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HMGB1 in inflammation - secretion and function

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With love to my family

ABSTRACT

Rheumatoid arthritis (RA) is a chronic inflammatory disease characterised by progressive joint destruction. The inflammatory and joint destructive processes in RA are mediated by resident synovial cells and cells recruited from the blood stream and bone marrow. A variety of cytokines, chemokines and proteases contribute to the cartilage and bone destruction.

High mobility group box chromosomal protein 1 (HMGB1) was discovered over three decades ago as a transcription-regulating protein. In addition to its nuclear role, HMGB1 expression was detected at the leading edges in motile cells and its active secretion from immune cells was demonstrated. An excessive HMGB1 expression has been recorded in arthritic joints and in synovial fluid from RA patients and HMGB1-blocking therapies have been demonstrated to attenuate the disease course in murine arthritis models, suggesting that HMGB1 is a key player in arthritis.

The focus of this thesis work has been to further the understanding of HMGB1 as an inflammatory mediator and its role in arthritis. More specifically, I have studied the induction of HMGB1 secretion from a variety of inflammatory cells, how HMGB1 blockade affects the proinflammatory cytokine pattern in cell cultures and how HMGB1-targeting therapy affects the disease development in collagen-induced arthritis (CIA). Finally, I have also studied the inflammation-inducing capacity of HMGB1 alone and in complex with other proinflammatory molecules.

In order to quantify HMGB1 secretion from different cell types an HMGB1-specific ELISpot method was developed. We could demonstrate that HMGB1 was secreted from macrophage/monocytic cells during inflammatory conditions and that the secretion could be inhibited by gold salts and oxaliplatin treatment as detected by ELISpot. We could demonstrate that oxaliplatin-treatment attenuated disease development in murine CIA. A rebound effect with severe and aggressive disease course was demonstrated after one week of treatment which correlated with an excessive extranuclear HMGB1 pattern in the affected joints, indicating an HMGB1-mediated joint inflammation.

Furthermore, we have demonstrated *in vitro* that the proinflammatory activity of HMGB1 is dependent on complex formation between HMGB1 and other inflammation-promoting molecules, such as IL-1 β , LPS and CpG-DNA. Studies using synovial fibroblasts obtained from arthritis patients demonstrated enhanced induction of TNF, IL-6 and IL-8 production and an enhanced production of matrix metalloproteinase-1 and -3 when stimulated with HMGB1 in complex with IL-1 β or LPS as compared to either substance alone. Thus, these results suggest that HMGB1 in complex with IL-1 β or LPS can mediate both inflammation and destruction in RA.

In conclusion, the studies presented in this thesis strengthen the view of HMGB1 as an inflammation- and destruction-promoting molecule. I have demonstrated HMGB1 secretion from cell types present in the arthritic joint, defined two therapies in clinical use which have the potential to block HMGB1 secretion and verified the anti-rheumatic effect of one of these therapies in murine CIA. By *in vitro* studies, I have extended the knowledge of the proinflammatory features of HMGB1 and demonstrated both a proinflammatory and prodestructive effect of HMGB1 on synovial fibroblasts. Taken together, the studies in this thesis suggest that HMGB1 is one of the key mediators of arthritic inflammation and joint destruction.

LIST OF PUBLICATIONS

- I. WÄHÄMAA H, Vallerskog T, Qin S, Lunderius C, LaRosa G, Andersson U, Erlandsson Harris H
HMGB1-secreting capacity of multiple cell lineages revealed by a novel HMGB1 ELISPOT assay
Journal of Leukocyte Biology 2007 Jan;81(1):129-36.
- II. Zetterström CK, Jiang W, WÄHÄMAA H, Östberg T, Aveberger AC, Schierbeck H, Lotze MT, Andersson U, Pisetsky DS, Erlandsson Harris H
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- III. Östberg T, WÄHÄMAA H, Palmblad K, Ito N, Stridh P, Shoshan M, Lotze MT, Erlandsson Harris H, Andersson U
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HMGB1 in complex with IL-1 β promotes an inflammatory phenotype in synovial fibroblasts
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LIST OF ABBREVIATIONS

ACPA	anti-citrullinated protein antibodies
ACR	the American College of Rheumatology
AP-1	activator protein-1
CIA	collagen-induced arthritis
DAF	decay-accelerating factor
DAMPs	damage associated molecular patterns
DC	dendritic cells
DMARDs	disease-modifying anti-rheumatic drugs
EC	endothelial cells
ELIspot	enzyme-linked immunospot
EPC	endothelial progenitor cells
FLS	fibroblast-like synoviocytes
HLA	human leukocyte antigen
ICAM-1	intracellular adhesion molecule 1
IFN	interferon
IL	interleukin
MC	mast cells
MMP	matrix metalloproteinase
MVB	multivesicular bodies
MyD88	myeloid differentiation primary response protein 88
NK cells	natural killer cells
NF-κB	nuclear factor κ B
PAMPs	pathogen associated molecular patterns
PDGF	platelet derived growth factor
PgE₂	prostaglandin E ₂
PRRs	pattern recognition receptors
RA	rheumatoid arthritis
RAGE	receptor for advanced glycation end products
RANKL	receptor activator of the nuclear factor κ B ligand
RANTES	Regulated on Activation Normal T Cell Expressed and Secreted
RF	rheumatoid factor
SCID	severe combined immunodeficiency
SE	shared epitope
SP	substance P
TGF-β	transforming growth factor- β
TIRs	Toll/IL-1 receptors
TLR	toll-like receptor
TIRAP	TIR-domain containing adaptor protein
TNF	tumour necrosis factor
Treg	T regulatory cells
VCAM-1	vascular cell adhesion molecule 1
VEGF	vascular endothelial growth factor

RHEUMATOID ARTHRITIS

Inflammation is a complex defence mechanism that aims to control and resolve infection, toxic stress or tissue damage, and which protects the integrity of human body. Chronic inflammation is a pathological condition which is characterised by a continuous inflammatory response, which is self-perpetuating, causing tissue damage and impairing the function of the affected organ.

Rheumatoid arthritis (RA) is a chronic inflammatory disease characterised by swelling and pain in multiple joints, often initially occurring in the joints of the hands, wrists and feet [1]. Extra-articular manifestations such as vasculitis, respiratory and cardiac dysfunctions occur in patients with more severe disease [2]. The prevalence is about 0.5-1%, with an annual incidence of 25/100 000 persons in Western countries [3], preferentially affecting women after menopause [4].

Etiology

A detailed epidemiological population-based study determined that the incidence of RA continues to increase with age. The yearly incidence of RA around the age of 30 is about 10 per 100 000 individuals and this is about 10-fold higher at the age of 60 years [4]. Age is thus considered to be one of the strongest risk factors for RA.

Although the etiology of RA is not known there is strong evidence that both genes and environmental factors play roles in its development. The genetic influence has been demonstrated by studies showing a greater concordance in monozygotic (12-15%) as compared to dizygotic twins (3-4%) [5]. The most important genetic risk factor for RA is linked to the human leukocyte antigen (HLA) class II genes. HLA contains three regions, DP, DQ and DR, and the association is particularly strong for HLA DRB1 alleles that code for a similar amino acid sequence termed shared epitope (SE). The five peptides at positions 70-74 are located in the third hypervariable region within the peptide binding groove of HLA [6, 7], suggesting an involvement in peptide presentation to T cells [8]. It has been suggested that the SE determines the severity rather than susceptibility of RA [9, 10] and recently it was demonstrated that SE was only associated with individuals displaying antibodies against citrullinated peptides (anti-CCP) (discussed in more details in the B cell chapter) [11]. Interestingly, other

genes associated with RA displayed a correlation with occurrence of anti-CCP antibodies, implying different etiologies and pathogeneses in RA patients respectively seropositive or seronegative to anti-CCP antibodies [11-14].

Hormonal influences also contribute in development and progression of RA. As the disease has a three-fold predominance in women [8] and the incidence of disease increases through the fifth and sixth decades of life, this suggests that alternation in sex hormone levels plays a role in RA. It has been proposed that androgen protects younger men against development of RA and loss of estrogen at menopause elevates the risk for RA in women. Additionally, oral contraceptives confer as reduced risk of developing RA [15]. A decreased disease activity during pregnancy with disease flare during breastfeeding [16, 17] further indicate that the hormonal balance is central to the development of RA.

Environmental factors are estimated to contribute to at least one-third of the risk for developing RA [18]. Smoking it self is a risk factor [19, 20] but the risk is further increased in patients with SE and anti-CCP antibodies [21] thus indicating an interaction between environmental and genetic factors. No specific viral or bacterial infection has consistently been proven to precede RA development, but Epstein-Barr virus (EBV) is commonly detectable in synovial membranes of RA patients but not in osteoarthritis patients [22] and about one-third of RA patients display occurrence of cytomegalovirus (CMV) in the synovial membrane [23]. Furthermore, the presence of retroviral particles in synovial fluid [24] and bacterial compounds such as LPS and bacterial DNA in the synovial membrane in RA patients [25-27] supports the idea of a viral and/or bacterial contribution to RA. Other environmental factors that have been suggested to increase the risk of RA development include exposure to silica [28] and mineral oils [29]. Dietary factors have also been suggested to be important in RA outcome [30, 31] while contradictory statements concerning obesity and RA development have been reported [32, 33]. Interestingly, alcohol consumption has a protective effect [34] and even protects mice from arthritis [35].

Clinical manifestations in RA

The symptoms of RA vary between patients, but general disease features include fatigue, lack of appetite, low-grade fever, muscle and joint aches accompanied by stiffness. Muscle and joint stiffness are usually most notable in the morning and after

periods of inactivity. During disease flares joints become swollen, painful and tender, caused by local inflammation in the synovia with an excessive production of synovial fluid and an influx of inflammatory cells into the joint.

Multiple joints are usually inflamed in RA in a symmetrical fashion beginning with the small joints of the hand and feet. Although RA is acute or subacute in about 25% of patients its onset can be palindromic or monoarticular, or it can begin with extra-articular synovitis (tendosynovitis, bursitis) or with polymyalgia-like symptoms such as fever, fatigue and weight loss [36].

Since RA is clinically a heterogenous disease, with no single diagnostic or pathognomic symptom or laboratory analysis, the diagnosis of RA is facilitated by use of The American College of Rheumatology (ACR) classification criteria from 1987 [37] (Table 1). Patients fulfilling at least four of seven of these criteria are classified as having RA and criteria 1 through 4 must have been present for at least 6 weeks.

Table 1. The 1987 ACR classification criteria for RA

Criterion	Definition
1. Morning stiffness	Morning stiffness in and around joints lasting at least one hour a day.
2. Arthritis of three or more joint areas	At least three joint areas simultaneously with soft tissue swelling or fluid. 14 possible areas: left and right proximal interphalangeal (PIP), metacarpo-phalangeal (MCP); wrist, elbow, knee, ankle, and metatarsophalangeal (MTP) joints.
3. Arthritis of the hand joints	At least one swollen area in the wrist, MCP or PIP joint.
4. Symmetry of arthritis	Simultaneous involvement of the same joint areas (defined in 2.) on both sides of the body PIP, MCP, or MTP joints are acceptable without absolute symmetry)
5. Rheumatoid nodules	Subcutaneous nodules over bony prominences, extensor surfaces, or juxtaarticular regions.
6. Rheumatoid factor	Detected by a method positive in less than 5% of normal controls.
7. Radiographic changes	Typical for rheumatoid arthritis on posteroanterior hand and wrist radiographs. Must include erosions or unequivocal bony decalcification adjacent to the involved joints.

However, the ACR 1987 classification criteria are not best adapted to diagnose early RA since some of the criteria are not fulfilled during the first year after onset. A recent study indicates that the sensitivity and specificity of the ACR 1987 criteria in early RA is low and should not be used as a diagnostic tool in early RA, suggesting a revision of the classification criterias [38]. The Leiden group recently developed new diagnostic criteria set for early arthritis with the ability to discriminate, at the first visit, between self-limiting, persistent non-erosive and persistent erosive arthritis. This set consists of 7 criteria: symptom duration at first visit, morning stiffness of at least 1 hour, arthritis in ≥ 3 joints, bilateral compression pain in the metatarsal phalangeal joints, IgM-RF positivity, anti-CCP positivity, and erosions on radiographs of the hands and feet [39, 40].

Joint anatomy

A normal synovial joint consists of opposing bones with surfaces of unmineralised cartilage. Between the bone and the surface cartilage there is a mineralised cartilage layer. The joint is surrounded by a capsule covered with a thin layer of synovial tissue.

Normal healthy synovial tissue consists of two anatomically distinct compartments: a lining layer and a sublining layer. The lining layer, which is one-to-three cell layers thick, is in direct contact with the intra-articular space. It is a loosely organised, avascular tissue not supported by a basement membrane. Macrophage-like synovocytes (type A) and fibroblast-like synovocyte (type B) are the predominant cell types in healthy synovial membrane (reviewed in [41]).

