to the progression of OA. Therefore, it appears of primary importance to better define the key components of inflammatory pathways in order to discover disease-modifying OA drugs in the future.

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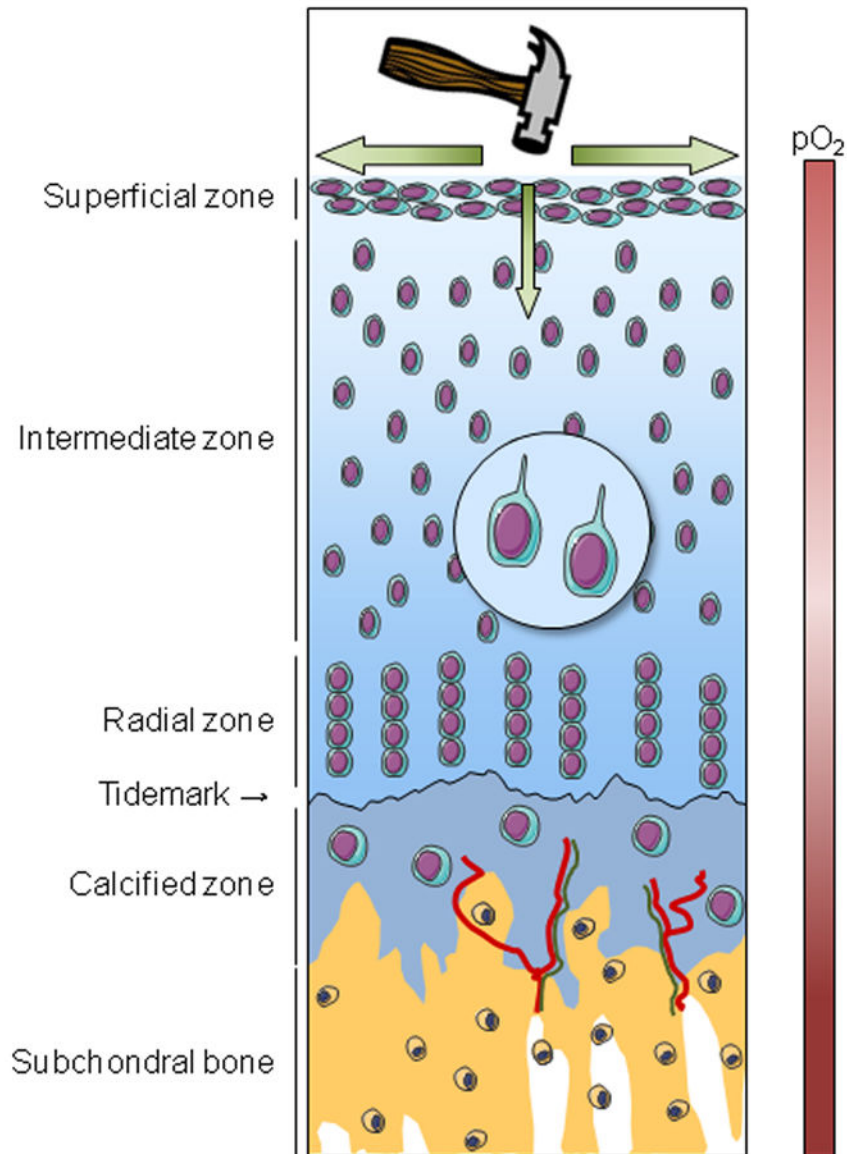


Figure 1. Schematic representation of cartilage organization in healthy joint

Healthy articular cartilage comprises four different areas: the superficial, intermediate, radial and calcified zones. Each is characterized by a peculiar chondrocyte phenotype and by distinctive extracellular matrix organization and composition. The calcified zone differs from the three other zones by the mineralization of its extracellular matrix, by the presence of vessels (red) and by nerve fibers (green) that originate from the subchondral bone. The calcified zone interfaces with the non-mineralized cartilage, from which it is separated by the tidemark, and the subchondral bone. Due to the absence of vessels within cartilage, chondrocytes live in a hypoxic environment. Hypoxia is important for chondrocyte function and viability. Oxygen and nutrients come from the vascular supply in the synovium and the subchondral bone. A main function of cartilage is the absorption and the dissipation of mechanical load, which is necessary to maintain cartilage homeostasis. The primary cilium

plays a crucial role in cartilage homeostasis, especially in the perception of mechanical load due to the presence of integrins and ion channels.

