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Chaperonins and the regulation of immunity
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Chaperonins have classically been thought of as intracellular molecules involved in the correct folding of proteins. Their expression is upregulated during times of stress such as heat. Hence their common nomenclature as heat shock proteins [HSP]. Chaperonins and reactive oxygen species [1]. These are conditions found in infected tissues or in tissues with chronic inflammation such as the rheumatoid synovium. In their intracellular location they protect the cell from apoptotic death due to stress. Increasingly chaperonins have been recognised to subserve extracellular functions for which they have received the name ‘chaperokines’ since they bind to specific receptors on the cell surface and activate cells of the innate immune system to secrete inflammatory cytokins, chemokines and small molecular weight mediators such as prostaglandins [2]. Indeed, an early event in inflammation is cell stress/necrosis leading to the release of HSP60 and HSP70 that binds via a CD14-mediated mechanism to Toll-like receptors 2 and 4 [2] as part of the ‘danger’ signal [3]. The secretion of tumour necrosis factor alpha, IL-1, IL-12 and other chemokines prepares the environment for a TH1 adaptive immune response. It is now recognised that some chaperonins, such as BiP and HSP27, may activate the innate immune system to secrete anti-inflammatory cytokins. BiP may downmodulate ongoing TH1 responses. Thus, it may be possible to suppress rheumatoid inflammation by administration of appropriate chaperonins such as BiP. Finally, chaperonins may be important system regulators determining the outcome between TH1 and TH2 immune responses.

References

Available online http://arthritis-research.com/supplements/7/S1
lates and biomarkers in patients suffering from RA, we searched for con-
spicuous differences in the abundance of soluble proteins between synovial fluids (SF) and plasmas of patients. Detailed analysis of two-dimensional gel elec-
trophoresis-separated protein spots by means of MALDI-MS and MALDI-QIT-
ToF-MS 
sequencing \cite{1,2} revealed that the haptoglobin $\alpha$-chain is present in both body fluids in at least four variants. This result suggests that specific post-
translational modification processes occur in SF that could be playing an impor-
tant role in the inflammatory degradation process of the joint.

We therefore analyzed pannus tissue from RA patients and compared the obtained protein pattern with that from tissues derived from patients with osteoarthritis (OA) first by RNA microarray-analysis (Affymetrix) \cite{3,4}. Our com-
bined approach started with screening the human genome for protease genes. There are 590 proteases encoded by the human genome, 397 of which are found on the Affymetrix chips, represented by 687 unique probe sets. In addition, from the 159 protease inhibitors in the genome, 106 are presented on the chips by 164 unique probe sets. Interestingly, only approximately 330 protease probe sets and approximately 70 inhibitor probe sets yielded in so-called ‘present calls’.

A comparison of the RNA abundances between RA and OA showed that approxi-
mately 40 protease and 16 inhibitor gene products could be identified as differ-
entially expressed. One of them was Cathepsin B, which was found approximately twofold more expressed in the pannus (RA) than in the tissue (OA).

We compared the protein abundances of both tissues and found a total of 1077 unique protein spots. In the OA tissues, 263 spots were detected with increased expression levels (more than twofold). Among these proteins, we could identify several components of the extracellular matrix, such as collagen, fibronectin, and laminin. In contrast, the RA tissues showed reduced expression levels of 237 proteins, including several matrix-degrading enzymes such as matrix metalloproteinases (MMPs).

Interestingly, we found that the abundance of Cathepsin B was significantly higher in the RA tissues compared to the OA tissues. This finding supports the hypothesis that increased protease activity is a key factor in the pathogenesis of RA. Further, we observed an increased expression of several inflammatory cytokines, including TNF-\alpha, IL-1\beta, and IL-6, in the RA tissues.

We also observed a decrease in the expression of several anti-inflammatory proteins, such as transforming growth factor-beta (TGF-beta) and IL-10, in the RA tissues. These findings suggest that the imbalance in pro-inflammatory versus anti-inflammatory cytokines might be a driving force in the progression of RA.

The results of our study highlight the importance of protease activity in the pathogenesis of RA and suggest that targeting these enzymes might be a promising therapeutic strategy. Further research is needed to validate these findings and to develop effective therapeutic interventions.
S10 Mechanisms of cartilage matrix turnover: synergistic interactions of proinflammatory cytokines with oncostatin M in upregulating matrix metalloproteinases and ADAMTS metalloproteinases

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Cartilage is a highly organized tissue where the arrangement of collagen and proteoglycan and minor components is carefully controlled. The chondrocytes maintain a precise balance between anabolic and catabolic processes that maintains this extracellular matrix. Proteoglycan removal is rapid and reversible while collagen removal is slower but, once removed, is difficult to replace. Our main research focus is to discover the mechanism of collagen turnover and we study the members of the matrix metalloproteinase (MMP) family that specifically cleave type II collagen to give characteristic one-quarter and three-quarter fragments; MMP-1, MMP-8, MMP-13 and also MMP-2 and MMP-14 cleave in this way. Oncostatin M (OSM) is a member of the IL-6 family that synergises with IL-1 to induce cartilage proteoglycan and collagen degradation in a cartilage explant culture system [1]. A significant finding is the synergistic induction of the collagenase, MMP-1, which occurs via interplay between the JAK/STAT, AP-1 and MAPK pathways. Other collagenases such as MMP-8 and MMP-13 are also upregulated along with MMP-14 and MMP-3. This latter enzyme can activate the collagenases, and an important feature of OSM may be its ability to promote the activation of enzymes that initiate activation cascades that lead to the production of active collagenases. OSM can also exacerbate the effects of other important proinflammatory mediators such as tumour necrosis factor alpha (TNF-α) and IL-17.

Molecular and cellular studies aim to discover the mechanism of action that leads to synergy. Affymetrix microarrays show that a specific cohort of genes are upregulated by these cytokine mixtures including MMPs, ADAMs (A disintegrin and metalloproteinases), activators, cell surface proteins and cytokines. Two-dimensional gel electrophoresis and proteomic analysis confirm that many of the corresponding proteins are made by chondrocytes after stimulation. Purification of specific proteins from conditioned culture medium has been undertaken to try and determine the enzymes responsible for collagen turnover.

In order to assess the effects of these cytokine combinations in vivo, we have injected OSM in combination with either IL-1 or TNF-α intra-articularly into murine knee joints using recombinant adenosine. Engineered adenosines were administered for only 7 days, after which time joints were fixed, decalcified and sectioned. Histological analyses indicated marked synovial hyperplasia and inflammatory cell infiltration for IL-1, TNF-α and OSM treated joints but not in controls (joints treated with an ‘empty’ adenovirus). The inflammation was more pronounced for both OSM + IL-1 and OSM + TNF-α combinations with evidence of extensive cartilage and bone destruction. Significant loss of both proteoglycan and collagen was also seen for these combinations, and an increased expression of MMPs with decreased tissue inhibitors of metalloproteinases was found in both articular cartilage and synovium. The effects of these combinations were significantly greater than those seen with any of the cytokines alone. Cytokine combinations also upregulated RANKL/RANK and increased the number of TRAP-positive cells showing an increase in osteoclast formation and bone damage. Taken together, these data confirm that, in vivo, OSM can significantly exacerbate the effects of both IL-1 and TNF-α resulting in inflammation and tissue destruction characteristic of that seen in rheumatoid arthritis.