The sublining layer is even more loosely organised, comprising a loose fibro-adipose tissue, interspersed with cells and blood and lymph vessels and nerves [42]. Two-thirds of native synovocytes are B-type fibroblast-like synovocytes (FLS), which in contrast to type A cells are CD68⁻. FLS appear to belong to specialised fibroblast populations. DAF and VCAM-1 are expressed by activated FLS while other fibroblasts, including skin fibroblasts, do not express these markers [41]. Currently the best markers to identify FLS are vimentin, prolyl-5-hydroxylase and Thy-1 [43]. FLS play critical roles in normal joint homeostasis by synthesising and secreting hyaluronan, proteoglycans and a balanced amount of cytokines and MMPs [44].

PATHOGENESIS IN RHEUMATOID ARTHRITIS

Synovial pathophysiology in RA is a complex and synergistic interplay between different cell populations within the joint characterised by chronic inflammation and progressive joint destruction. Each cell type within the synovium contributes significantly to the initiation and perpetuation of RA. The resident cells within the synovia are the adipocytes, nerve cells, macrophage-like synovicytes, fibroblasts-like synovicytes and endothelial cells. These cells are described first, as they build up the “host-tissue” of RA inflammation. A schematic picture of synovial inflammation and pannus formation is presented in figure 1.

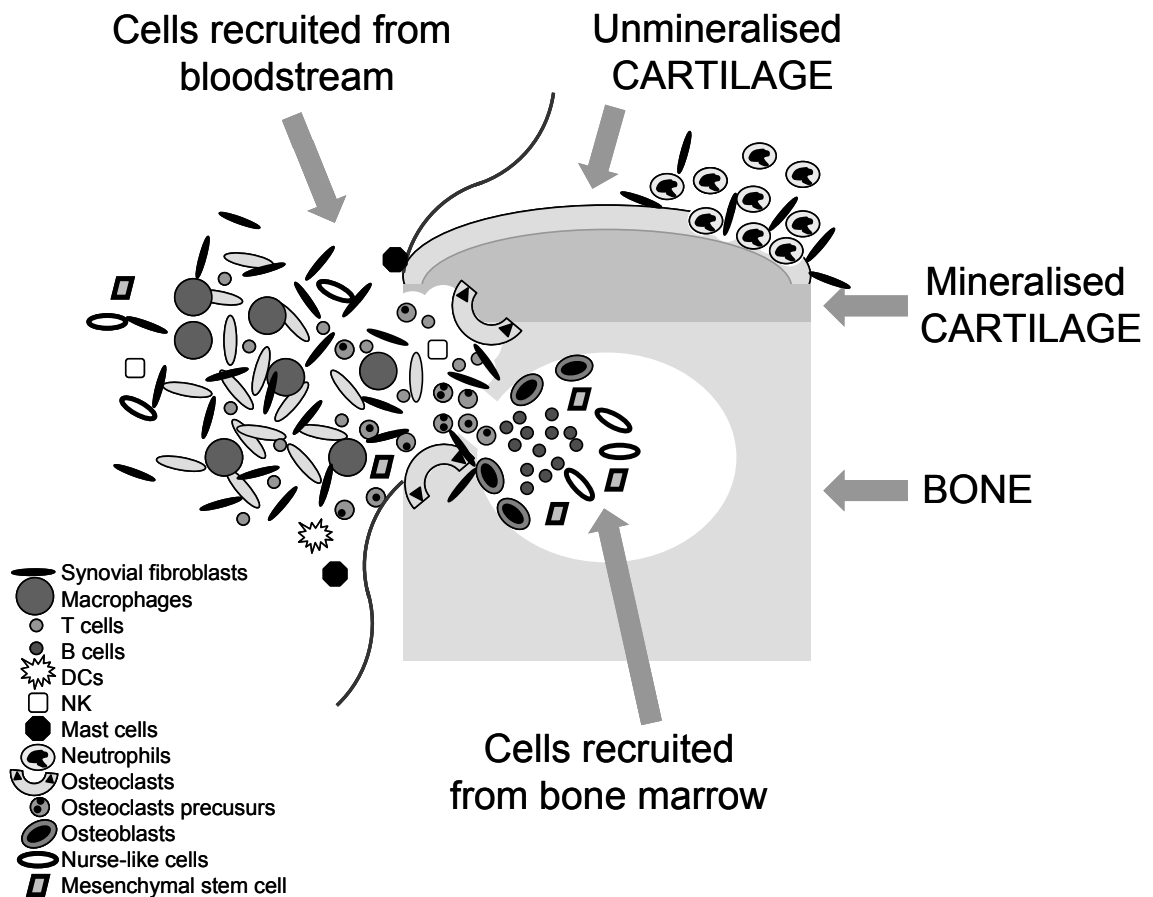


Figure 1. Hyperproliferating pannus tissue, with influx of inflammatory cells from bloodstream and bone marrow.

Adipocytes

Adipocytes have the general ability to synthesise and release proinflammatory cytokines, complement factors, growth factors and adhesion molecules [45] thus having a capacity to promote inflammation. However, the biological function of articular and synovial adipose tissue in RA is not well characterised, and conflicting data exists regarding the inflammatory and anti-inflammatory function of adipocytes in RA [46, 47]. It has been demonstrated that cytokines can regulate FLS differentiation to adipocyte-like cells [48] and further that adipocytes can dedifferentiate into fibroblast-like cells in a reversible manner [49]. Thus the phenotype of adipocytes might vary depending on the stage of the pathological process (metabolic or inflammatory) or the differentiation/maturation stage.

Nerve fibres

The innervation of RA synovia is altered, with loss of sympathetic nerve fibres [50, 51]. Instead, substance-P (SP) produced by sensory nerve fibres contributes to the severity of experimental arthritis [52] with activation of synovial fibroblasts [53] and enhanced proinflammatory cytokine secretion from different cell types [54-56]. A predominance of SP positive sensory nerve fibres in RA patients compared to OA patients further supports the importance of SP in the inflammatory process in RA [57].

Macrophage-like synoviocytes

Macrophage-like synoviocytes or type A synoviocytes are considered to be tissue resident macrophages even though they are derived from blood-borne mononuclear cells. Type A cells have a round morphology and are located in the synovial lining layer with about half of the cell bodies projected over the surface line of the synovial membrane. These cells play an important role in maintaining normal joint homeostasis by absorbing and degrading extracellular constituents, cell debris and microorganisms in the synovial fluid and intimal matrix. Type A synoviocytes have the ability to phagocytose foreign substances that enters into the joint cavity, demonstrated with latex particles, iron dextran and colloidal gold particles (reviewed in [58]). As an antigen-presenting cell, type A synoviocytes express MHCII and have a broad spectrum of lysosomal enzymes facilitating the degradation of ingested material [59]. Latex

particles ingested by type A cells are gathered at the synovium cartilage junction which is highly vascularised, suggesting that intra-articular particles are drained via blood circulation. However, it has also been suggested that type A cells could remove the ingested material to lymphatic channels of the sublining layer (reviewed in [58]).

Fibroblasts-like synoviocytes

The most common cell type at the sites of bone and cartilage invasion is synovial fibroblasts that play crucial roles in both joint damage and the propagation of inflammation [41, 60, 61] FLS differ considerably from synovial fibroblasts from healthy joints. FLS in RA have been demonstrated to accumulate a number of mutations similar to those evident in malignancy [62] but these appear to be a consequence of the inflammatory environment rather than a primary cause of RA. However, once established these mutations facilitate FLS invasiveness, proliferation and resistance to apoptosis.

The specific features of RA FLS are now described in more detail, namely their: *invasiveness*, *hyperplasia* and their *inflammation*-promoting characters.

Invasiveness

The primary mechanism by which FLS erode cartilage appears to be via the synthesis and secretion of matrix metalloproteinases (MMPs), including MMP 1, 3, 8, 9, 10 and 13 (reviewed in [41]). MMP1 (collagenase-I) has the capacity to digest collagen type II which is an abundant cartilage compound and MMP3 (stromelysin-I) degrades matrix proteins [63]. Levels of MMP1 and MMP3 are elevated in synovial fluid and serum of RA patients [64-66] and are suggested to be useful predictive markers for an erosive disease [64-66]. In cell culture FLS produce MMP1 and MMP3 in response to the proinflammatory cytokines IL-1 β and TNF, TLR ligands, direct cell-cell contact with T cells and under hypoxic condition [67-70]. These are all features characterising the arthritic joint. In addition to protease-mediated cartilage destruction, *in vitro* studies have revealed that FLS have the capacity to ingest cartilage by phagocytosis [71]. Studies of joints have demonstrated mineralised cartilage is rapidly resorbed by osteoclasts, whereas unmineralised surface cartilage remains intact for a longer time. Unmineralised cartilage degradation is mediated by FLS, neutrophils and chondrocytes themselves [72].

FLSs are also important key players in bone destruction. A key factor for osteoclastogenesis is the production of the receptor activator of the nuclear factor κ B ligand (RANKL), which is produced and expressed on the surface of FLS following stimulation with proinflammatory cytokines and TLR ligands [73-75]. Activation of resident osteoclast progenitors in the bone or recruited macrophages [76] or DC [77] are able to mature to osteoclasts through RANKL-mediated activation. Additionally, FLS have been demonstrated to directly invade bone and to mediate osteoclast-independent bone resorption [78].

The invasive phenotype of FLS is suggested to be induced through expression of cellular proto-oncogenes, a feature occurring abundantly at the sites of invasion into cartilage and bone [79] although distinct from inflammation [80]. The inflammation-independent activation of synovial fibroblasts was confirmed by studies performed in the severe combined immunodeficiency (SCID) mouse. RA synovial fibroblasts were co-implanted with cartilage explants from the same donor into SCID mice, and even after 60 days the implanted fibroblasts retained their activated appearance and grew into the cartilage. This feature was not detected in synovial fibroblasts obtained from osteoarthritis or healthy individuals [81] further underlining the activated phenotype of RA synovial fibroblasts.

Synovial hyperplasia

Another hallmark of RA is synovial hyperplasia. The lining layers expand from 1-2 cell layers to being 15 cell layers depth or even more. Despite that the sublining layer becomes infiltrated with a variety of inflammatory cells, the FLS population in this region is also expanded [82]. In addition to the inflamed environment in which several growth factors from adjacent cells promote FLS proliferation, at least three different mechanisms in FLSs themselves can contribute to increased FLS populations in RA, namely: hyperproliferation, decreased apoptosis and decreased senescence (reviewed in [41]).

Hyperproliferation of FLS can be driven by both over-expression of proteins and mutations in genes that regulate proliferation. Indeed, both pathways seem to be affected in RA. Excessive expression of growth factors such as platelet-derived growth factor (PDGF) and basic fibroblast growth factor (bFGF) is evident in FLS [83] as is increased expression of Erk that regulates mitosis in FLS [84].

Decreased apoptosis: In the absence of apoptosis cells survive and accumulate abnormally. Death signals that promote apoptosis include oxidants that damage mitochondria as well as specific pro-death ligands promoting cell death through specific receptors. Human studies indicate dysregulated CD95-receptor mediated apoptosis in FLS [85] and a high expression of Bcl-2 which suppress apoptosis. Heterogeneous mutations of the tumour suppressor gene *p53* have been documented in RA FLS, permitting cell division in the presence of DNA damage [62, 86]. Mutations in *p53* are suggested to be a consequence of oxidative and inflammatory stress rather than being the primary etiology of RA [87].

Decreased senescence: Senescence denotes the process by which aging cells enter a permanently non-proliferative state. The mitotic life of a cell is principally determined by telomeres, the repeating DNA sequences at the ends of chromosomes. With each cell division, telomere number is usually decreased while in stem cells, cancer cells and RA FLS the enzyme telomerase replaces lost telomeres and permits unlimited mitosis [88, 89].

Inflammation

Another important feature of RA FLS is their capacity to produce and secrete a wide range of proinflammatory mediators including cytokines, growth factors and lipidic mediators of inflammation.

Chemokines and their receptors are crucial elements in the migration of leukocytes during inflammation. FLS can produce chemokines constitutively due to hypoxia [90] or following stimulation by proinflammatory cytokines, microparticles [91] or TLR ligands [92] An early activation and chemokine production of FLS by exogenous and endogenous TLR ligands might be a crucial step in the initiation of the chronic inflammatory process in RA. TLR pathways can be activated by exogenous stimuli such as bacteria and viruses that are evident in RA joints [26, 27, 93] and endogenous stimuli such as mRNA and fibrin [94, 95].