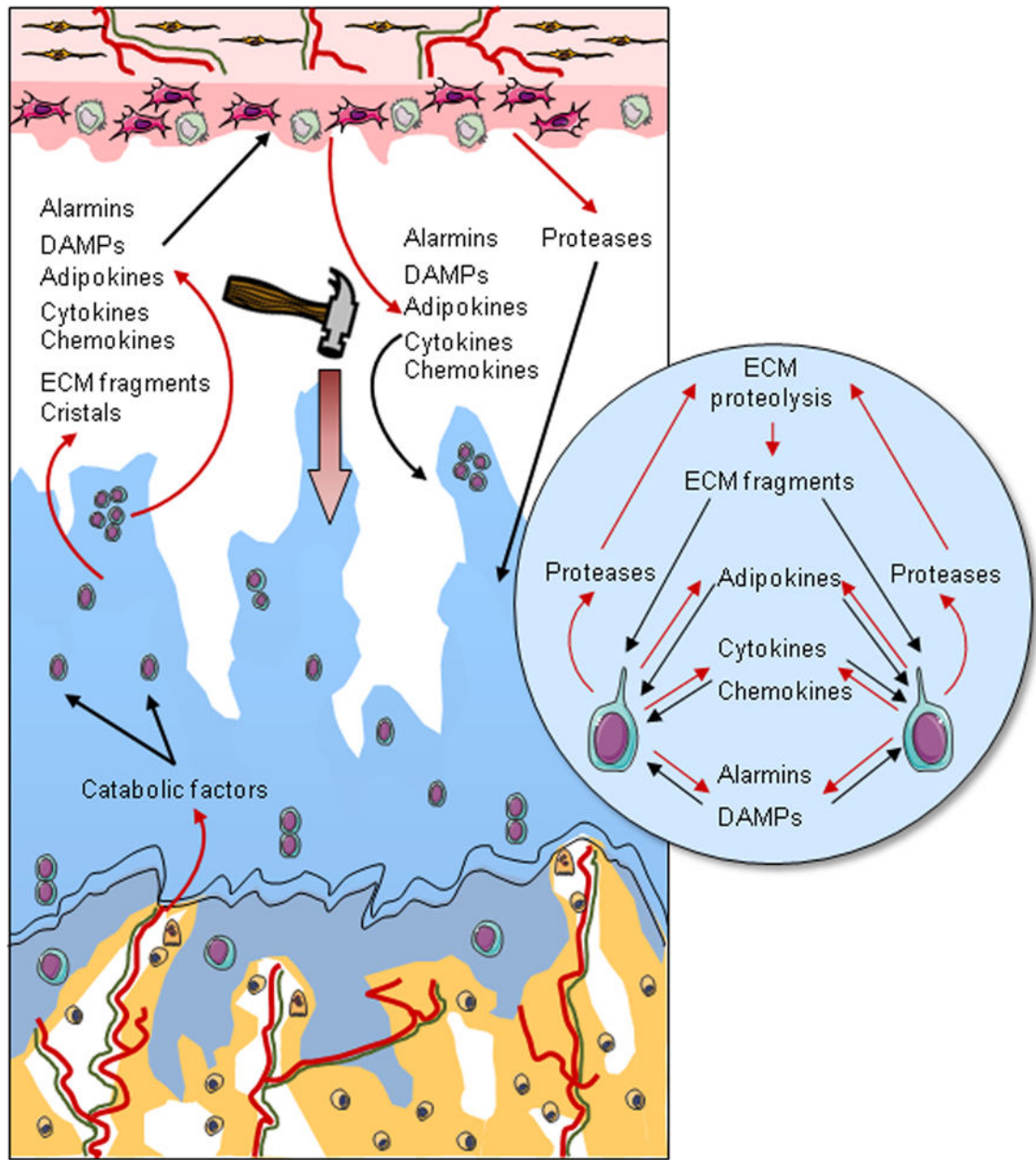


Figure 2. Schematic representation of cartilage alterations in OA

In OA, there is a progressive disappearance of cartilage associated with chondrocyte loss and phenotypic modifications, including the formation of clusters, the activation of a catabolic phenotypic and hypertrophic differentiation. In addition to cartilage damage, remodeling of the subchondral bone occurs with the development of vessels (red) located in structures called vascular channels, which also contain osteoblasts, osteoclasts, and sensory nerves (green). Vascular channels are supposed to facilitate biochemical communication between the bone and the cartilage. In response to several stimuli, including inappropriate mechanical loading and catabolic factors coming from the subchondral bone, chondrocytes modify their phenotype and express a subset of factors, such as cytokines, chemokines,

alarmins, DAMPs, and adipokines. All of these mediators act as paracrine factors and initiate a vicious circle of cartilage degradation but also reach the synovium and provoke an inflammatory process with the production by synovial macrophages and fibroblasts of factors, which both promote inflammation in the synovium and participate in cartilage damage.