Reference

S11 Collagenases and aggrecanases: understanding the role of non-catalytic domains in cartilage matrix breakdown

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Degradation of cartilage matrix, which mainly consists of collagen fibrils and aggrecan, seriously impairs the function of joints. The primary cause of this process is elevated proteolytic enzymes. Collagen fibrils are degraded by a group of matrix metalloproteinases (MMPs) including collagenases (MMP-1, MMP-8 and MMP-13), gelatinase A (MMP-2) and MT1-MMP (MMP-14). Aggrecan is degraded by MMPs and ‘aggrecanases’ belonging to the ADAMTS family. Inhibitors of these metalloproteinases are considered as potential therapeutic agents to protect cartilage degradation, and many active site-directed inhibitors with a zinc-chelating moiety have been developed. Unfortunately, these compounds have serious side effects possibly due to lack of selectivity [1]. In the hope of developing new types of inhibitors we have been investigating the mechanisms of action of collagenases and aggrecanases. Collagenases are unique as they can degrade triple helical collagen into three-quarter and one-quarter fragments, a crucial step for collagenolysis in the tissue. Typical collagenases consist of a catalytic domain and a hemepxin domain that are connected by a linker peptide. Both domains are essential for collagenolysis. The three-dimensional structure of MT1-MMP (MMP-14), however, indicated that the active site of the enzyme is too narrow to accommodate triple-helical collagen. We have recently shown that collagenase locally unwinds triple helical collagen before it hydrolyses the peptide bonds [2]. Based on a series of mutagenesis mutageneses we predict that the collagen binding site is created by a catalytic and the hemepxin domain. The collagen binding groove is partially blocked by the prodomain in the zymogen of MMP-1 (proMMP-1), explaining its inability to bind to collagen unless it is activated. Overall pro-MMP-1 has a ‘closed’ configuration in contrast to the ‘open’ configuration of the active MMP-1.

The exact mechanism of how collagenase unwinds collagen is under investigation. Another key collagenase is MT1-MMP. It is highly expressed in rheumatoid synovial lining cells invading into the cartilage. Overexpression of recombinant MT1-MMP in COS7 cells in vitro degrades reconstituted type I collagen filaments. This reaction requires dimerisation of the enzyme on the cell surface through the hemepxin domain. When dimerisation of MT1-MMP is prevented by overexpression of the membrane-anchored MT1-MMP hemepxin domain, the collagenolytic activity was blocked, but not its general photolytic activity.

Among 19 ADAMTSs in humans, six have been shown to have aggrecanase activity. These are disintegrin, one or more thrombospondin, one or more hemepxin and one or more hemepxin domains. The aggrecanase activity of ADAMTS-4 expressed by a ‘closed’ configuration of the active MMP-1. Further deletion of the cysteine-rich and thrombospondin domains greatly reduces both activities [3].

These studies suggest that activities of collagenases and aggrecanases will be attenuated by inhibitors or antibodies that interact directly with their non-catalytic ancillary domains (exosite/allosteric inhibitors). Such molecules will be attractive for therapy as they will be highly selective because they are based on the unique mechanism of each proteinase.

References

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S12 The effects of inflammatory arthritis on bone remodeling

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Rheumatoid arthritis (RA) represents an excellent model for gaining insights into the adverse effects of inflammatory arthritis on skeletal remodeling. Bone erosions at the margins of diarthrodial joints represent the radiographic hallmark of RA. Histopathologic examination of the bone–pannus interface in patients with RA reveals the presence of a heterogeneous population of cells lining the bone surface, including multinucleated cells expressing the full phenotypic repertoire of osteoclasts, the cells that mediate bone resorption in physiologic remodeling. Further evidence implicating osteoclasts in the pathogenesis of marginal joint erosions is derived from animal models of inflammatory arthritis in which animals lacking the capacity to form osteoclasts fail to develop joint erosions. Studies have shown that the RA synovial tissue contains abundant osteoclast precursors and that the RA synovium is a rich source of factors with potent osteoclast differentiation and activation activity. Particular attention has focused on receptor activator of NFκB ligand (RANKL), a member of the tumor necrosis factor ligand family, because of the requirement of this factor for osteoclastogenesis. RANKL is expressed by synovial fibroblasts and activated T cells in RA synovial tissues and in sera of a proportion of RA patients. RANKL interacts with osteoprotegerin (the soluble receptor that inhibits RANKL activity) results in marked suppression of focal bone erosions. In addition, mice possessing the null mutation for RANKL are protected from focal bone destruction in the serum transfer model of inflammatory arthritis. An additional observation in patients with active RA is the absence of bone remodeling on the unaffected side of the joint. This finding suggests that the processes that regulate coupling of bone resorption and formation under physiologic conditions have been disrupted and that the enhanced focal bone

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resorption is not matched by a compensatory increase in bone formation. In addition to the disordered focal bone remodeling associated with the synovial lesion, patients with RA also exhibit evidence of generalized axial and appendicular bone loss at sites that are distant from inflamed joints. Assessment of biochemical markers of bone turnover indicates that there is a generalized increase in bone resorption, and that there is a correlation between disease activity and the rate of systemic bone resorption. It is likely that this generalized hemoedematous bone loss is mediated by synovial cytokines with osteoclastogenic activity that enter the circulation and act as ‘endocrine’ factors to adversely affect systemic bone remodeling. Recent studies indicate that agents, such as the bisphosphonates, that target osteoclast-mediated bone resorption have the capacity to reduce not only generalized bone osteoporosis but also may have efficacy in retarding the progression of focal joint erosions.

S13 Genetics and bone disease

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Bone diseases are a common cause of morbidity and mortality in developed countries, and genetic factors play an important role in the pathogenesis of these diseases. The most common form of bone disease is osteoporosis, which is characterized by reduced bone mineral density (BMD) and an increased risk of fracture. Environmental factors such as diet and exercise influence BMD but genetic factors play a predominant role, accounting for up to 85% of the variation in peak BMD. Several candidate genes have been identified that regulate BMD and susceptibility to fracture, including bone morphogenic protein 2, collagen type I alpha 1, the vitamin D receptor, the estrogen receptor and lipoprotein receptor related protein 5 (LRP5). Paget’s disease of the bone (PDB) is characterised by focal abnormalities of increased bone turnover. Mutations in several genes have been identified as causes of PDB and related syndromes including receptor activator of NF-κB (RANK), osteoprotegerin, sequestosome 1 and valosin containing protein. All of these genes play a role in the RANK signaling pathway, which is essential for osteoclast activation. Rare bone diseases such as osteopetrosis and hereditary osteosclerosis are also caused by mutations in genes that affect bone cell function. Osteopetrosis is characterized by increased BMD, and failure of osteoclastic bone resorption due to mutations in genes that encode proteins that are essential for osteoclast activity like the chloride pump and proton pump, or mutations in genes like cathepsin K, which breakdown bone matrix. Although the bones are dense, fractures are common in osteopetrosis because of reduced bone quality. Osteosclerosis occurs because of mutations in genes that increase osteoblast activity, including SOST, transforming growth factor beta and LRP5. Osteosclerotic patients also have increased BMD but fractures are rare, because bone quality is normal. From a clinical standpoint, advances in knowledge about the genetic basis of bone disease offers the prospect of developing new markers for assessing fracture risk and the identification of new molecular targets that will form the basis for the design of new treatments.

S14 Defining a role for fibroblasts in the persistence of chronic inflammatory joint disease

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One of the most important but as yet unanswered questions in inflammation research is not why chronic inflammation occurs but why it does not resolve. Current models of inflammation stress the role of antigen-specific lymphocyte responses and attempt to address the causative agent. However, recent studies have begun to challenge the primacy of the lymphocyte and have begun to focus on an extended immune system in which stromal cells, such as macrophages and fibroblasts, play a role in the persistence of the inflammatory lesion.

In this lecture I will illustrate how fibroblasts play an important role in regulating the switch from acute to chronic persistent inflammation associated with the pathology of diseases such as rheumatoid arthritis [1]. In chronic inflammation the normal physiological process of the death and emigration of unwanted inflammatory effector cells becomes disordered leading to accumulation of leucocytes [2–4] with effector properties that resemble those of effector T cells in lymphoid tissue [5]. I will describe how fibroblasts from the rheumatoid joint provide survival and retention signals for leucocytes leading to their inappropriate and persistent accumulation within inflamed tissue [6]. Our work suggests that targeting the stromal microenvironment is likely to be an important strategy for future anti-inflammatory therapies.