Endothelial cells

Under normal circumstances the adult vasculature is mostly quiescent, and angiogenesis does not take place except during wound healing and the female

reproductive cycle. Dysregulated angiogenesis and vasculogenesis contribute to RA pathology. Angiogenesis describes the formation of new vessels by activating pre-existing mature endothelial cells (EC) [96] and vasculogenesis describes the *de novo* formation of blood vessels by recruiting circulating CD34⁺ endothelial progenitor cells (EPCs) to ischemic tissues [97].

Vascular endothelial growth factor (VEGF) is the key regulator of both angiogenesis and vasculogenesis. The expression of VEGF is induced under hypoxic conditions in the RA joint and induces EC proliferation, migration and survival [98, 99] thereby promoting EPC recruitment to the sites of vascular injury [100].

Endothelial activation during inflammation involves upregulation of vascular cell adhesion molecule-1 (VCAM-1) that together with increased angiogenesis and increased vascular permeability of endothelial cells facilitates the influx of inflammatory cells from the bloodstream into the joint [41, 101].

Cells infiltrating the sublining layer

The specific features of the different cell populations recruited to the arthritic joint are further described cell-by-cell.

Nurse-like cells and mesenchymal stem cells

A specific cell population distinct from fibroblasts, called *nurse-like cells* [102] is present in the synovial tissue and bone marrow. These fibroblastic bone marrow stromal cells migrate into the joint cavity through bone canals and proliferate in the synovial tissue [103]. Nurse-like cells have the capacity to adhere and allow lymphocytes to crawl beneath them, a process termed *pseudoemperipolesis* (adhesion and holding beneath). These cells interact with lymphocytes and monocytes, promoting cytokine production, cell proliferation, IgG production [104, 105] and osteoclast maturation from monocytes [106]. Multipotent mesenchymal stem cells from bone marrow are yet another cell population present in the arthritic synovium, with the multipotency to develop into cartilage, bone, fat and muscle cells [107] and reviewed in [102].

T cells

Substantial evidence for a T cell influence in RA pathogenesis include the association of HLA-DR1 and HLA-DR4 alleles, the presence of activated T helper cells within inflamed RA synovium, the ability to actively transfer RA to immunodeficient mice using T cells from human RA synovium and the anti-arthritic effects of T cell-directed therapies (reviewed in [108]).

Of the infiltrating cells, 30-50% are T cells, predominantly of the CD4⁺ subtype [109]. The vast majority of T cell clones from the human synovial membrane and synovial fluid represent Th1 cells producing IFN γ and IL-2. Activated CD4⁺ T cells are also present in the peripheral blood and the frequencies of IFN γ producing cells in patients with new-onset synovitis correlate well with disease activity, emphasizing the role of Th1 cells in the initiation of disease (reviewed in [108]).

Pregnancy improves the symptoms of RA in about 75% of women, with significant resolution of inflammation. Interestingly, during pregnancy a marked decrease in Th1-mediated immunity has been determined and recently, a placental-derived protein (placental protein 14) was determined to inhibit Th1 immune responses and to synergise with IL-4 promoting Th2 immunity [110]. This further strengthens the evidence of a Th1-mediated immune response in RA.

It has become apparent that in RA the CD4⁺ T cell subsets with regulatory capacity are functionally impaired, thus allowing Th1-driven immunity to progress into chronic inflammation. A T cell subset with regulatory capacity is the CD4⁺CD25⁺ T regulatory cells (Tregs). Between 5% and 15% of CD4⁺ T cells in the peripheral blood of healthy individuals are Treg cells, which have the capacity to inhibit activation-induced proliferation of autologous Th1 cells (reviewed [108]). Despite the high levels of Tregs in the synovial fluid of RA patients, they are ineffective/defective in their capacity to control inflammatory responses. A recent study suggested that TNF inhibits the suppressive activity of Treg cells, as treatment with anti-TNF antibody could restore the suppressive function of Tregs [111, 112].

A second CD4⁺ T cell population with the potential to counteract T cell-driven inflammation in RA is the Th2 cell population. Th2 cells produce IL-4 and can prevent the generation of Th1 and Th17 cells, and downmodulate their effector functions [113]. However, the majority of RA patients already have an impaired Th2 cell differentiation at the initial phase of disease and it is demonstrated that reduced Th2 cell generation is

associated with persistently aggressive and erosive disease (reviewed in [114]). Furthermore, an association between RA severity and impaired IL-4R signalling has been demonstrated [115].

T cells are also important contributors to the pathogenesis of bone erosion in RA through an antigen-independent process. CD4⁺ Th17 cells are distinct from Th1, Th2 and Treg cells and are present in the synovium and circulation of RA patients. Recent studies have identified Th17 cells as an exclusive osteoclastogenic T cell subset among the CD4⁺ T cell lineage [116, 117] and IL-17 mRNA levels in synovial membranes have been demonstrated to be predictive of joint damage in RA [118]. RANKL expression by Th17 cells is thus the key link between immune activation and bone loss.

CD8⁺ T cells produce high levels of TNF and IFN γ , thereby contributing to RA pathogenesis. Interestingly, subgroups of CD8⁺ T cells recognising Cytomegalovirus, Epstein-Barr virus and influenza virus, respectively, are enriched in the synovial fluid compared to in peripheral blood, reflecting the enrichment of memory T cells specific for foreign antigens [119]. CD8⁺ T cells are also required for the formation of germinal-like centre structures in RA synovia [120, 121] and these structures facilitate the interaction between T and B cells, as well as between T cells, macrophages and fibroblasts [122]. Direct cell-cell interactions of FLS with T cells were demonstrated to prevent programmed cell death of T cells [123, 124] and induced IL-6, MMPs and PGE2 production in fibroblasts. T cell contact with macrophages induces IL-1, TNF and IL-6 production [69, 125-127], demonstrating that T cells are able to drive chronic inflammation through an antigen-independent mechanism.

B cells

Successful treatment of RA through B cell depletion provides evidence for the relevance of B cells in RA pathogenesis [128-130]. B cells are apart from being Ig producing cells, very efficient antigen presenting cells and contribute to T cell activation through expression of costimulatory molecules. B cells both respond to and produce chemokines and cytokines, thereby promoting synovial inflammation [131]. Direct cell-cell interactions of B cells with FLS were demonstrated to prevent programmed cell death of B cells [123, 124] and stimulation of FLS with TNF and IFN γ induce production of B cell activation and survival factor (BAFF) [132] thus increasing the longevity of plasma cells.

Several different autoantibodies have been detected in RA patients but only rheumatoid factor (RF) and anti-citrullinated protein antibodies (ACPA) have sufficient sensitivity and specificity to be used in clinical practice (reviewed in [133]).

RF is an autoantibody directed against the Fc portion of IgG and can be detected in 75-80% of patients suffering from RA [134]. Combined elevation of IgM-RF and IgA-RF appears to be more specific for RA than IgM-RF alone [135] and high titer IgA-RF is associated with more rapid disease progression, worse outcome and extra-articular manifestations [136].

Although circulating RF has been considered as an important marker for RA, autoantibodies directed against citrullinated peptides have recently been identified in RA patients termed as *anti-citrullinated protein antibodies* (ACPA). Citrullination is a post-translational modification of arginine catalyzed by the enzyme family peptidylarginine deaminase (PAD) [137]. Citrullinated proteins are detectable in the arthritic synovium in humans [138] and in animal models of arthritis [139].

ACPA provide greater diagnostic specificity than RF and have high predictive value for RA several years before disease onset [140] with erosive disease being more likely to develop in ACPA⁺ positive patients compared to in ACPA⁻ patients [141]. ACPA producing B cells have been observed in synovial tissue and the abundance of ACPA is higher in synovial fluid and synovial tissue than in sera from RA patients [142, 143] suggesting a local antibody production against citrullinated antigen within the joint. This could indeed be the case, since germinal center-like structures are formed within the synovial tissue [144] and hypermutation and terminal B cell differentiation is suggested to occur within these germinal centre-like structures [145].

Macrophages

Macrophages are important key players in the pathogenesis of rheumatoid synovitis. Macrophages present in the inflamed synovium have two origins: the resident synovial lining layer type A synovocytes, and sublining macrophages which have migrated from blood circulation as monocytes and become tissue macrophages [146]. The number of type A synovocytes is higher in the inflamed synovial lining layer than in healthy conditions [147] and the number of macrophages in the pannus tissue correlates well with both radiological joint damage [148] and with joint pain and inflammation [149]. Macrophages, together with fibroblasts and endothelial cells, thus promote cartilage

destruction [150, 151] and through stimulation by RANKL and M-CSF monocytes are able to differentiate to osteocasts [152] promoting bone destruction.

In RA tissue macrophages have been demonstrated to be resistant to apoptosis [153] contributing to the persistent release of growth factors, cytokines, chemokines [154] and MMPs-1, -2 and -9 (reviewed [155]). Growth factors released by tissue macrophages include platelet derived growth factor (PDGF) [156] basic and acidic fibroblast growth factor (bFGF, aFGF), vascular endothelial growth factor (VEGF), hepatocyte growth factor (HGF) and transforming growth factor- β (TGF- β) [154].

TNF, IL-1 β , IL-6, IL-12, IL-15 and IL-18 are some of the proinflammatory cytokines produced by tissue macrophages [154]. Interestingly, IL-10 produced by monocytes is no longer considered to be an anti-inflammatory cytokine in RA [157] since IL-10 was determined to induce TNF receptor expression on monocytes [158]) and an increased expression of interferon- γ -inducible genes [157]. Among chemokines, IL-8 produced by macrophages functions as a recruiting factor for neutrophils [154] and fractalkine, while promoting angiogenesis, also acts as a chemotactic agent for monocytes and lymphocytes [159].

Neutrophils

Neutrophils are the most abundant cell population in the synovial fluid but are sparsely distributed in the synovial membrane.

A variety of chemokines produced by FLS, among others IL-8, MCP-1 and RANTES, attract neutrophils to the inflamed RA joint (reviewed in [160]) and locally produced complement components [161] followed by complement activation generates anafylatoxin C5a which also functions as chemoattractant for neutrophils [162]. C5a further induces the expression of FcR γ III on neutrophils [162] and facilitates Fc-receptor mediated phagocytosis of immune complexes in the synovial fluid. Phagocytosis further triggers the release of hydrolytic enzymes, production of reactive oxygen species [163] and production of IL-1 α and IL-1 β thereby promoting local joint inflammation and tissue degradation, and as such are important mediators of surface cartilage degradation (reviewed in [164]). During neutrophil activation and degranulation nociceptin is released, which is a neuropeptide associated with pain [165] thus accounting for joint pain in RA.

NK cells

NK cells are distributed throughout lymphoid and non-lymphoid tissues. NK cells are a minor cell population of human peripheral blood, comprising 2%-18% of the total lymphocyte count (reviewed in [166]). NK cells mediate clearance of antibody-coated cells, mediate early protection against viruses and kill cancer cells (reviewed in [167]).

In humans NK cells are divided into CD56^{dim} NK cells which express perforin and produce IFN γ , and CD56^{bright} NK cells which lack perforin and produce cytokines upon stimulation. NK cells are able to induce maturation and activation of DCs, macrophages and T cells but are also able to kill immature cells DCs, activated CD4⁺ T cells, hyperactivated macrophages and cells not expressing MHC class I molecules (reviewed in [166]).

Since NK cells are able to skew the immune system towards a Th1 or Th2 response depending on the cytokine milieu and tissue localisation these cells can both promote or protect from autoimmunity [167]. The function of NK cells in RA is not fully elucidated but CD56^{bright} NK cells accumulate in both lymph nodes [168] and in chronically inflamed RA joints [169]. CD56^{bright} NK cells are also detected in synovial fluid from RA patients and they spontaneously produce IL-10 and TGF β [170]. It has been demonstrated that NK cells have the ability to induce TNF production from monocytes [171] and can trigger CD14⁺ monocytes to differentiate into DCs [172].

Dendritic cell

Dendritic cells (DC) play a pivotal role in T cell immunity and tolerance due to their ability to stimulate naïve T cells and to direct effector cell function. Human DCs are divided into two different subsets: myeloid- (mDC) or plasmacytoid dendritic cells (pDC) and both mDCs and pDCs are present in the synovial tissue in RA patients.

Myeloid DCs are found in peripheral blood, synovial fluid and in synovial tissue. In the synovial tissue they are localised in the vicinity of T cells, where they express IL-12 and IL-23, important cytokines for the induction/expansion of Th1 and Th17 T cell subsets, respectively. TLR ligands induce chemotaxis and production of various chemokines from mDCs, in particular IL-8. Peripheral blood CD14⁺ monocytes are able to differentiate into a specific type of myeloid DCs, designated as CD1a⁺ mDC (mo-DC). In chronically inflamed tissues or in lymph nodes NK cells trigger the differentiation of mo-DC into potent Th1-promoting cells. These cells are abundant in

the RA synovium and are primarily located in the perivascular areas and lymphoid-like structures (reviewed in [173]).

Plasmacytoid DCs are found with reduced numbers in peripheral blood in RA patients compared with healthy donors while a higher concentration of pDC was reported in synovial fluid and synovial tissue in RA patients compared in osteoarthritis patients [174]. Importantly, pDCs induce both T cell-dependent and -independent B cell differentiation into antibody-producing plasma cells. Interestingly, pDC numbers are especially increased in ACPA positive RA patients (reviewed in [173]).

Mast cells

Mast cells (MCs) are multifunctional cells containing a vast numbers of preformed granules with proinflammatory and fibrogenic mediators. An increased number of MCs occurs in the synovial tissues of RA patients, especially at the sites of cartilage destruction [175] where the activation and degranulation of MCs are also detected [176]. Upon activation MCs are able to produce or release the preformed granules containing cytokines, chemokines and proteolytic enzymes. MCs are also a major source of vasoactive and chemotactic factors, facilitating the recruitment of other inflammatory cells into the joint (reviewed in [131]). Interestingly, a MC-membrane stabilising agent was shown to suppress arthritis progression in a collagen-induced arthritis model (reviewed in [177]).

ANTI-RHEUMATIC THERAPIES

In the normal healthy joints there is a balance between pro- and anti-inflammatory cytokines, whereas in the arthritic joint an imbalance between these mediators causes the persistence of inflammation and joint destruction [178]. Therapy in RA aims to suppress chronic inflammation and structural protection of cartilage and bone. The available therapies for RA are directed against individual proinflammatory cytokines or against individual effector cells, including therapies inhibiting the Th1/Th17 cytokine-driven disease through favouring Th2 differentiation.

Cytokine-inhibiting therapy

TNF

TNF is a major mediator of structural damage in RA by inducing osteoclast formation. This is accomplished by: *i*) inducing the expression of RANKL on mesenchymal cells and lymphocytes; and *ii*) direct engagement of TNF receptor type I on the surface of osteoclast precursors. TNF has also a primary role in RA pathogenesis by inducing production of adhesion molecules facilitating the influx of osteoclast precursors (monocytes) and other inflammatory cells [179].

TNF additionally induces the production of MMPs, IL-1 and other proinflammatory cytokines, thereby sustaining both inflammation and in turn promoting cartilage and bone destruction (reviewed in [180]). TNF stimulates macrophages to produce reactive oxygen [181, 182] that induce other synovial cells to produce more TNF [183] creating an intrinsic loop for sustained TNF production.

Available targeted therapies are: **Infliximab (Remicade[®])**; a humanised chimeric monoclonal antibody which binds to both soluble and membrane bound TNF. **Adalimumab (Humira[®])**; a human monoclonal antibody (produced by phage display) that binds TNF. **Etarnecept (Enbrel[®])**; a soluble TNF receptor with a human IgG Fc that binds to TNF and lymphotoxin.

IL-1

Several reports demonstrate that IL-1 (in particular IL-1 β) is a key mediator of joint damage. Osteoclast formation is dependent on IL-1 since the abolition of IL-1 in TNF-transgenic mice completely protected these animals from cartilage breakdown, and reduced bone destruction considerably despite ongoing synovitis [184]. An earlier study also demonstrated that therapy with IL-1RA or induced IL-1R1 abolition completely rescued TNF-initiated bone loss [185]. In addition, mice that are IL-1RA-deficient spontaneously develop destructive polyarthritis [186]. Furthermore, high IL-1 levels are correlated with joint inflammation and are responsible for the articular destruction in RA by inhibiting proteoglycan synthesis [187] and by stimulating the release of MMP1 and MMP3 [188].

Available targeted therapy: **Anakinra (Kineret[®])**; a soluble IL-1 receptor antagonist. Novartis has an anti-IL-1 β mAb in clinical trials. This antibody works well in IL-1 β caused disorders like Muckle-Wells and CINCA syndromes.

IL-6

IL-6 is the major inducer of CRP synthesis in the liver and mediates systemic inflammation [179]. IL-6 is also one of the cytokines that induces RANKL expression on mesenchymal cells and T cells, which in turn can activate osteoclastogenesis and bone degradation [189]. A recent study demonstrated that blockade of IL-6 by neutralising antibodies against the IL-6 receptor effectively blocked the inflammatory process in RA [190].

Available targeted therapy: **Tocilizumab**: an antibody directed against the IL-6 receptor.

Effector cell-directed therapy

B cell depletion

B cell depletion appears to inhibit inflammatory responses by: i) decreasing the amount antigen presenting cells; ii) impairing the formation of immune complexes; and iii) blockade of proinflammatory cytokine production. Activated B cells express RANKL and support osteoclastogenesis; thus B cell depletion could affect the structural damage in RA.

Available targeted therapy: **Rituximab**; CD20⁺ B cell depleting antibody, detects B cells in the periphery but does not deplete plasma cells.

Costimulation blockade

Endogenous CTLA4 expressed on Treg cells (and activated T cells) binds with high affinity to CD80 and CD86 expressed on the surface of antigen presenting cells, inhibiting the costimulatory signal for T cells. Thus recombinant soluble CTLA4 has anti-inflammatory properties by inhibiting T cell activation [191] but also by targeting CD80/CD86-bearing monocytes and thereby inhibiting the differentiation of monocytes into osteoclasts [192].

Available targeted therapy: **Abatacept**; recombinant CTLA4 with IgG Fc.

Modulation of Th1 toward Th2 balance

Disease-modifying anti rheumatic drugs (DMARDs)

The majority of T cell clones from the human synovial membrane and synovial fluid represent CD4⁺ Th1 cells producing IFN γ and IL-2. (reviewed in [108]).

It has become apparent that in RA T cell subsets with regulatory capacity, such as Th2 cells and CD4⁺CD25⁺ Treg cells, are functionally impaired, thus allowing the progression of Th1- mediated inflammation (reviewed in [108, 114])

The concept of modulating the Th1/Th2 balance has been successful in animal models of arthritis [193, 194]. Several recent studies have indicated that several DMARDs and glucocorticoids appear to be able to modulate the Th1/Th2 balance.

Available targeted therapies are: **Methotrexate** [195], **Leflunomide** [196], **Sulfasalazine** [197], **Cyclosporine** [198] and **Glucocorticoids** [199, 200].

ANIMAL MODELS OF ARTHRITIS

Experimental arthritis models are appropriate tools for the study of a complex disease with interactions between genetic and environmental factors. Different animal strains have specific genetic backgrounds, where every strain may resemble one subgroup of RA patients. This offers the possibility to study how different disease inducers influence the disease course and to evaluate the effects of different anti-rheumatic therapies. The advantage of using animal models includes the possibility to study the entire disease course, from the induction phase to the progressive erosive disease.

Collagen-induced arthritis

In this thesis work, I have used Collagen-induced arthritis (CIA) in mice as a model of human arthritis. CIA is the most commonly used experimental model of arthritis and has been used since the late seventies [201]. Injection into the tail base of heterologous type II collagen (CII) suspended in mineral oil together with inactivated mycobacteria (complete Freund's adjuvant, CFA) induces a severe destructive arthritis in DBA/1 mice [202, 203]. The susceptibility to CIA is related to MHC class II alleles. Mouse strains bearing MHC I-A^q, I-A^r or I-A^b develop arthritis following challenge with CII [204]. In CIA both cellular and humoral immune responses drive the inflammation, resulting in cartilage and bone erosion. CIA has many similarities to human RA being chronic, symmetric, affecting peripheral joints and inclusion of formation of synovial pannus tissue [203, 205].

Although an adaptive immune response to CII is pivotal for the development of disease, macrophages and their products (ie TNF, IL-1, IL-6) play a major role in the disease pathogenesis [186, 206-208]. Blockade of these cytokines ameliorate, as in RA, the disease symptoms [209-211]. The differences between mouse CIA and RA are: the absence of lymphoid aggregate-formation, that no difference in sex predisposition exists and that no RF can be demonstrated in mouse CIA [203, 205].

HMGB1

HMGB1 as a nuclear protein

The human HMGB1 gene is located on chromosome 13q12 [212] and encodes a 215 amino acid polypeptide. HMGB1 is highly conserved between species with 99% identity between rodent, bovine and human proteins [213]. HMGB1 has a tripartite domain organisation: the A- and B- HMGB boxes, each around 75 amino acids in length, are connected by a short linker and an acidic tail formed by 30 consecutive glutamate and aspartate residues. The A-box consists of 3 α -helices folded in an L-shape and the B-box is also folded in an L-shape similar to the A-box [214-219]. The acidic tail modulates interaction with DNA and its helix-distorting ability [220-222] which modulates the interaction with nucleosomes and chromatin remodelling machineries [223, 224]. The acidic tail also modulates the acetylation of HMGB1 mediated by histone acetyltransferases [225] (reviewed in [215]).

HMGB1 is an abundant and highly conserved non-histone chromosomal protein that binds to the minor groove of DNA without sequence specificity. It associates with high affinity to DNA with highly bent structures, such as four-way junctions and cisplatin-modified DNA [226]. HMGB1 has a functional importance as a regulator of transcription, either by remodelling chromatin and nucleosome structure or direct interaction with transcription factors such as steroid hormone receptors, p53 and NF- κ B [227]. Furthermore, HMGB1 knockout mice die shortly after birth due to hypoglycemia and exhibit a defect in the transcriptional function of the glucocorticoid receptor [228]. HMGB1 is expressed in all nucleated cells but the expression level of HMGB1 is much higher in transformed cell types compared to in non-transformed cells [229-232].

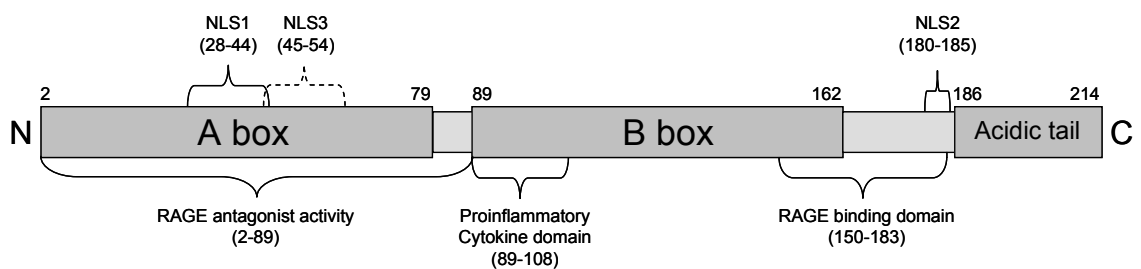


Figure 2. Structure of HMGB1

Extracellular functions of HMGB1

The cytoplasmic occurrence of HMGB1 was already demonstrated in 1979 [233] and HMGB1 expression at leading edges in spreading and motile cells was demonstrated in 1987 [229, 234]. HMGB1 binding to plasminogen and plasminogen activator [235] was demonstrated to play a crucial role during cell invasion and tissue remodelling by activating MMP2 and MMP9 that degrade the extracellular matrix [236, 237]. HMGB1 was also found in the cytoplasm of resting platelets and to be expressed on platelet surface upon activation [238].

In 1999 HMGB1 was discovered as an extracellular mediator of inflammation released by macrophages [239]. The cytokine activity of HMGB1 is ascribed to the B-box structure while the A-box behaves as a competitive inhibitor of HMGB1 [240-243]. The structure and the functional domains of HMGB1 are further described in Fig 2. During the last decade HMGB1 has been demonstrated to be secreted from various types of cells, promoting both inflammation and tissue regeneration [244] and to possess bactericidal effects [245].

Secretion of HMGB1

Active HMGB1 secretion

HMGB1 is an extremely mobile nuclear protein which rests at a specific DNA site for only fractions of a second [246] and in most cells HMGB1 shuttles between the nucleus and cytoplasm. The nuclear import is an active process while the cytoplasmic translocation may occur via passive diffusion or by CRM1-mediated active export. Activation of monocytes with proinflammatory agents induces hyperacetylation of HMGB1 which inhibits the active transport of HMGB1 to the nucleus, resulting in cytosolic accumulation [247]. In myeloid cells HMGB1 is then accumulated in secretory lysosomes followed by lysophosphatidylcholine (LPC)-mediated exocytosis [248]. In addition, the ATP binding cassette transporter 1 inhibits both HMGB1 and IL-1 β secretion from monocytes and macrophages [249, 250] and recently a specific ABC transporter (multi-drug resistant protein 1, MRP-1) was suggested to mediate active HMGB1 secretion from macrophages [251]. The mechanism by which cell types lacking the secretory lysosomal pathway, such as smooth muscle cells and endothelial cells [252, 253] secrete HMGB1 is not yet elucidated.