References


Buckley: Why do leucocytes accumulate within chronically inflamed joints? Rheumatology Research Group, Division of Immunity and Infection, MRC Centre of Experimental Rheumatology, University Hospital, Muenster, Germany; 1Department of Experimental Rheumatology, University Hospital Magdeburg, Germany; 2Center of Experimental Rheumatology, Department of Rheumatology, University Hospital, Zurich, Switzerland; 3Department of Traumatology, Hand and Reconstructive Surgery, University Hospital, Muenster, Germany


In this lecture I will illustrate how fibroblasts play an important role in regulating the switch from acute resolving to chronic persistent inflammation. Fibroblasts, effector cells becomes disordered leading to accumulation of leucocytes [2–4]. Recent studies have begun to challenge the primacy of the lymphocyte and have begun to focus on an extended immune system in which stromal cells, such as macrophages and fibroblasts, play a role in the persistence of the inflammatory lesion. Fibroblasts, play a role in the persistence of the inflammatory lesion.
S16 Innate immunity and the anti-viral state of rheumatoid synovium
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Rheumatoid arthritis (RA) is an immune-mediated disease with synovial inflammation and invasion of the extracellular matrix. While adaptive immunity plays a key role in the pathogenesis of RA, the contribution of innate immune responses has been increasingly appreciated in recent years. Toll-like receptors (TLRs) and cytokines in the rheumatoid synovium can activate signal transduction pathways that induce proinflammatory genes and perpetuate synoviocytes. Understanding these signaling mechanisms helps us understand the pathogenesis of disease and identify novel therapeutic targets. Among the signaling pathways that are potentially involved in inflammation, the IKK-related kinase, inducible IKK (IKKγ or IKKε), appears to play a key role in innate immune responses in the joint and modulates synovial inflammatory responses. This kinase, along with a second IKK-related kinase TANK binding kinase 1 (TBK1), was originally identified as a NF-κB activating enzyme that phosphorylates IkB. It is now clear, however, that this represents only one of several substrates for this family. For instance, IKKγ also phosphorylates interferon regulatory factor (IRF) and coordinates the activation of IRF and NF-κB after TLR ligation. IKKγ may also link the NF-κB and CCAAT enhancer binding protein (C/EBP) pathways in lipopolysaccharide-stimulated cells. The novel roles for IKKγ suggests that it contributes to the signaling pathways involved in synovial inflammation. Moreover, IKKε appears to play a key role in the establishment of an ‘anti-viral state’ through the activation of IRF3 and c-Jun with subsequent production of interferon beta (IFN-β) and other genes involved in host defense. We previously demonstrated that IKKε is constitutively expressed in RA synovial tissue and fibroblast-like synoviocytes (FLS), and that the gene can be induced by cytokine stimulation. More recent studies now show that functional activity of IKKε in cultured synoviocytes is rapidly increased by exposure to proinflammatory cytokines and TLR agonists. We have also shown that IRF3 is activated in RA synovium, which represents an early step in the IKK-mediated expression of anti-viral genes like IFN-β. Additional preliminary data with human FLS suggest that the IKKγ pathway can activate other signaling cascades, such as c-Jun, which play a role in assembly of the interferon enhancerosome to increase IFN-β expression. Using FLS from IKKγ knockout mice, we have shown that IKKγ can act as a key link between TLR/cytokine receptor ligation and expression of cytokines and matrix metalloproteinases. IKKγ might serve in an alternative signaling pathway for activation of innate immunity in RA and establishing an anti-viral state in the synovium, especially through the activation of IRF3-driven and c-Jun-driven genes.

S17 Signal transduction in T lymphocytes
D Cantrell
Division of Cell Biology & Immunology, School of Life Sciences, University of Dundee, Dundee, UK

S18 Title to be confirmed
J Kalden
University Erlangen-Nuremberg, Erlangen, Germany

Poster abstracts

P1 Differential effects of T-cell specific PKC-theta inhibition or selective intra-articular NF-κB inhibition on synovial inflammation in rat adjuvant arthritis
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Objective NF-κB is a key regulator of synovial inflammation. In the initiation phase of rheumatoid arthritis (RA) dendritic cells and T cells are likely to be important, whereas in established arthritis other cells play a key role as well. We investigated the relative effect of upstream NF-κB inhibition specifically in T cells versus non-cell type specific NF-κB inhibition in different stages of rat adjuvant arthritis (AA), using either the T-cell specific PKC-theta inhibitory factor (PIF) peptides or non-cell type specific IKK-beta blocking NEMO binding domain (NBD) peptides. The effects of the NBD peptide on human RA synovial tissue in culture were also evaluated. Methods AA was induced in Lewis rats by intradermal injection of heat-killed mycobacteria. Rats develop clinical signs of arthritis 10–12 days after immunization. PIF or NBD peptides (150 μg) were administered either intraperitoneally or intra-articularly into the ankle joint at different time-points. The course and severity of arthritis was monitored using water-displacement plethysmometry. On day 21 rats were sacrificed and tissue specimens were collected for routine histology and X-rays of the ankle joints. Human RA synovial tissue was collected by arthroscopy and cultured ex vivo and NBD (100 μM). Tumor necrosis factor alpha induced IL-6 production was measured in the supernatant after 7 days by ELISA.

Results Intra-articular injection of the T-cell specific PKC-theta inhibitor PIF on days 10 and 12 did not result in amelioration of arthritis nor reduced bone erosion. However, intraperitoneal injection of PIF on days –1, 1, and 3 resulted in reduced T-cell proliferation on day 5 in response to TCR triggering (50%; P = 0.03) or cognate antigen (PPD) (30%; P = 0.05). Furthermore, this resulted in a slightly reduced severity of arthritis (area under the curve 18.47 versus 22.96; P = not significant) and radiological damage (erosion score 4 versus 6; P = not significant). Non-cell type specific NF-κB blockade by the NBD peptide resulted, however, in significantly reduced severity of arthritis (P < 0.0001) and radiological damage (P = 0.04) when injected intra-articularly on days 10 and 12. In addition, proinflammatory cytokine expression was significantly lower in synovial tissue of NBD-treated rats. Incubation of human RA synovial tissue with NBD peptides resulted in 33% inhibition of tumor necrosis factor alpha induced IL-6 production in the supernatant (P = 0.01).

Conclusions Specific NF-κB blockade using a small molecular inhibitor of IKK beta has anti-inflammatory effects in AA and human RA synovial tissue. Inhibition of PKC-theta has clear effects on T-cell proliferation when administered around the induction of arthritis, but very limited effects on the clinical course of arthritis, suggesting that NF-κB activity in other cell types contributes significantly to the inflammatory response. These results indicate that IKK-beta-targeted NF-κB blockade is superior to T-cell specific PKC-theta inhibition in established arthritis.

Acknowledgement This study was supported by a EULAR Young Investigator Award to SWT.

P2 Positive cytoplasmic indirect immunofluorescence on HEp2 cells of unknown pattern: what to report to rheumatologists
Z Rotar, B Božič, B Rozman, T Kveder
University Medical Centre, Department of Rheumatology, Ljubljana, Slovenia
The aim of our study was to evaluate antibodies against ‘specific liver’ antigens in selected sera from patients with positive ‘AMA like’ and unidentified (UD) Hep2 cytoplasmic immunofluorescence (cIF, IF).

Sera of 75 inpatients and outpatients from the Department of Rheumatology, Ljubljana met the inclusion criteria: 36 with AMA-like and 39 with UD pattern. All sera were also negative for anti-M2 and/or antibodies against pyruvat dehydrogenase complex as well as negative to other defined cIF patterns according to European Consensus Finding Study: lysosomal-like, Golgi-like, vimentin-like and actin-like. The majority of patients fulfilled the criteria for connective tissue diseases and rheumatoid arthritis.

Antibodies against intracellular antigens were screened by IIF on HEp2 cells (Immunoncepts, Sacramento, CA, USA). Antibodies against LKM1, SLA, LC1 and Sp100 were performed by line immunoassay (Imtecs, Berlin, Germany). There was no difference in AMA-like and UD cIF concerning antibodies against ‘specific liver’ antigens. A surprisingly high prevalence of positive anti-LKM1 was found in sera regardless of the IF pattern (Table 1).