Passive HMGB1 release

The other setting in which HMGB1 release occurs is during cell death. Since HMGB1 is loosely bound to chromatin it may leave the nucleus when membrane integrity is lost. Induction of necrotic cell death through physical or metabolic injury leads to HMGB1 release [246]. Late apoptotic cells undergoing secondary necrosis also release HMGB1 [254-257]. One recent report suggests that hypoxia may even induce active HMGB1 release, that precedes hypoxia-induced apoptosis or necrosis [257].

Exosomal HMGB1 release

Exosomes are small, 30-100 nm membrane vesicles believed to originate from late endosomal compartments called multivesicular bodies (MVBs). MVBs are involved in transporting proteins for degradation in lysosomes. Intraluminal vesicles are formed by inward budding of the endosomal membrane of MVB and may be released when MVB fuse with the plasma membrane, these intra luminal vesicles are then called exosomes [258, 259]. HMGB1 has been detected in exosomal compartments and in exosome-depleted supernatants of Caco-2 cells suggesting that HMGB1 was released by several routes from these cells [374].

Modifications of HMGB1

HMGB1 is further directed to diverse post-translational modifications. ADP ribosylation of HMGB1 regulates gene transcription and is a cellular response to DNA damage [260, 261]. HMGB1-ADP ribosylation can be induced by alkylating agents and was shown to induce HMGB1 relocalisation from the nucleus to cytoplasm and subsequent release during necrotic cell death [262].

During apoptosis caspases 3 and 7 mediate oxidation of HMGB1 in HeLa cells [263]. Activation of RAW 264.7 cells induced phosphorylation of HMGB1 and inhibited the nuclear transport of HMGB1 by reduced binding to nuclear cargo carrier protein KAP- α 1 [264]. Furthermore, mono-methylated HMGB1 was detected in the cytoplasm but not in the nucleus of neutrophils [265].

Depending on the activation status of cells at the time point of passive HMGB1 liberation, it is therefore likely that all these different HMGB1 isoforms may occur extracellularly. HMGB1 can also be cleaved by Thrombin-thrombomodulin complexes

[266] and extracellular HMGB1 can further make complexes with IgG [267, 268], LPS, CpG [269-271, *paper IV*] and IL-1 β [272, *papers IV,V*]. All these modifications of HMGB1, (both post-translational and the binding to other molecules), influence the mode of receptor binding, the choice of receptor/receptors and the subsequent signalling cascade (Figure 3).

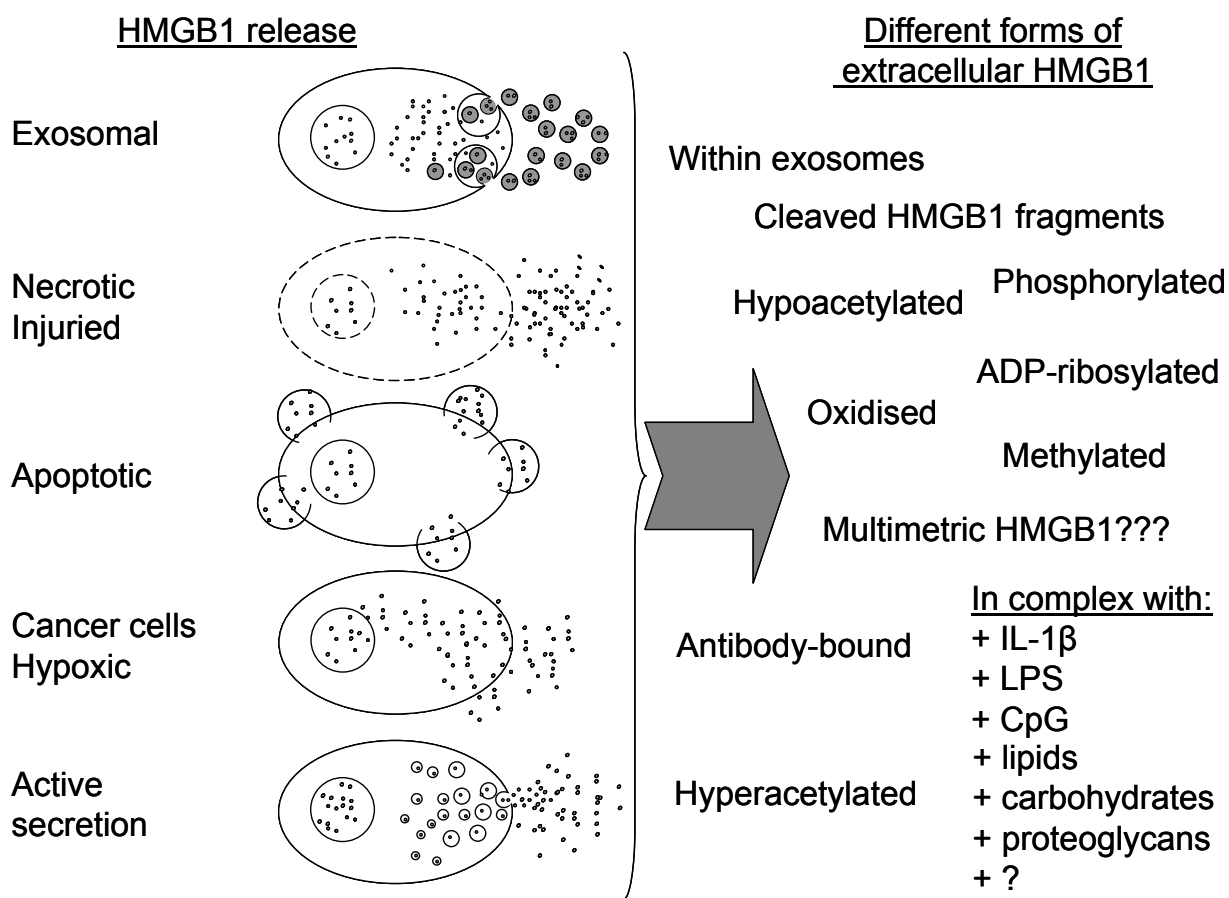


Figure3. SUMMARY: HMGB1 release and different forms of extracellular HMGB1

HMGB1 receptors

HMGB1 has been demonstrated to interact with a wide range of proteins including proteoglycans [273, 274] lipids and carbohydrates [275] transcriptional factors [227, 276-278] and viral proteins [279, 280]. Using a phage display approach HMGB1 was demonstrated to bind to more than 12 different peptide sequences, some being strictly associated with the A-box or B-box, respectively, while several were associated with both A- and B-box structures [281]. The heterogeneity of peptide and protein binding to HMGB1 thus implies interaction with several extracellular receptors. The suggested receptors for HMGB1 are summarised in Table 2 and the following receptors are discussed more detailed in next section: Receptor for advanced glycation end products (RAGE), TLR2, TLR4 and TLR9.

Receptor for advanced glycation end products (RAGE)

RAGE belongs to the immunoglobulin superfamily of cell-surface molecules and is composed of an extracellular region containing of one V-type and two C-type immunoglobulin domains [282, 283] followed by a hydrophobic transmembrane-spanning domain and a highly charged cytoplasmic domain which is essential for RAGE signalling [284, 285]. RAGE has several isoforms that code for both transmembrane and soluble proteins (sRAGE) [286, 287]. sRAGE has been suggested to function as a decoy receptor since higher plasma levels of sRAGE are associated with a reduced risk for arthritis and many other inflammatory diseases (reviewed in [288]).

HMGB1 interaction with membrane-bound RAGE was originally described to promote neuronal outgrowth [229, 289, 290]. The A- and B-boxes can independently promote cell migration in rat smooth muscle cells via a RAGE-dependent manner [291] while the neuronal outgrowth is promoted by the C-terminal motif [217]. It is therefore likely that additional molecules are involved in the regulation of cell migration. It was recently demonstrated that both RAGE and Mac-1 β 2 integrin interaction was required in HMGB1-mediated neutrophil recruitment in an *in vivo* model of peritonitis [292].

RAGE is also described to be the major receptor for HMGB1-induced cytokine production and cell migration in macrophages [250, 293]. However, the cytokine-inducing capacity of HMGB1 is ascribed to the B-box domain [240, 263, 294-296] whereas the interaction with RAGE is located to amino acids 150-183, just before the

C-terminal acidic tail [217] implying an interaction between HMGB1/RAGE and additional receptor/receptors. Full-length RAGE has two potential N-linked glycosylation sites which occur in the ligand-binding V-domain [283] and the subsequent glycosylation of RAGE was reported to enhance the binding to HMGB1 [297].

Interestingly, S100, which is a ligand for RAGE, has been detected as a tetrameric state in the human brain. Ostendorp and colleagues proposed that these S100 complexes could trigger multimerisation of RAGE and initiation of signal transduction [298, 299]. Since HMGB1 has a charged dipolar structure it has a strong tendency to form polymeric structures, which was first described for the protein isolated from brain tissues [234]. There are no studies addressing whether multimeric HMGB1 is needed for RAGE signalling and/or if a multimerisation of RAGE is needed for HMGB1-mediated signal transduction. Conversely, it has been demonstrated that RAGE/TLR9 associates in HMGB1/CpG-mediated signalling in pDCs [271].

Toll-like receptors

The primary response to pathogens in the innate immune system is triggered by Pattern Recognition Receptors (PRRs) that bind Pathogen Associated Molecular Patterns (PAMPs). Toll-like receptors (TLRs) are well-characterised signal generating receptors among PRRs and recognise a vast number of complex PAMPs [300] and Disease Associated Molecular Patterns (DAMPs), thereby initiating key inflammatory responses [301]. All known TLRs (presently 14) known in mammals are type I integral membrane glycoproteins containing an extracellular domain with leucine-rich repeats responsible for ligand recognition [302]. Most of TLRs are cell-surface receptors but TLR3, TLR7, TLR8 and TLR9 reside in intracellular organelles [303]. TLRs act as homo- or heterodimers or together with other PRRs recognising diverse bacterial and viral ligands [304] and even host DNA [305, 306]. The cytoplasmic domains of TLRs and IL-1-receptors are homologous, thus called Toll/IL-1 receptors (TIRs) [302]. TIR is required for signalling pathways activating the transcription factors nuclear factor κ B (NF κ B), activator protein-1 (AP-1), which is common to all TLRs, and interferon regulatory factor 3 (IRF) and IRF7. NF κ B and AP-1 leads to proinflammatory cytokine production while IRF 3 and IRF7 promote the production of IFN β and IFN α , -type I interferons.

TLR2 and TLR4

Both TLR2 and TLR4 are membrane-bound receptors. Among a vast number of ligands, TLR2 recognises lipoteichoic acid from gram-positive bacteria and TLR4 binds LPS from gram-negative bacteria (reviewed in [307]). While both TLR2 and TLR 4 are membrane-bound receptors they can be expressed as soluble proteins. Soluble TLR2 is produced through a post-translational modification and is detectable in human plasma and milk, while soluble TLR4 in mice is a result of alternative splicing (reviewed in [300]).

More recently a direct interaction of HMGB1 with TLR2 and TLR4 was determined using fluorescence resonance analysis and immunoprecipitation [308] and HMGB1-mediated TNF release from macrophages obtained from TLR2^{-/-} and TLR4^{-/-} mice was determined to be compromised in comparison to wild-type mice [309].

HMGB1-mediated NFκB activation via TLR2 is dependent on Myeloid differentiation primary response protein 88 (MyD88) and TIR-domain containing adaptor protein (TIRAP) binding to TIR. Furthermore, expression of dominant-negative forms of IL-1R associated kinase 1 (IRAK1), IRAK2, IRAK4, TGF-β activated kinase 1 (TAK1), Tak 1 binding protein 2 (TAB2), TNF receptor-associated factor 6 (TRAF6) or p38 inhibited HMGB1-mediated NFκB activity in macrophages. The signalling cascades initiated by TLR2 and TLR4 exhibit significant overlap but HMGB1-mediated TLR4 signalling seem to be less dependent on TAK1 and TAB2 pathways [310].

A partial overlap exists between RAGE and TLR2 and TLR4 signalling pathways, as depicted in Fig 4 [311, 312]. This sharing of signalling components makes genetic studies and heterologous expression systems difficult to interpret, and has led to contradictory conclusions regarding the roles of TLR2, TLR4 and RAGE, respectively, in HMGB1 signal transduction [293, 310]. Furthermore, the signalling cascades and substrate specificities are also modulated by TLR homo- and hetero-oligomerisation. Thus the binding of HMGB1 to homo- or heterodimeric TLRs remains to be determined. Furthermore, the fact that HMGB1 is very prone to form complexes with several TLR ligands such as LPS and endogenous molecules such as IL-1β complicates the issue of defining HMGB1-specific receptors.

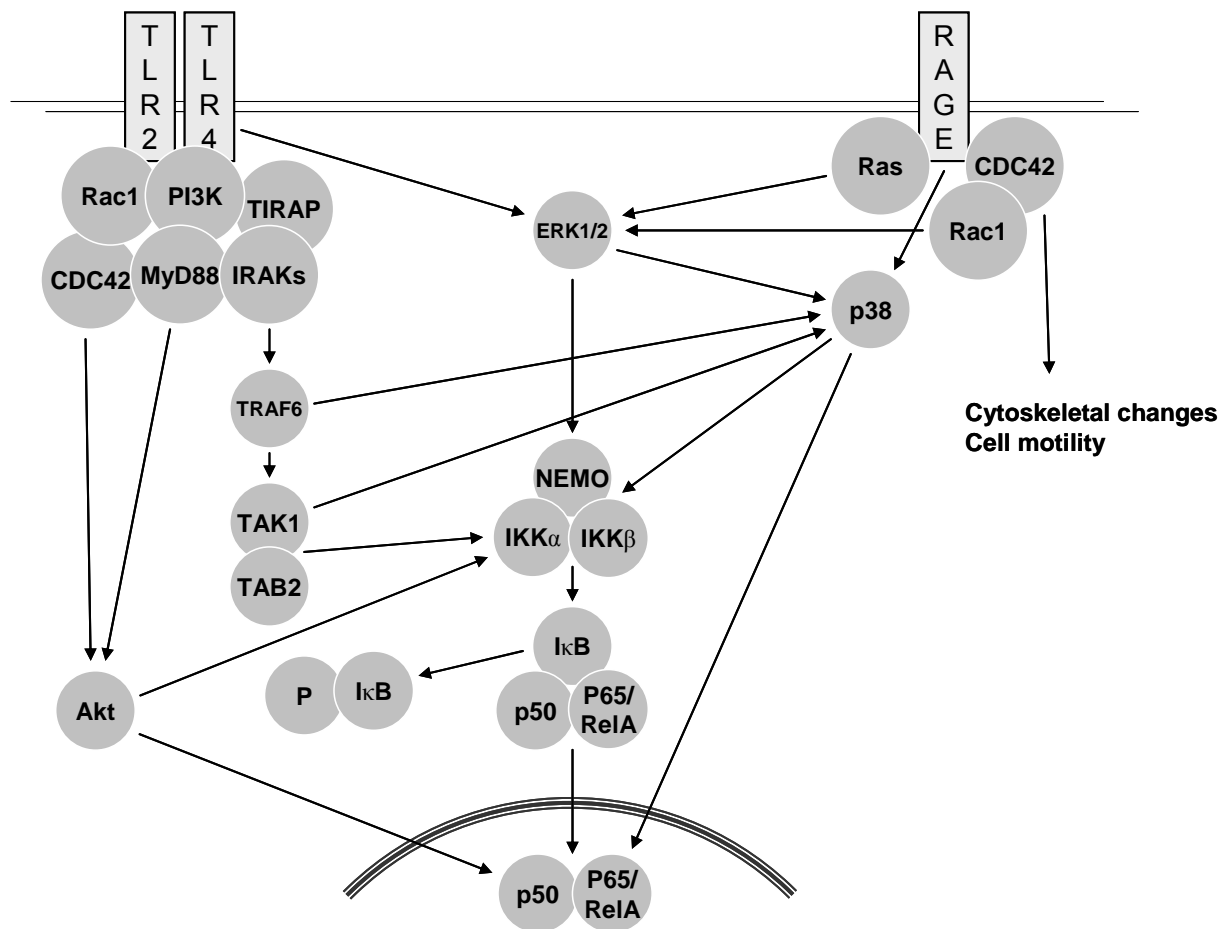


Figure 4. Convergence of TLR2 ,4 and RAGE signalling.
 Picture modified from van Beijnum et al. (ref.311)

Apetoh and colleagues illustrated the importance of adequate interaction between HMGB1 released from dying tumour cells and TLR4 expressed on DCs. The cross-presentation of tumour antigens and the promotion of tumour-specific cytotoxic T-cell responses required both HMGB1 and TLR4. Mutation in TLR4 (Asp299Asp to Asp299Gly) decreased its binding to HMGB1 and individuals bearing this mutation failed to cross-present antigens to CTLs from dying melanoma cells. Furthermore, knockdown of HMGB1 with siRNA or treatment with neutralising antibody directed against HMGB1 blunted antigen presentation of tumour antigens and inhibited T-cell priming. However, addition of recombinant HMGB1 could not restore the effects of HMGB1 released from Doxorubicin-treated tumour cells, indicating a requirement of tumour-specific HMGB1 [313, 314] (reviewed in [315]).

Interestingly, the way of dying and the resulting post-translational modifications of HMGB1 seem to be important for HMGB1-mediated DC responses. Kazama and colleagues demonstrated that oxidation of Cysteine 106 alone was sufficient to block the immunogenic activity of HMGB1. Thus DCs are activated by HMGB1 released from necrotic cells which is not oxidised while oxidised HMGB1 released from apoptotic cells induces tolerogenic signals in DCs. Oxidation of HMGB1 was reported to be mediated by caspase 3- and 7-induced ROS activation [263, 316].

ADP-ribosylation of HMGB1 occurs in cells treated with alkylating agents. How this affects the cross-presentation of tumour antigens is as far as I know not yet studied. It is interesting that cell supernatants from cells deficient in the enzyme (PPAR-1) responsible for polyadenylation fail to induce inflammation [262].

TLR9

TLR9 is primarily confined to cells of the immune system and is highly expressed in plasmacytoid DCs but not in conventional DCs [317]. It is initially localised in the endoplasmic reticulum, but redistributes to early endosomes upon stimulation with CpG-DNA [318]. TLR9 recognises synthetic CpG oligonucleotides and unmethylated CpG motifs in bacterial and viral DNA [317] but also host DNA and RNA [305, 319].

While the exact mechanism leading to TLR9 activation by CpG-DNA remains unclear, HMGB1 was recently determined to be an important regulator in this process. It was demonstrated that HMGB1 interacts with TLR9 in the endoplasmic reticulum Golgi intermediate compartment (ERGIC) in quiescent macrophages and accelerates the redistribution of TLR9 to early endosomes in response to CpG-ODN stimulation. Thus immune cells lacking HMGB1 demonstrated a delayed redistribution of TLR9 to early endosomes and an impaired cytokine response to CpG-ODN. Interestingly, the decreased response to CpG-ODN in HMGB1-defective cells could be restored by addition of extracellular HMGB1, suggesting a common feedback loop in which innate immune cells secrete HMGB1 and HMGB1 sensitises immune cells to CpG-DNA through interaction with TLR9 and RAGE [270, 271].

Table 2. HMGB-1 receptors and signaling

Receptor	Comment
RAGE [217, 289, 293]	Interactions with HMGB1 result in MAP kinase activation, enhanced tumor growth, metastases, and release of MMPs. RAGE-HMGB1 also interact with the Rho family of GTPases, Cdc42 and Rac to regulate cell motility.
TLR2/TLR4 [308]	Interaction with HMGB1 results in activation of macrophages and maximal stimulation of NFκB activity in macrophages, along with induction of neovascularization in periods of innate immune system activation.
TLR9 [270, 271]	Interaction with HMGB1 within the ERGIC in quiescent macrophages and accelerates the redistribution of TLR9 to early endosomes upon CpG activation.
Syndecan [274]	HMGB1 links syndecan to the extra cellular matrix participates in cell adhesion and migration of simple epithelial cells, particularly in early cell spreading.
Phosphacan/protein-Tyr Phosphatase γ/β [273]	This receptor participates in proteoglycan-mediated regulation of cell adhesion, neurite growth and cell migration during central nervous system development. It links phosphacan in the extracellular matrix or the transmembrane phosphatase on adjacent cells, to cell surface glycoproteins such as contactin to which phosphacan alone binds only minimally.
Plasminogen [235]	This activates plasmin via formation of ternary complexes, also binds tissue-type plasminogen activator.
TREM -1 [320, 321]	TREM is expressed broadly on myeloid cells. Interaction with HMGB1 amplifies the immune response on THP-cells.

Modified from JE Ellerman 2007, Clin Cancer Research

HMGB1 expression in the arthritic joint

High levels of HMGB1 are present in serum and synovial fluid in rheumatoid arthritis patients [257, 322] with a higher concentration in synovial fluid from RA patients compared with osteoarthritis patients [323]. The hyperplastic synovial tissue in RA patients demonstrates a significant increase in extracellular HMGB1 expression [257, 324].

Tissue hypoxia occurs in the inflamed RA joints due to accelerated oxygen consumption in accumulated inflammatory cells and due to the hyperproliferation of synovial cells. Hypoxia has been considered to have a pathological role in arthritis development through induction of cytokines, matrix-degrading enzymes and angiogenic factors [325]. Thus the increased number of blood vessels detected within the inflamed synovial tissue is suggested to be a consequence of the hypoxic environment. Recently, hypoxia was demonstrated to induce HMGB1 release in cell-based *in vitro* experiments and HMGB1 detected in synovial fluid collected from patients suffering from RA correlated with lactic acid concentrations, which is a tissue hypoxia marker [257]. Thus HMGB1 released during hypoxia is yet a source of extracellular HMGB1 within RA tissue.

Putative role of HMGB1 in RA

In the collagen-induced arthritis model both the protein and mRNA levels of HMGB1 were elevated at the areas of cartilage bone destruction [326].

Interestingly, FLS in the arthritic joint express RAGE [323, 327, 328] and binding of HMGB1 induces invasive feature of FLS. HMGB1-mediated invasiveness could be completely inhibited by antibody treatment targeting RAGE, suggesting that RAGE-targeted therapy could inhibit the cartilage and bone invasion by FLS [329]. In our studies we have demonstrated that HMGB1 in complex with trace amounts of LPS or IL-1 β induced TNF, IL-6 and IL-8 production from FLSs and enhanced their MMP1 and MMP3 production, thus increasing the inflammatory and destructive phenotype of FLS (*Paper V*).

HMGB1 promotes vasculogenesis by inducing chemotactic migration of adult human peripheral blood-derived endothelial progenitor cells (EPC), an important mechanism in rescue of ischemic tissues. The enhanced adhesion of EPCs at a site of ischemia and active angiogenesis is mediated by HMGB1/RAGE-induced β -integrin upregulation on EPCs [330].

The initiation of angiogenesis, the growth of new blood vessels from pre-existing ones, begins with the degradation of the basement membrane by activated endothelial cells. These proliferate and migrate, leading to the formation of solid sprouts to the stroma. Macrophages produce a number of potent angiogenic cytokines and growth factors, e.g. TNF, IL-8 and VEGF. Recently, HMGB1 has been demonstrated to promote

angiogenesis in a dose-dependent manner in an *in vitro* angiogenesis assay [331]. Blocking of RAGE inhibited HMGB1-induced neovascularisation *in vivo* and endothelial cell proliferation and membrane ruffling *in vitro*, demonstrating HMGB1 and RAGE dependency during blood vessel formation and in wound healing [332].

Interestingly, a high HMGB1 expression pattern was demonstrated in the endothelial cells of RA synovial tissue samples despite local glucocorticoid treatment [324], and an active HMGB1 release has been demonstrated from activated endothelial cells [252, 333] and from smooth muscle cells lining the arteries [252] suggesting that local HMGB1 production could promote angiogenesis in RA.

An activated endothelium is required for the transmigration and accumulation of immune cells to the site of inflammation. Recent publications demonstrate that HMGB1 possesses the capacity to both activate the endothelial cells by upregulating the adhesion molecules ICAM-1, VCAM-1 and E-selectin, and through attracting inflammatory cells to the site of inflammation by inducing IL-8 and MCP-1 production [242, 246, 295, 334]. Treutiger and colleagues demonstrated that neutrophil adhesion to activated endothelial cells was partly mediated by RAGE. Furthermore, it was recently demonstrated that both RAGE and Mac-1 β 2 integrin interaction was required in HMGB1-mediated neutrophil recruitment in an *in vivo* model of peritonitis and for increased adhesion to ICAM-1 *in vitro* [292, 335]. Since Mac-1 expression is only restricted to neutrophils and macrophages it is plausible that recruitment of other proinflammatory cells requires interaction with other molecules together with RAGE. Additionally, HMGB1 activates neutrophils [336].

When NK cells are in physical contact with immature DCs they start to produce IL-18 that stimulates NK cells to produce HMGB1 [337]. Extracellular HMGB1 in turn has been demonstrated to promote DC migration [338] and maturation [339, 340]. HMGB1 is further secreted from stimulated DCs, creating an intrinsic loop of inflammation-promoting events. HMGB1 secreted from DCs is crucial for T cell proliferation, survival and polarisation to a Th1 phenotype, and this is mediated by HMGB1/RAGE interaction [340, 341]. Among T cells, Th1 cells are the most prominent cell population in the inflamed RA synovial tissue [108, 109] mediating inflammation and bone destruction.