<p>| Antibodies against ‘liver specific’ antigens in sera with AMA-like and UD cIF |
|-----------------------------|-----------------|-----------------|</p>
<table>
<thead>
<tr>
<th>n</th>
<th>Sp100</th>
<th>LKM1</th>
<th>SLA</th>
<th>LC1</th>
</tr>
</thead>
<tbody>
<tr>
<td>AMA-like</td>
<td>42</td>
<td>4</td>
<td>19 (45%)</td>
<td>0</td>
</tr>
<tr>
<td>Unidentified</td>
<td>33</td>
<td>4</td>
<td>14 (42%)</td>
<td>2</td>
</tr>
<tr>
<td>All</td>
<td>75</td>
<td>8 (11%)</td>
<td>33 (44%)</td>
<td>2 (3%)</td>
</tr>
</tbody>
</table>

Anti-LKM1 has been considered as one of the markers for autoimmune hepatitis type II characterised by fulminant onset and high inflammatory activity according to Imtecs data. None of our patients with positive anti-LKM1 had any serious
hepatic involvement, therefore they had not been histopathologically evaluated. Only few of them exhibited minor deviations in liver enzymes (less than 1 x upper normal limit). There was slightly lower prevalence of connective tissue disease patients found among UD ctp IIF (Table 2).

Table 2

<table>
<thead>
<tr>
<th>Patients</th>
<th>n (%)</th>
<th>Sp100</th>
<th>LKM1</th>
<th>SLA</th>
<th>LC1</th>
</tr>
</thead>
<tbody>
<tr>
<td>AMA (n = 42)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Connective tissue diseases</td>
<td>25/42(60%)</td>
<td>3</td>
<td>8</td>
<td>0</td>
<td>1</td>
</tr>
<tr>
<td>Rheumatoid arthritis</td>
<td>6/42 (14%)</td>
<td>0</td>
<td>5</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Other</td>
<td>11/42 (26%)</td>
<td>1</td>
<td>6</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Unidentified (n = 33)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Connective tissue diseases</td>
<td>15/33 (46%)</td>
<td>3</td>
<td>6</td>
<td>2</td>
<td>0</td>
</tr>
<tr>
<td>Rheumatoid arthritis</td>
<td>6/33 (18%)</td>
<td>0</td>
<td>2</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>Other</td>
<td>12/33 (36%)</td>
<td>1</td>
<td>6</td>
<td>0</td>
<td>0</td>
</tr>
</tbody>
</table>

An UD ctp IIF pattern is a frequent laboratory finding but it seems not to be of much help to rheumatologists. A search for antibodies against ‘specific liver’ antigens seems not to be justified for delineation of hepatic involvement in patients with rheumatic diseases. According to the literature in patients with autoimmune hepatitis the meaning of these antibodies is different.

P3 Synoval hypoxia inducible factor-1α expression is inversely related to tissue oxygen levels in vivo in inflammatory arthritis

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Background Tissue hypoxia in inflammation induces the upregulation of a gene program associated with angiogenesis, glycolysis and adaptation to pH via the hypoxia-inducible transcription factors (HiFs). In this study we investigate the relationship between synovial tissue oxygen levels in inflammatory arthritis and tissue expression of HIF-1α and vascular endothelial growth factor (VEGF).

Methods Novel silver microelectrode technology was used to measure synovial tissue oxygen levels under direct vision during arthroscopy in six patients with inflammatory arthritis of the knee. A sterile silver needle electrode comprising a tetfon-insulated silver wire was embedded in a 19 G hypodermic needle of 10 cm length and introduced to the intra-articular space via a medial suprapatellar approach such that the electrode tip could be directly visualised by the arthro-scope introduced from a standard lateral infrapatellar approach. The voltage applied was adjusted to give a diffusion-limited current for the reduction of oxygen. Synovial biopsies were taken under direct vision from exactly the point at which tissue oxygen levels were measured and snap-frozen immediately. HIF-1α, HIF-2α and VEGF were detected by immunohistochemistry in fixed synovial biopsy sections and the immunopositive area fraction was determined by quantitative digital image analysis.

Results The mean and standard deviation for oxygen tension in the synovial tissue of the joints sampled was 15.4 ± 9.6 mmHg, range 24.4 ± 44 mmHg. The mean and standard deviation for immunopositive area fraction for HIF-1α was 0.64 ± 0.39% and for HIF-2α was 4.9 ± 6.7%. HIF-1α and HIF-2α staining were detected predominantly in the synovial lining layer. There was a significant, inverse relationship between synovial tissue oxygen measurement in vivo and tissue expression of HIF-1α (Pearson r = -0.86, P = 0.03) and similarly between synovial tissue oxygen and tissue expression of VEGF (Pearson r = -0.89, P = 0.02). There was a positive, highly significant correlation between synovial expression of HIF-1α and VEGF (Pearson r = 0.97, P = 0.0005).

Conclusions In this study we directly demonstrate that intra-articular pO2 is markedly reduced in inflammatory arthritis. Furthermore, in the same patients, synovial tissue oxygen tensions are inversely proportional to HIF-1α and VEGF expression, suggesting that this environment contributes to the perpetuation of inflammation and associated tissue destruction.

P4 Prophylactic administration of abatacept (CTLA4-Ig; BMS-188667) prevents disease induction and bone destruction in a rat model of collagen-induced arthritis

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Background and objectives Rheumatoid arthritis is an autoinflammatory disease in which activated T cells play an important role orchestrating the autoimmune reaction giving rise to the immune cascade required for joint inflammation and bone destruction. The CD28/B7 costimulatory pathway is critical for full T-cell activation, and modulating this pathway has been shown to provide significant improvement in the signs and symptoms of rheumatoid arthritis in a phase II trial. Here, we examine the effect abatacept administration has on disease induction, anti-collagen antibody production, and bone destruction in a rat model of collagen-induced arthritis.

Methods Female DA rats were immunized subcutaneously on day 0 with 300 µg bovine type II collagen in incomplete Freund’s adjuvant at the base of the tail. Immunized rats were administered either 1 mg/kg abatacept or a control human IgG IP on days –1, 0, 2, 4, 6, 8 and 10. Disease progression was monitored by measuring the paw volume in milliliters with a plethysmometer. Both hind paws were measured and the change in volume from baseline measurements (day 0) was recorded. At the conclusion of study (day 27), synovia were collected from each animal for measurement of collagen-specific antibodies by ELISA as well as serum cytokine measurements. Legs from the rats were removed and placed in formalin and prepared for histological analysis as well as analysis of bone morphology by micro-CT.

Results By day 16 of the study, significant paw swelling was observed in the IgG-treated control animals and continued to increase throughout the study until reaching a plateau (~ 3–3.5 ml) on day 21. Administration of abatacept abrogated paw swelling throughout the course of the study. The IgG-treated rats reached 100% incidence while no incidence was observed in the abatacept-treated group. Serum anti-collagen antibody levels correlated well with the paw swelling data where abatacept administration resulted in 90% inhibition of collagen-specific antibodies. We also found that abatacept decreased the expression of many of the circulating cytokines and chemokines that were upregulated in diseased animals. The micro-CT data revealed that abatacept treatment protects the bone from destruction as the knees and ankles of these rats appear to be normal. Conclusions Abatacept, a selective co-stimulation modulator, significantly inhibited the onset and progression of disease in a rat collagen-induced arthritis model. In these studies, paw swelling, collagen-specific antibodies and bone destruction were all inhibited by the treatment.

P5 The transcription T-bet is required for optimal proinflammatory trafficking of CD4+ T cells

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Background The transcription factor T-bet is a critical regulator of Th1 effector function. Animals deficient in T-bet are protected from a variety of inflammatory diseases, including systemic lupus erythematosus and inflammatory arthritis. An essential function of Th1 cells is the ability to traffic appropriately to sites of inflammation, which is largely dependent on the expression of specific selectin ligands and chemokine receptors. We therefore hypothesised that T-bet would modulate lymphocyte trafficking in vitro and in vivo by direct regulation of both selectin binding and chemokine function.

Methods Balb/c mice deficient in, or transgenic for, T-bet had been generated previously. T-bet+/− × DO11.10 TCR and T-bet+× IFN-γ−/− mice were generated by backcrossing for >10 generations. CD4+ T cells were generated from primary lymph nodes from all these mice by positive selection and stimulation with appropriate antigen. Functional analysis used the following four methods: adoptive transfer into WT Balb/c mice, which were then injected with OVA, cells were harvested from the spleen, lymph nodes and peritoneum; selectin binding, interactions with immobilised P-selectin and E-selectin under conditions of laminar flow were examined in a parallel plate flow chamber; expression of selectin ligands, using flow cytometry, real-time PCR and 32P incorporation; and chemokine receptor expression and function, using flow cytometry, real-time PCR, transwell chemotaxis and endothelial binding under flow conditions.
Results Selective migration of T-bet–/– CD4+ T cells in a Th1-dependent model of periarticular inflammation was completely abrogated. Further investigation revealed that this effect was due to a 50% reduction in binding to P-selectin but not E-selectin. The reduction in vivo flow conditions abrogated the defect in vitro flow conditions. A similar pattern was found in a transwell chemotaxis and binding to endothelial cells. RETROViral transfer impaired tyrosine sulfation of PSGL-1. In addition, mRNA and surface expression of E-Selectin and CCR5 binding are unimpaired, this reveals a level of control on trafficking of TH1 lymphocytes not recognised by previous paradigms.