Phagocytosing macrophages release HMGB1 [342] and extracellular HMGB1 can further induce monocyte migration [250] and enhance the expression and secretion of

other proinflammatory cytokines such as TNF, IL-1 β , IL-6 and IL-8 [343, *paper V*]. All these cytokines occur in the arthritic joint, promoting inflammation and bone destruction. Bone destruction in RA is mainly mediated by osteoclasts and HMGB1 and RAGE are mediators of osteoclastogenesis [344]. HMGB1 is also released by osteoclast precursor cells, osteoclasts and osteoblasts [345]. It is also demonstrated that HMGB1 promotes chemotaxis and osteoblast differentiation from mesenchymal stem cells [346] indicating a bone anabolic activity of HMGB1.

Taken together, HMGB1 is an abundant molecule in the arthritic joint and different cell populations, namely endothelial cells, neutrophils, NK-cells, DCs, T-cells, monocytes and macrophages, are potent sources of secreted HMGB1. Extracellular HMGB1 is a potent amplifier of local inflammatory responses by enhancing the release of cytokines, chemokines and by promoting osteoclastogenesis and pannus invasion into the cartilage and bone. Modulating HMGB1 activity may provide a new strategy to block the intrinsic loop of inflammation and joint destruction.

HMGB1 targeting therapies

The importance of HMGB1 in arthritis has been further demonstrated by use of animal models, in which the blocking of HMGB1 activity using different strategies has had beneficial effects on arthritis development. To inhibit HMGB1-mediated activities the strategies which have been used include: *i*) targeting of extracellular HMGB1; *ii*) receptor blocking (may be different for inflammation and invasiveness); and *iii*) inhibition of HMGB1 secretion.

Targeting extracellular HMGB1

HMGB1 neutralising polyclonal antibody and the antagonistic A-box residue ameliorated the disease course of collagen-induced arthritis in both the mouse and rat. The mean arthritis score, disease-induced weight loss and histological severity of arthritis as well as IL-1 β expression in the synovial tissue were significantly reduced in the treated animals [257, 347].

Thrombomodulin is an endogenous endothelial anticoagulant that binds to HMGB1 and prevents the extracellular proinflammatory activities of HMGB1 [348]. Treatment with truncated forms of thrombomodulin was a successful therapy in several forms of experimental arthritis [349].

Receptor blocking

Administration of sRAGE suppressed clinical and histological signs of arthritis and decreased the RAGE expression, TNF, IL-6, MMP-3, -9 and -13 levels in DBA/1 mice joints, limiting both inflammation and bone and cartilage destruction [350].

Inhibition of HMGB1 secretion

Ghrelin (GHR) is a 28-aa polypeptide mainly produced by stomach cells and is involved in the control of growth hormone secretion and adiposity [351]. Collagen-induced arthritis treated with GHR attenuated the arthritis severity, with decreased HMGB1 levels in serum compared with untreated animals. Translocation of HMGB1 from the nucleus to the cytoplasm in LPS-stimulated macrophages was inhibited by GHR treatment, indicating a decreased secretion of HMGB1 [352].

Oxaliplatin a commonly used anti-cancer drug creating platinated DNA adducts where HMGB1 is sequestered [353]. Systemic treatment with oxaliplatin ameliorated collagen type-II induced arthritis in mice and blocked the nuclear translocation of HMGB1. However, the treatment effect was not persistent and a rebound effect was determined with an increased disease induction and severe synovial inflammation. This rebound effect correlated with an increased extracellular HMGB1 expression (*Paper III*).

METHODS USED IN THE PAPERS

Cell cultures

<i>C1MC/C57.1</i>	(I)
<i>HCT 116</i>	(I)
<i>HMC-1.2</i>	(I)
<i>PBMC</i>	(IV)
<i>RAW264.7</i>	(I, II, III)
<i>Synovial fibroblasts</i>	(V)
<i>THP-1</i>	(II)

Detection of cytokines and MMPs

<i>CBA</i>	(V)
<i>ELISA</i>	(II, IV)
<i>TNF ELISpot</i>	(II, IV)
<i>Western blotting</i>	(II, IV)

Detection of HMGB1

<i>ELISpot</i>	(I, II, III)
<i>Immunohistochemistry</i>	(III)
<i>Immunocytochemistry</i>	(I, II, III)
<i>Western blotting</i>	(III, IV)

Induction and evaluation of arthritis

<i>CIA</i>	(III)
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RESULTS & DISCUSSION

Development of an HMGB1-specific ELISpot assay and determination of HMGB1 secreting capacities of several cell lines.

(Paper I)

In the first study an HMGB1-specific ELISpot method for both adherent and non-adherent cells was developed. Several different antibodies were screened in order to elucidate the optimal combination of antibodies to detect HMGB1 secretion from cells. The capture antibody in our HMGB1 ELISpot is a non-commercial mouse monoclonal antibody, 2G7 CTI (Boston, MA, USA) that recognises the amino acid sequence 53-63 within the A-box region of the HMGB1 molecule. The detection antibody is a commercial affinity-purified rabbit polyclonal antibody PharMingen (San Diego, CA, USA) detecting amino acids 166-181 at the linker region between the B-box structure and the acidic tail of HMGB1. The specificity of the ELISpot assay was confirmed by replacing the capture or detection antibodies with isotype- or irrelevant control antibodies, or by omitting the detection antibody. No spots were detected with these control antibodies from either stimulated or unstimulated RAW246.7 cells.

The kinetic pattern of HMGB1 release could be determined by discriminating between low- and high- intensity spots. Low intensity spots reflect the initial phase of HMGB1 secretion and high intensity spots signify high output HMGB1 secretion. Stimulation with IFN γ alone induced a fast HMGB1 release from RAW264.7 cells detected as the highest amount of low intensity spots after 24h of stimulation. Conversely, TNF was a poor inducer of HMGB1 secretion. Stimulation with LPS alone or with IFN γ +LPS generated a granular HMGB1 pattern after 24h of stimulation as detected by immunocytochemistry, indicating that HMGB1 was secreted via secretory lysosomal pathway from the RAW264.7 cells. However, in IFN γ stimulated cells this pattern occurred after 48h of stimulation, demonstrating that HMGB1 secretion was not always preceded by HMGB1 granule formation, suggesting additional pathways for HMGB1 secretion.

HMGB1 is known to be highly expressed in malignant cells [229, 354]. In my study I could demonstrate that not all transformed cell lines tested were able to actively secrete HMGB1. The human colon cancer cell line HCT 116 had a high spontaneous secretion of HMGB1, while the mast cell lines C57 and HMC-1.2 did not even release HMGB1 following stimulation. HMGB1 release was further detected from water-disintegrated cells (resembling necrotic cells), but was not detected from apoptotic cells (induced by p53 activator PRIMA-1).

Although we did not detect HMGB1 release from apoptotic or all transformed cell lines tested, we should consider the possibility that it might depend on conformational differences or post-translational modifications of HMGB1 [260-265]. For instance, PRIMA-1 induces apoptosis by activating p53 which in turn activates the caspase proteinases which induce oxidation of HMGB1 [263]. It is possible that oxidised HMGB1 is not detected by the antibody pair used in our ELIspot assay. It is therefore crucial to evaluate the specificity of HMGB1 antibodies that are used in different bioassays.

HMGB1 secreted by the exosomal pathway would neither be detected by ELIspot or ELISA, since HMGB1 is then encircled by membrane, pinpointing the necessity to combine different techniques when studying HMGB1 secretion.

Inhibition of HMGB1 secretion by inducing nuclear retention of HMGB1

(Paper II & III)

In the second and third studies we investigated the capacity of gold sodium thiomalate and oxaliplatin to inhibit HMGB1 secretion.

The first clinical trial with gold compounds was led by a French physician, Forestier in 1929. Thirty years later (1960) gold therapy was demonstrated to be clinically efficient in a controlled study (reviewed in [355]). The intramuscular gold treatment in subgroups of patients with RA reduced both disease activity [356] and cartilage destruction [357]. Although the clinical efficacy of gold salts is well established in RA the mechanism of action is not fully understood. The so far described anti-

inflammatory effects of gold salts include suppression of the proinflammatory mediators IL-1 β , NO and PGE2 [358] and inhibition of NF- κ B activity [359].

After absorption the gold complex dissociates rapidly in blood plasma, generating gold-albumin complexes and the thiomalate moiety is converted to a free thiolate form. After repeated administration gold is concentrated in the kidneys, liver, spleen and synovial tissue. It is taken up by macrophages and the gold is almost exclusively deposited in lysosomes in macrophages (reviewed in [355]).

I wanted to elucidate whether Myocrisin (GST), the most commonly used gold compound, could inhibit HMGB1 secretion from human THP-1 monocytes and murine RAW264.7 macrophage cell lines. We started to investigate whether IFN γ +LPS- or p(I:C)-induced-HMGB1 secretion could respectively be inhibited by GST treatment.

THP-1 and RAW264.7 cells pretreated with GST and followed by IFN γ +LPS stimulation displayed a dose-dependent decrease in HMGB1 secretion determined by both ELISpot and Western blotting analyses. Intracellular HMGB1 staining of IFN γ +LPS stimulated RAW264.7 cells displayed a cytoplasmic HMGB1 pattern compared with GST-treated cells, which display a more nuclear HMGB1 staining indicating a nuclear retention and a decreased HMGB1 secretion. Similarly, GST-mediated inhibition of HMGB1 secretion was determined by p(I:C)- or LPS-stimulated RAW264.7 cells (determined by Western blot). In agreement with previous data [358], TNF production was not affected by GST treatment.

NO and type I IFNs have been reported to be downstream key mediators of HMGB1 release [254]. NO production is triggered by LPS, p(I:C), IFN γ and TNF stimulation and IFN β production is induced by LPS and p(I:C). We therefore further investigated whether GST also influenced the production of these key mediators and if GST could inhibit HMGB1 secretion induced by NO and IFN β . Indeed, RAW264.7 cells pretreated with GST followed by stimulation with either LPS or p(I:C) demonstrated decreased IFN β and NO levels as determined by ELISA and the Greiss method, respectively. Furthermore, the IFN β and NO donor NOC-15-induced HMGB1 secretion was attenuated by GST-treatment as determined by Western blotting, demonstrating that GST-treatment affects LPS-, p(I:C)-, IFN β - and NO-induced HMGB1 release.

We also verified that the GST-mediated inhibition of HMGB1 was related to the gold component itself rather than to the thiomalate moiety in the GST, since the thiomalate

moiety itself did not induce HMGB1 attenuating effects. We could also demonstrate that AuCl₃, another gold compound, attenuated both HMGB1 and NO secretion from RAW264.7 cells, which further strengthens the view that gold compounds in general function as inhibitors of HMGB1 secretion.

We did not elucidate whether the phagocytosis of gold particles *per se* inhibited HMGB1 release from monocytes/macrophages. There is one report concerning increased HMGB1 release during phagocytosis of apoptotic material [342] thus describing a distinct event from gold particle phagocytosis.

Paper III

Oxaliplatin and other platinated anti-tumour compounds generate DNA adducts, leading to nuclear sequestration of HMGB1 [360]. In the third study we aimed to verify the oxaliplatin sequestering capacity of HMGB1 both in *in vitro* and *in vivo* models and to study whether that influenced the course of collagen type II-induced arthritis.

In vitro studies using RAW264.7 cells stimulated with IFN γ +LPS demonstrated a nuclear retention of HMGB1 when co-cultured with oxaliplatin. In addition, the secretion of HMGB1 was inhibited by oxaliplatin treatment as determined by ELISpot. Conversely, TNF production was not affected by oxaliplatin treatment. Cultures with lymph node cells challenged with ovalbumin displayed an inhibited proliferative activity in the presence of oxaliplatin, an important finding since CIA is a T cell-dependent arthritis model.

DBA/1 mice were challenged with bovine collagen type II and treated with one intraperitoneal injection of oxaliplatin at the expected onset of CIA. Administration of oxaliplatin in early arthritis delayed the disease onset and ameliorated the clinical signs of arthritis. In an attempt to prolong the positive effect of oxaliplatin treatment the study was repeated and the animals were treated with an additional injection of oxaliplatin. The additional dose of oxaliplatin prolonged the period of reduced arthritis but did not affect the arthritis incidence. In both settings an aggressive disease flare was observed one week after the last dose of oxaliplatin was given. Analysis of articular tissue demonstrated a nuclear HMGB1 staining pattern which correlated well with the low clinical arthritis score, while an excessive cytoplasmic and extracellular HMGB1 pattern correlated with the time point of disease flare.