Conclusions These data establish that T-bet imparts a specific migratory program onto developing CD4+ cells via control of PSGL-1 sulfation (and thus P-selectin binding) and CXCR3 expression and function. Furthermore, as E-selectin and CCR5 binding are unimpaired, this reveals a level of control on trafficking of TH1 lymphocytes not recognised by previous paradigms.

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P6

Specificity of CD4 T-cell responses to aggrecan in BALB/c and DR1 transgenic mice

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Background It has been suggested that rheumatoid arthritis (RA) is initiated or perpetuated by CD4 T cells activated by presentation of joint antigens by susceptible MHC class II molecules including HLA-DR4 and DR1. A number of candidate antigens have been investigated including cartilage-derived type II collagen and aggrecan. Immunisation of susceptible strains of mice with aggrecan, including BALB/c (H-2d), induces autoimmune arthritis, providing an animal model of human RA [1]. Immunisation with peptides predicted to bind to HLA-DR4 and DR1 also elicits T-cell responses in HLA-DR4 transgenic mice [2]. The autoimmune T-cell response focuses on only a few epitopes within restricted regions of aggrecan such as the Gd globular domain, for reasons that are poorly understood. One explanation is a failure of self-tolerance due to poor presentation of these aggrecan epitopes in the thymus, and presentation of the same epitopes in joints following release and processing of the normally sequestered aggrecan induced by early inflammatory events. T-cell responses have also been observed in RA patients mapping epitopes within the Gd domain.

Aim

To characterise aggrecan-specific T-cell hybridomas from BALB/c (H-2d) and DR1 to investigate the mechanisms of antigen presentation of arthritogenic CD4 T-cell epitopes of aggrecan.

Methods

Aggrecan-specific T-cell hybridomas were generated from spleen cells of BALB/c (H-2d) and DRB1*10101-transgenic mouse (DR1-tg) mice immunised with deglycosylated bovine aggrecan. Synthetic peptides of three known arthritogenic H-2d-restricted epitopes (amino acids 58–70, 84–93 and 169–189) and three DR1-restricted epitopes (amino acids 148–165, 201–213 and 292–311) from the Gd domain of bovine aggrecan were used to define the specificity of T-cell hybridomas. Cultured bone marrow macrophages were treated with deglycosylated bovine aggrecan or synthetic peptides and used as antigen-presenting cells. T-cell hybridoma responses were measured by proliferation of CTL-2 indicator cells to T-cell hybridoma supernatants in the presence of titrated thymidine and expressed as counts per minute.

Results The specificity of most aggrecan-specific T-cell hybridomas mapped to the aggrecan Gd domain using synthetic peptides representing known H-2d-restricted or DR1-restricted CD4 T-cell epitopes. However, most cloned (and reconstituted) T-cell hybridomas recognised two of the H-2d-restricted epitopes (84–103 and 169–189) as well as two of the DR1-restricted epitopes (148–165 and 292–311). The same synthetic peptides were not recognised by H-2d-restricted and DR1-restricted T-cell hybridomas. Unreliable specificities and were not mitogenic for spleen cells from BALB/c or DR1-tg mice. None of the T-cell hybridomas recognised aggrecan epitopes 68–82 or 201–213.

Conclusion We are investigating this unexpected pattern of cross-reactivity between a number of known arthritogenic epitopes of aggrecan using lymph node T-cell responses of peptide-immunised BALB/c and DR1-tg mice. In addition we are investigating the mechanisms of antigen presentation of these epitopes, which may shed light on why this particular region of aggrecan is antigenic for auto reactive T cells.

References


P7

The role of hypoxia in rheumatoid tendon disease

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Background Tendon disease is often the first presentation of rheumatoid arthritis (RA). Tenosynovial proliferation results in scarring and adhesion formation. Synovial invasion into tendons occurs in 50% of cases and is associated with multiple tendon ruptures and a poorer prognosis. Recent work on diseased joints suggests that hypoxia may play a key role in synovial invasion. We hypothesised that hypoxia promotes and maintains the inflammatory response in RA tenosynovium via neovascularisation.

Objectives To measure oxygen tension (pO2) within the synovium of rheumatoid tendons and joints in vivo. To study markers of hypoxia and neovascularisation in invasive and non-invasive tendon synovium by immunohistochemistry. To investigate the effects of hypoxia on in vitro cultures of invasive and non-invasive tenosynovium.

Methods Patients undergoing elective hand surgery for RA were recruited into the study. In vivo oxygen tension measurements were taken intra-operatively using an established microelectrode technique. Readings were taken from tendon and joint synovium. Diseased tissue was harvested from areas of oxygen sampling for immunohistochemical analysis of CD31 expression.

Results Tissue was also harvested from invasive and non-invasive tenosynovium. Joint tissue was used as a control. Serial sections of tissue were stained for the pro-angiogenic factor vascular endothelial growth factor (VEGF) and the hypoxia-regulated transcription factor hypoxia inducible factor (HIF)-2α.

Separate tissue from these three areas of interest was enzymatically digested and cultured in hypoxia (1% oxygen) and normoxic (21% oxygen) conditions. Supernatants were harvested at 24 hours and analysed for expression of key inflammatory cytokines by ELISA.

Results We observed profound hypoxia in the synovium of RA tendons and joints in vivo despite immunohistochemical evidence of markedly increased vascularity, measured as expression of CD31. Immunohistochemical analysis revealed twofold greater VEGF expression in tenosynovium (P < 0.05), compared with joint synovium from the same patient. Levels of HIF-2α were found to be similar in tendon and joint synovium.

One of the consequences of synovial hypoxia could be the modulation of inflammation by angiogenic cytokines. We found that hypoxia upregulated in vitro expression of pro-angiogenic cytokine VEGF in both joint and tenosynovial cultures (P < 0.05) by an average of 128%, and in parallel increased levels of the pro-inflammatory cytokine tumour necrosis factor alpha by an average of 105%. In contrast, hypoxia downregulated expression of monocyte chemoattractant protein-1 (P < 0.05) by an average of 44%.

Conclusions Hypoxia is a feature of rheumatoid tenosynovitis. Key cytokines are regulated by hypoxia in this disease process. HIF-2α may represent the link between hypoxia and VEGF-driven angiogenesis in rheumatoid tendon disease.

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P8

Short-fibre modification facilitates adenovirus-mediated gene delivery in rheumatoid arthritis synoviocytes and synovium: role of RGD and non-RGD binding integrins

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Objective Adenovirus (Ad5) receptors other than Cocksackie-ad receptor have not been well explored in rheumatoid arthritis (RA) human fibroblast-like synoviocytes (FLS). Defining these receptors may enable development of improved Ad5 vectors to specific synovial targets. As Cocksackie-ad receptor is absent in RA FLS, we investigated the efficacy and receptor usage of fibre-modified Ad5 vectors for gene delivery in vitro and ex vivo.

Methods Short fibre modified vectors with seven fibre repeats (Ad5GFP-R7-knob, Ad5GFP-R7-RGD) were compared with wild-type (WT) 22 repeats...
P9

Laminin type 1 augments the transforming growth factor beta-induced expression of matrix metalloproteinase 3 in synovial fibroblasts
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Background and objective Elevated expression of laminin (LN) and integrins in the synovial membrane of rheumatoid arthritis (RA) versus osteoarthritis patients has been reported but metabolic effects of attachment of synovial fibroblasts (SF) to LN are not well studied. We therefore investigated gene expression patterns in SF upon attachment to LN1 (EHS laminin) in comparison with LN10.

Methods Expression of IL-1α, IL-1β, IL-6, IL-8, IL-16, IL-18 as well as matrix metalloproteinase (MMP)-1 and MMP-3 were investigated in RA SF (n = 6) or osteoarthritis SF (n = 7) in primary or early passage cultures. Fibroblasts were seeded onto LN1-coated vessels (BD BioCoAT®) for 24–72 hours and cells attached to cell culture vessels served as controls in all experiments. In addition, cells were activated with cytokines and growth factors such as transforming growth factor beta (TGF-β). After activation, transcript amounts of individual genes were enumerated by quantitative RT-PCR. A recombinant cytokine standard and GAPDH RT-PCR served as controls in each sample. Expression of the α1, β1 and γ1 chains of LN1 laminin by SF was investigated by quantitative RT-PCR and immunochemistry. The secretion of MMPs was enumerated by ELISA in SF supernatants.

Results Growth of SF on LN1-coated surfaces without additional stimuli induced a significant IL-8 mRNA response (3.1-fold, ± 1.24, P ≤ 0.001) and lower responses for IL-1α, IL-1β, IL-6, IL-8, IL-16 and IL-18. MMP-1 mRNA was upregulated 2.3-fold (± 0.79, P ≤ 0.001), and MMP-3 mRNA only 1.5-fold. Upon incubation of SF on LN10, cytokine and MMP expressions were not changed. Addition of TGF-β (10 ng/ml, 24 hours) to SF attached to tissue culture vessels showed a different induction profile. Here IL-6, IL-1α, IL-1β, IL-8, IL-16 and MMP-1 mRNA were induced to some degree, IL-18 mRNA was reduced whereas MMP-3 mRNA was induced (3.15-fold, ± 0.7, P ≤ 0.04), when compared with controls. Next combinations of activation by TGF-β and laminin signaling were investigated. For cytokine expressions no additive effects of combining these signals were seen and MMP-1 mRNA was induced to some extent (threefold, ± 1.76). In contrast, MMP-3 mRNA was induced more that 10-fold (12.8 ± 0.7, P ≤ 0.025) and MMP-3 secretion was elevated almost 20-fold (19.67 ± 6.9, P ≤ 0.006). In SF, mRNA encoding α1, β1 and γ1 laminin — which encode the proteins for LN1 — was determined by quantitative RT-PCR and transcript amounts encoding the α1 and β1 chains of LN1 were higher in mRNA encoding the LN1 γ1 chain. Using an anti-EHS serum, LN1 was detected on SF by immunochemistry. However, using monoclonal antibodies to laminin α1 or γ1 proteins, staining signals were very weak.

Conclusions Attachment to LN1-laminin in the presence of TGF-β induces elevated MMP-3 expression in SF. However, an autocrine stimulation of MMP-3 expression by SF via TGF-β and LN1 seems rather unlikely, as LN1 is not expressed in high amounts in the adult synovial membrane. Still, activation of SF by LN1 may serve as a model for activation of fibroblasts by extracellular matrix compounds in the presence of growth factors or cytokines, and both pathways contribute to the aggressive invasive growth of SF in the course of RA.
P12  
Close association between valvular heart disease and central nervous system manifestations in antiphospholipid syndrome  
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Objectives Heart valve lesions and central nervous system (CNS) involvement are among the most common manifestations of antiphospholipid syndrome (APS). We evaluated possible inter-relationships between these manifestations in a large group of APS patients.  
Methods Two hundred and eighty-four APS patients were retrospectively evaluated, 159 of whom had primary APS (PAPS). Cardiac–CNS associations were determined for the entire study population, and for subgroups of patients with PAPS or APS secondary to systemic lupus erythematosus (SLE).  
Results Significant associations were found between cardiac valvular disease and migraine (P < 0.01). In subgroups with APS secondary to either SLE or PAPS, significant associations were detected between migraine and psychosis/depression.  
Conclusions Our study points to potentially different biological behaviors in PAPS versus APS secondary to SLE. According to our results, the presence of cardiac valve pathology may be a risk factor for several CNS involvements in PAPS.  

P13  
Elevated titers of anti-ribosomal-P antibodies in systemic lupus erythematosus  
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Objective Ribosomal P is located in the cytoplasm. The detection of antibodies is to the 60 kDa fraction. Anti-ribosomal-P antibodies are highly specific for systemic lupus erythematosus (SLE), and are detected at a 15–20% frequency according to the literature. Elevated anti-ribosomal P titers correlate with disease activity and are specifically associated with neuropsychiatric disease such as psychosis/depression, and coexist with anti-dsDNA antibodies. The aim of our study was to evaluate the frequency of anti-ribosomal P antibody titers and the correlation with manifestations in SLE patients.  
Methods Sera samples from 174 individuals were evaluated for titers of anti-ribosomal P antibodies: 77 samples from SLE patients, 22 patients with antiphospholipid syndrome (APS), 20 patients with inflammatory rheumatic disease, 12 patients with infections, and 43 healthy controls. Anti-ribosomal P antibody titers were tested by ELISA. Manifestations of SLE at the time of serum sampling were determined by the SLEDAI score.  
Results Six SLE patients (11%) harbored elevated anti-ribosomal P antibody titers. Five SLE patients were females, mean age 44.3 years (range, 18–73 years old), and the mean SLEDAI mean score was 7 (range, 3–10) indicating moderate disease. Elevated titers of anti-dsDNA were detected in 50% of SLE patients with elevated anti-ribosomal P antibodies. One patient had secondary APS. One patient with elevated titers of antinuclear had renal disease and psychosis. Three patients had a rash, while none of the patients had arthritis or leukopenia. Anti-ribosomal P titers were not elevated in patients with primary APS, inflammatory rheumatic disease, infections, or in healthy controls.  
Conclusion The prevalence of elevated titers of anti-ribosomal P antibodies was restricted to SLE patients. No correlation with a specific manifestation was found.  

P14  
Human type II collagen is processed in lysosomal compartments of macrophages for presentation of the glycosylated arthritogenic epitope hCII259-273 to CD4 T cells in HLA-DR1 transgenic mice  
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Background Post-translational modification of human type II collagen (hCII) in the form of hydroxylation of Pro and Lys residues and glycosylation of some hydroxylated Lys residues has been shown to correlate with hCII arthritogenicity in susceptible strains of mice [1,2]. At the epitope level, O-linked glycosylation of Lys264, located within the arthritogenic region hCII259-273, has been implicated in the creation of neoplastic cells recognized by arthritogenic T cells [3]. Macrophages and to lesser extent primed B cells have been implicated in processing hCII for presentation of hCII259-273 epitope to specific T cells [4,5], whereas Langerhans dendritic cells are unable to process CII [6]. Macrophages may thus play a pivotal role in the activation of autoreactive T cells during collagen-induced arthritis. However, no information is available on the mechanisms of antigen processing of the glycosylated arthritogenic epitope, although it is likely to be crucial for an understanding of the activation of autoreactive T cells in rheumatoid arthritis.  
Objective We investigated the mechanisms of intracellular processing of hCII for presentation of the glycosylated epitope hCII259-273 to CD4 T cells in macrophages from HLA-DR1-transgenic mice.  
Methods HLA-DRα*0101/C57BL/6J-transgenic mice (designated HLA-DR1-tg) were developed by backcrossing HLA-DRα*0101 mice onto a MHC class II-deficient background. T-cell hybridomas specific for the glycosylated and non-glycosylated hCII259-273 epitope were developed to study antigen presentation of the glycosylated epitope by bone marrow macrophages used as antigen-presenting cells. Subcellular fractions of macrophages were used as a source of enzyme activity to digest hCII at pH 4.5 in the presence and absence of enzyme inhibitors to localize stages of processing in lysosomal/endosomal compartments and to identify the families of enzymes involved.  
Results HLA-DR1-tg mice lacking mouse MHC class II were susceptible to collagen-induced arthritis. Macrophages from DR1-tg mice processed intact hCII for presentation of the glycosylated epitope hCII259-273 to T-cell hybridomas. T-cell hybridomas specific for the glycosylated peptide did not cross-react with the non-glycosylated peptide. Intracellular processing of hCII for presentation of the glycosylated epitope was prevented by inhibitors of serine-proteases, cysteine-proteases, aspartic-proteases and metallo-proteases or agents that raise endosomal pH, suggesting a requirement for extensive lysosomal processing. Lysosome-enriched subcellular fractions of macrophages were identified as the main organelles involved in processing and presentation of the glycosylated epitope from hCII, as these compartments contained: proteolytic enzymes of the serine-protease and cysteine-protease families that could generate the glycosylated hCII epitope; the glycosylated hCII epitope itself generated by intracellular processing of hCII; peptide-receptive HLA-DR1 molecules; and complexes of HLA-DR1 molecules with the glycosylated and non-glycosylated hCII259-274 epitopes.  
Conclusion We showed stringent conditions for intracellular lysosomal processing of hCII for presentation of the arthritogenic glycosylated epitope by HLA-DR1 molecules to CD4 T cells, which may explain the lack of tolerance to glycosylated collagen and induction of arthritis in HLA-DR1-tg mice.  
References  
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P15  
Does the burden of inflammation determined prospectively in patients with early inflammatory arthritis determine the progression of atherosclerosis?  
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Background Accelerated atherosclerosis accounts for the increased mortality seen in patients with established rheumatoid arthritis (RA). Recent research has
shown that RA is associated with an increase in the carotid intimal medial thickness (IMT). To date, there is no prospective study in RA that examines this question and none that includes an inflammatory disease control.