Apetoh and colleagues reported that HMGB1 is released from oxaliplatin-treated cells undergoing apoptosis, thereby confirming our results [313, 314]. They further described that cross-presentation of tumour antigens and the promotion of tumour-specific cytotoxic T-cell responses required tumour-derived HMGB1 to bind to TLR4 on DCs. It is currently not known if disease flares in oxaliplatin treated CIA mice are dependent on such DC-mediated immune responses. Alkylating agents have been demonstrated to induce ADP-ribosylation of HMGB1 [262]. Oxaliplatin belongs to this group of drugs and it is therefore plausible that the released HMGB1 is ADP-ribosylated. Whether ADP-ribosylated HMGB1 is more immunogenic than unmodified HMGB1 or if ADP-ribosylation is required for TLR4 binding is yet to be determined.

It is also possible that the rebound effect with aggressive arthritis in oxaliplatin-treated CIA mice could depend on HMGB1-mediated chemoattraction of proinflammatory cells.

Studies of the cytokine inducing capacity of HMGB1 alone or in complex with inflammation promoting molecules

(Paper IV & V)

Highly purified HMGB1 batches have been demonstrated to possess low or no cytokine-inducing activity [275, 361]. In these last two studies I wanted to further study the cytokine-inducing capacity of highly purified HMGB1. I studied HMGB1 alone or in complex with IL-1 β , LPS, Pam3CSK4, CpG-ODN, TNF, RANKL, p(I:C) or IL-18, respectively.

In study IV we used peripheral monocytes (PBMCs) to investigate the proinflammatory capacity of HMGB1. Native HMGB1 purified from calf thymus or recombinant HMGB1 purified from viral or bacterial sources were used. None of these HMGB1 batches induced IL-6 production from freshly isolated PBMCs. In contrast, IL-6 production was synergistically enhanced when PBMCs were stimulated with HMGB1/LPS complexes. These HMGB1/LPS complexes contained suboptimal concentration of LPS, which alone did not induce IL-6 production. HMGB1 together with Pam3CSK4 or CpG-ODN also displayed synergistic effects on IL-6 production in

PBMCs, even though the effect was not as pronounced as was the HMGB1/LPS complex-induced IL-6 production. Monocytes express high levels of TLR1/TLR2 that mediates Pam3CSK4 signalling while the TLR9 expression is very low on monocytes. It has been reported that the pDC-containing monocyte population is sensitive to CpG-ODN-mediated stimulation while pure monocyte populations do not respond to stimulation with CpG-ODN. The authors further suggested that monocyte activation within human PBMCs is due to secondary effects of CpG-ODN-mediated signalling via pDCs [362]. It is therefore not surprising that the CpG-ODN was a weak inducer of IL-6 production from our PBMC cultures.

HMGB1 together with TNF, RANKL, p(I:C) or IL-18 failed to induce IL-6 production from PBMCs. A recent publication reported that HMGB1 had only a weak association to TNF, while HMGB1 was shown to bind avidly to IL-1 β [272]. In our study we did not investigate if these latter molecules failed to form complexes with HMGB1, but we clearly demonstrated that HMGB1 acts selectively together with certain molecules, and that the synergistic activity of HMGB1 is not only dependent on non-specific interaction with each and every protein.

Paper V

In study V we investigated the proinflammatory effect of HMGB1 alone or in complex with IL-1 β or LPS on synovial fibroblasts (RASf) from RA and osteoarthritic (OASf) patients. Cells were stimulated for 9h and the number of TNF producing cells was determined by ELISpot. After 24 hours of stimulation the supernatants were collected and IL-1 β , IL-10, IL-6 and IL-8 levels were determined using a CBA assay and MMP-1 and MMP-3 levels were analysed by ELISA. HMGB1 alone did not induce cytokine or MMP production. In contrast, stimulation with HMGB1 in complex with IL-1 β or LPS had a synergistic effect on TNF, IL-6 and IL-8 production, respectively, and enhanced the MMP-1 and MMP-3 production as compared with stimulation by IL- β or LPS alone. This is the first report to demonstrate the effects of HMGB1-complex-mediated activation of synovial fibroblasts.

In my study, I could not determine any difference between the HMGB1/IL-1 β -induced cytokine and MMP production between RA and OA fibroblasts. Interestingly, high levels of IL-1 β are evident in RA synovial tissues and to a lesser extent in OA patients. The quantities of HMGB1 in the synovial fluid from OA patients are much lower

compared to the levels in RA patients [323]. It is therefore possible that the complex formation between HMGB1 and IL-1 β occurs more frequently in the arthritic joint, leading to a more pronounced inflammation with an increased bone and cartilage destruction in RA patients compared to in OA patients.

CONCLUDING REMARKS & FUTURE PERSPECTIVES

The scientific messages and innovations in this thesis work can be summarised as follows:

- An HMGB1-specific ELISpot assay was developed that enabled assessments of active and passive HMGB1 release from both adherent and non-adherent cells.
- Gold salt was determined to reduce HMGB1, IFN β and NO secretion from macrophages, while it did not influence their TNF secretion.
- Oxaliplatin ameliorated experimental arthritis by inducing nuclear retention of HMGB1. The observed disease rebound effect correlated well with increased amounts of extracellular HMGB1, indicating the importance of HMGB1 as a pro-inflammatory mediator in arthritis.
- The inflammatory and destructive activity of HMGB1 was demonstrated to be mediated by complex formation of HMGB1 with other inflammation-inducing molecules.

Rheumatoid arthritis is a chronic systemic inflammatory disease encompassing severe inflammation and destruction of synovial joints. An increasing body of evidence suggests that HMGB1 has a central role in RA pathogenesis since increased levels of HMGB1 are evident in the synovial fluid and an extracellular HMGB1 pattern can be demonstrated in the synovial tissues of RA patients. HMGB1 is released by a variety of cells in the inflamed RA joint and reportedly promotes a vast number of inflammation-promoting features such as angiogenesis, endothelial activation, inflammatory cell recruitment and tissue destruction [363].

Changes that occur in the synovial lining layer during RA development resemble the peritoneal lining during chronic ambulatory dialysis in which epithelial cells become hyperplastic and exhibit a transformed mesenchymal (myofibroblast) phenotype. These changes are induced in a process called 'epithelial-to-mesenchymal transition' (EMT) [364]. In a recent study, Steenvoorden and colleagues demonstrated that the myofibroblast marker α -sma was expressed in RA FLS but not in healthy subjects, indicating a transformed EMT phenotype in RA FLS. Interestingly, α -sma expression

in healthy FLS could be induced by stimulation with synovial fluid obtained from RA patients [365]. TGF- β is the most well known inducer of EMT, but it can also be induced by the RAGE ligands S100 calgranulins and AGEs [240]. Increased levels of TGF- β , AGEs and S100 calgranulins are detected in synovial fluid in RA patients [366, 367]. Several S100 proteins and AGEs are ligands to RAGE. Together with increased expression of RAGE in FLS the induction of the EMT phenotype may be promoted by RAGE/RAGE-L interaction in RA. Since it has been reported that HMGB1 competes with AGEs for binding to the RAGE ectodomain [284] it would be interesting to investigate if HMGB1 could induce EMT in healthy synovial fibroblasts and thereby reveal if HMGB1 may be an important molecule already at the early phase of RA.

Pullerits and colleagues demonstrated that intra-articular HMGB1 injections did not induce arthritis in IL-1R gene deficient mice [243] demonstrating co-operation between HMGB1 and IL-1 β . My results presented in this thesis demonstrate a distinct co-operation between HMGB1 in complex with IL-1 β , generating a synergistic effect on proinflammatory cytokine and MMP production in synovial fibroblasts (*paper V*). Such complex formation between HMGB1 and IL-1 β may occur *in vivo* since both HMGB1 and IL-1 β are highly expressed within the arthritic joint [323].

Interestingly, several reports demonstrate that IL-1 β is able to drive both bone and cartilage destruction independently of TNF [184]. TNF gene deficient animals displayed a similar degree of joint inflammation as the corresponding control TNF wildtype animals when challenged with intra-articular HMGB1 [368] thus demonstrating that HMGB1-mediated joint inflammation is not dependent on TNF induction. Furthermore, a recent study from Sundberg and colleagues demonstrated that the extracellular HMGB1 expression pattern did not decrease in the synovial tissues following anti-TNF treatment [369]. All these results together indicate that TNF and HMGB1 may act independently of each other and that HMGB1-mediated joint inflammation and destructive features of synovial fibroblasts may be dependent on IL-1R-mediated signalling.

Taken together, these results suggest new approaches to treat patients who do not respond to anti-TNF therapy.

It will be a future challenge to develop drugs which specifically target the disease-promoting HMGB1 molecule since an increasing body of evidence suggests that pure HMGB1 promotes tissue regeneration and cell migration [275] whereas in complex with inflammation-promoting agents such as CpG, IL-1 β and LPS it promotes inflammation and tissue destruction [269-272, *papers IV,V*].

It is also apparent that HMGB1 also undergoes diverse post-translational modifications [260-263, 265]. It can be cleaved by Thrombin-thrombomodulin complexes [266] and is also able to make complexes with IgG [267, 268]. These modifications and molecular interactions of HMGB1 most likely influence the wide receptor binding capacity and diverse functions of HMGB1.

A recent report illustrated the importance of HMGB1 in the error-free repair of DNA damage. The lack of HMGB1 led to increased mutagenesis and reduced cell survival in mammalian cells following exposure to DNA-damaging agents [373] thus emphasising the importance of targeting only the disease-promoting form of HMGB1.

Protein transduction domains which promote cargo delivery cross cell and organell membranes are typically rich in basic amino acids (lysine, arginine and histidine) [370]. HMGB1 has an exceptional dipolar structure with a highly basic amino-terminal structure, consisting of 184 amino acids there on an average every fourth amino acid is a lysine [229]. Thus, the structure of HMGB1 might influence the capacity of HMGB1 to enter cells through non-receptor mediated mechanism. Since HMGB1 has been used as a nonviral gene delivery agent [371, 372] it is a possibility that therapies directed against HMGB1 could be delivered into cells in a cargo dependent manner.

One potential approach to identify HMGB1 suppressive agents is to study the HMGB1-suppressing capacity of already known drugs that have been shown to be safe in clinical use. In this thesis two well-known compounds were studied regarding their capacities to inhibit HMGB1 secretion. Both oxaliplatin and gold salt induced nuclear HMGB1 retention and decreased HMGB1 release. From a clinical point of view regarding arthritis it was interesting to study gold salts which are used as efficacious anti-rheumatic drugs in a subgroup of RA patients. Gold salt treatment of macrophages displayed a suppressive effect on HMGB1 release but did not suppress their TNF secretion. Thus patients with HMGB1- (and IL- β)-specific cytokine profiles might in particular benefit from therapy based on gold salt treatment.

SVENSK SAMMANFATTNING

Reumatoid artrit eller som sjukdomen i allmänhet kallas: reumatism, är en inflammatorisk sjukdom som främst drabbar lederna med påföljande vävnadsskada och invaliditet. Forskarna och läkarna är överens om att den ihållande inflammationen drivs av olika proteiner bland andra TNF och IL-1 β . Terapier riktade mot dessa proteiner hjälper många patienter, men det finns fortfarande en stor grupp av reumatiker som har en aktiv sjukdom med pågående inflammation som ger upphov till vävnadsskador i både ledbrosket och i benet.

Färska studier visar att det finns ytterligare andra proteiner som kan vara viktiga i den reumatiska inflammationen. HMGB1 är ett protein som har påvisats i stora mängder i den artritiska leden samt i ledvätskan hos reumatiker. Djurstudier har visat att behandlingar riktade till att hämma HMGB1 minskar ledinflammationen och vävnadsskadorna hos försöksdjuren.

Syftet med mina studier har varit att vidare studera betydelsen av HMGB1 i reumatism. Vi utvecklade en känslig metod för att på cellnivå kunna mäta utsöndringen av HMGB1 från olika celletyper. Genom att studera inflammatoriska celler och deras förmåga att aktivt utsöndra HMGB1 har vi kunnat med hjälp av läkemedel påverka utsöndringsgraden av HMGB1. Vi har kunnat visa att en hämning av HMGB1-utsöndring resulterar i ett minskat inflammatoriskt svar från celler och i en minskning av ben- och brosknedbrytning. Vi har vidare kunnat visa att HMGB1 samarbetar med andra inflammatoriska proteiner och därmed intensifierar inflammationen och den vävnadsskadande förmågan hos ledspecifika celler.

Våra studier har därmed bekräftat att HMGB1 är en central molekyl i den reumatiska inflammationen och därmed en potentiell målmolekyl för kommande terapier.

Vår förhoppning är att våra studier ska leda till, att fler patienter med svår reumatism ska kunna få en mer effektiv behandling.

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