**Objectives** To evaluate prospectively the burden of inflammation in a cohort of patients with early inflammatory arthritis, including RA and psoriatic arthritis (PsA). To correlate inflammatory burden with IMT in this cohort and to compare with normal age-matched control subjects.

**Methods** RA and PsA patients with disease duration of more than 5 years were selected from the early arthritis clinic database for further study. Controls without inflammatory conditions were recruited from the general clinic. Men older than 40 years and women older than 50 years were excluded. Patients with known predisposing risks for ischaemic heart disease were also excluded. At the time of clinical assessment blood samples were collected for erythrocyte sedimentation rate (ESR) and C-reactive protein (CRP) together with fasting lipid samples, and carotid artery ultrasound was performed at the same time. The mean IMT was then calculated by averaging the values at three points, 1 cm above, at, and 1 cm below the area of maximal IMT for each carotid artery.

**Results** To date, 61 patients (29 RA, 26 PsA and six control subjects) have been reviewed. Twenty-one (72%) of the RA patients compared with 11 (42%) of the PsA patients had an increased IMT (normal IMT < 0.5 cm). Mean ± standard deviation ESR values in the RA cohort (0.6 ± 0.14) and in the PsA cohort (0.5 ± 0.15) were significantly greater than controls (P = 0.003, P = 0.03, respectively). IMT values in the RA cohort were greater than in PsA (P = 0.017). There was a significant correlation between IMT and age in the RA cohort. However, mean age in the three groups was not different and no correlation between IMT and age was seen in either the PsA or the control group. The area under the curve (AUC) ESR correlated with the AUC CRP in the group as a whole and in both RA and PsA separately.

**Conclusions** Patients with inflammatory arthritis (RA > PsA) are at a greater risk of developing atherosclerosis compared with control subjects. No correlation has been found to date between IMT values and the burden of inflammation as measured by ESR or CRP over time. Additional mechanisms of accelerated atherosclerosis in inflammation, yet to be determined, may well apply. The results are preliminary and recruitment with additional analysis is ongoing.

**P16**

**Altered composition of CD97 splice variants in rheumatoid synovial tissue**

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The intimal lining of synovial tissue consists of fibroblast-like synoviocytes (type A synoviocytes) and macrophages (type B synoviocytes). These cells are able to interact through the CD97/CD55 receptor ligand system. The CD97 receptor is a heterodimer receptor composed of α and β subunits. The CD97α/β subunit may exist as three isoforms due to alternative spliced transcripts, each having a different affinity for CD55. When comparing synovium of rheumatoid arthritis (RA) patients with synovium of patients with osteoarthritis (OA), no increase in the level of total CD97α/β or in the level of CD97βα transcripts was found. However, in RA synovium a relative increased expression of CD97 transcripts encoding isoforms with an increased affinity for CD55 (CD97αβ2α2 and CD97αβ2α3 mRNA) was detected. A difference in CD97 splice variants between RA and OA tissues could not be attributed to differences in composition of cells as in both tissues the majority of CD97+ cells are CD14+ macrophages/monocytes – 93% in RA and 94% in OA, respectively. These data indicate that during inflammation CD97 splicing is regulated, and we propose that this is likely to affect trafficking and function of CD97-positive leukocytes.

**P17**

**Improvement of T-cell function in rheumatoid arthritis (RA) patients in clinical remission is associated with the recovery of IL-7 expression and depends on a familial history of RA**

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**Background** Rheumatoid arthritis (RA) is a chronic, inflammatory disease with a number of phenotypic and functional T-cell defects. We previously demonstrated abnormal differentiation and hyperproliferation of RA patient T cells [1], in relation with inflammation and associated with reduced thymic activity as measured by T-cell receptor excision circle (TREC) content. However, it is still not clear whether these dysfunctions are a primary feature of RA or only secondary to the presence of inflammation. Therefore we aimed to evaluate RA patients in clinical remission in whom systemic inflammation was controlled.

**Methods** Patients were defined as ‘in remission’ when they had controlled disease, with no change of activity for at least 6 months, C-reactive protein below 15, no swollen or tender joints and on stable treatment (with or without therapy). Measurements of TREC content in CD4+ T cells was by real-time PCR. IL-7 quantification was by ELISA. Proliferation assay in response to mitogen, IL-2, TCR stimulation or recall antigen.

**Results** The TREC content of CD4+ T cells in these patients was heterogeneous (n = 35). However, two groups of patients could be defined: group 1 (TREC anti) similar to healthy controls (n = 17); group 2 (TREC poor), close to active disease (n = 19). No conventional clinical parameter such as age, sex, disease duration, remission duration, treatment, clinical scores or rheumatoid factor could explain this difference. However, age at disease onset was significantly distributed between these two groups (P = 0.021) and correlated with a familial maternal history of RA. IL-7 is essential to thymic T-cell development and to T-cell activation in the periphery. We found large variations in IL-7 circulating levels between RA patients in remission (n = 57). There was a positive correlation between the circulating levels of IL-7 and the TREC content (r = 0.701, P < 0.0001), suggesting that recovery of thymic activity was limited by the availability of IL-7. We investigated T-cell responses to mitogen, antigen, recall antigen and IL-2 in patients with high and low levels of circulating IL-7 (n = 5 for each group). Low levels of IL-7 were associated with hyporesponsiveness to all stimuli, which could be overcome by adding IL-7 to the cultures. In contrast, high levels of IL-7 were associated with optimal responses to all stimuli including recall antigen and were not greatly affected by supplementation with high and low IL-7.

**Conclusion** RA patients in clinical remission are clearly separated in two groups, according to their ability to express IL-7 and the associated consequences on thymic activity and T-cell responses. This ability was dependent on the age of the patients at disease onset. This was only associated with a maternal family history of RA and suggests that genetic anticipation may be involved.

**Reference**


**P18**

**T-bet expression in rheumatoid arthritis patients with early, disease-modifying anti-therapeutic drug naïve disease is low and correlates with low levels of IL-7 and T-cell dysfunctions**

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**Background** Rheumatoid arthritis (RA) exact pathogenesis remains uncertain, although autoimmune processes appear to play a role, and RA is often referred to as a Th1-driven disease. However, it is well known that RA patients have a reduced capacity to produce IL-2 and interferon gamma (IFN-γ). IL-7 is an important cytokine during early events leading naïve T cells towards Th1 polarisation. We have associated low levels of circulating IL-7 with reduced thymic T-cell development and T-cell functions in the periphery. The origin of IL-7 in the circulation is not clear and stromal cells in the bone marrow, liver, gut and lymph nodes are potential production sources. The only cytokines known to regulate the expression of IL-7 in different tissues are IFN-γ (bone marrow), transforming growth factor beta (TGF-β) (skin) and both IL-7 and tumour necrosis factor alpha (TNF-α) (synovium). We therefore investigated the relationship between levels of circulating IL-7, a Th1 (IFN-γ) and a Th2 (TGF-β) cytokine, a proinflammatory cytokine (TNF-α) and two transcription factors essential for T-cell polarisation (T-bet and GATA3).

**Methods** Patients ‘in remission’ were defined as having controlled disease, with no change of activity for at least 6 months, C-reactive protein below 15, no swollen or tender joints and on stable treatment (with or without therapy). A cohort of these patients was selected on the basis of the expression of circulating IL-7. RA patients with active, early, disease-modifying anti-rheumatic drug (DMARD) naïve disease were also recruited. Circulating levels of cytokines were measured by ELISA and the expression of T-bet and GATA3 by real-time PCR on mRNA extracted from peripheral blood mononuclear cells.

**Results** We selected 10 patients with either low or high levels of circulating IL-7. Levels of IFN-γ, TGF-β and TNF-α were measured. High levels of IL-7 were significantly associated with higher levels of IFN-γ (P = 0.04) and a tendency for lower levels of TGF-β but no difference was found for TNF-α. Furthermore, there was a
The signalling signature downstream of the notch receptor in CD4+CD25+ regulatory T cells in RA defines anergic cells: insight into resistance to anti-tumour necrosis factor therapies

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Background We have previously reported on the abnormal expression of the different members of the Jagged/Notch signalling pathway in early rheumatoid arthritis (RA) patients and Detex are two members of the Jagged/Notch signalling molecules resulting from the transduction of notch signals. We have shown that signalling through the Jagged/Notch pathway is involved in the development of an anergic phenotype in a T-cell clone model in vitro. We have also used this model to establish a Notch signalling signature characteristic a T-cell suppression reaction. We analysed the Notch signalling signature of effecter CD4+ T cells and CD4+CD25+ regulatory T cells in RA patients and compared it with healthy controls.

Methods The HA1.7 CD4+T-cell clone develops an anergic phenotype associated with high CD25 expression when stimulated with its cognate peptide in the absence of co-stimulation. These cells were used in a suppression assay of fresh HA1.7 (CD25high) cells, activated by anti-CD3/CD28 antibodies in proliferation assays. Real-time PCR for the quantification of gene expression was undertaken. CD4+CD25- T cells and CD4+CD25+ regulatory T cells were sorted using flow cytometry from 50 ml blood from five RA patients with early, disease-modifying anti-rheumatic drug naive disease and seven healthy controls. Gene expression was quantified by real-time PCR.

Results During a suppression reaction of fresh HA1.7 cells (CD25high) by anergic HA1.7 expressing high levels of CD25, the expression of HES1 was induced; however, Detex was inhibited. This signature is unique and differs from either an anti-CD3 or an anti CD28 signal. HES1 and downregulated Detex).

Conclusions CD4+CD25+ regulatory T cells in RA appear anergic and may be able to suppress an undesirable auto-immune reaction very early in the RA disease process. Altogether, our results on the abnormal baseline expression of Jagged/Notch molecules and these atypical signalling signatures suggest that the Jagged/Notch pathway may be involved in the pathogenesis of RA.

Acknowledgment This work was supported by the Arthritis Research Campaign (arc).

Abatacept (CTLA4-Ig) modulates human T-cell proliferation and cytokine production but does not affect lipopolysaccharide-induced tumor necrosis factor alpha production by monocytes

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Background and objectives Activated T cells play a central role in the inflammatory cascade leading to the joint inflammation and destruction characteristic of rheumatoid arthritis (RA). The cytokines secreted by activated T cells are thought to both initiate and propagate the immunologically driven inflammation associated with RA. Abatacept, the first of a new class of agents for the treatment of RA that selectively modulates the co-stimulatory signal required for full T-cell activation, was evaluated for its ability to regulate human T-cell proliferation and cytokine production in vitro. The effect of abatacept on lipopolysaccharide (LPS)-induced tumor necrosis factor alpha (TNF-α) from monocytes was evaluated to distinguish the impact of this agent on innate versus adaptive, antigen-specific immune responses.

Method T cells were isolated from normal healthy human volunteers. The effect of abatacept on antigen-dependent T-cell activation was evaluated using either an irradiated human B-cell line (PM-LCL), or autologous EB-PMCs as APCs for a primary mixed lymphocyte reaction (MLR), or autologous EB-PMCs as APCs.
for a recall response to tetanus toxin (TT). Cytokines were measured at various times post activation, with proliferation determined on day 5. Monocytes were iso-
lated by elutriation, challenged with LPS and TNF-α levels measured at 6 hours. Chi-squared analysis was included as a non-specific fusion protein control. Results Abatacept significantly downmodulated T-cell proliferation, in both primary and recall responses, at concentrations between 0.3 and 100 μg/ml, with maximal inhibition (~80-90%) observed at ~3–10 μg/ml. These concentrations are below the trough plasma levels observed in patients receiving a clinically effective dose [1]. Under conditions of maximal inhibition of proliferation, and similar to trough plasma levels in patients (30 μg/ml), abatacept also inhibited IL-2, TNF-α and interferon gamma secretion in both primary and TT-dependen
t recall responses. However, the extent, kinetics and rank order of cytokine
inhibition by abatacept was somewhat different between primary and recall responses. In contrast, abatacept did not inhibit LPS-induced TNF-α production in primary human monocytes, demonstrating that its action is restricted to antigen-dependent T-cell responses. Conclusion Abatacept, a selective co-stimulation modulator, significantly inhibited the activation (as measured by cytokine production) and proliferation of human T cells in the context of a primary MLR or TT-dependent memory response. This inhibition occurred at concentrations below the serum Cmax levels observed in patients receiving a clinically effective dose of abatacept [1] (10 mg/kg monthly), consistent with suppression of T-cell activation in vivo. There was no effect of abatacept on LPS-stimulated TNF-α production in monocytes indicating that this agent may largely preserve innate immune responses. Reference 1. Kremer JM, Westhovens R, Leon M, Di Giorgio E, Alten R, Steinfeld S, Russell A, Dougados M, Emery P, Nuamah IF, et al.: Treatment of rheuma

P22 Intra-articular gene therapy blocking NF-κB using adeno-
associated virus type 5 ameliorates adjuvant arthritis in rats J Adriaensen1, SW Tas1, N Hajji1, A Bakker2, MJ Vervoordeldonk1, PP Tak1
Objective NF-κB is highly activated in synovium of RA patients, and can induce transcription of proinflamatory cytokines, adhesion molecules, and inducible nitric oxide, among others. Phosphorylation of the inhibitor of NF-κB (IκB) proteins is an important step in NF-κB/Rel activation and is regulated by IκB kinase (IκK). The IκK complex consists of at least three subunits, including IκKα and IκKβ (also called IKK1 and IKK2) and the regulatory subunit IκKγ. In an initial study in Lewis rats with adjuvant arthritis (AA) adeno-associated dominant-negative IKK2 (Ad.IKK2dn) significantly decreased the severity of disease as evidenced by decreased paw swelling compared with Ad.GFP-treated rats [1]. However, adenoviral vectors are known to be very immunogenic, compromising stable long-term expression of the transgene. Adeno-associated virus (AAV) is considered the most promising vector for gene therapy in RA. In a comparative serotype study we found that direct injec
tion of the ankle joints of rats with Ad.IKK2dn resulted in the highest synovial transduction, with good expression of the transgene at the protein level until the end of the study, followed by AVV2. In the present study we investigated the effect of inhibiting NF-κB in AA in rats using AAV-mediated intra-articular gene therapy. For this purpose we used the following vectors: AAV5 containing the IKK2dn gene (AAV5.IKK2dn) or AAV2 containing the IκBα-suppressor gene (AAV2.IκBα SR). Methods AAV5.IKK2dn (2.5 x 1010vp), AAV2.IκBα SR (2.5 x 1010vp) or AAV5/
AAV2.GFP were injected into the right ankle joints of rats with AA on day 11 after adjuvant immunization. Subsequently, the effect of both genes on paw swelling was measured by water displacement plethysmometry. Animals were sacrificed 2 weeks after intra-articular injection and joints were collected for analysis. Bone
degradation was examined using X-rays of the ankle joints and histology was performed to assess synovial inflammation and joint damage. Results In the rats treated with IKK2dn, significantly reduced paw swelling was observed (P < 0.05, AAV5.dnIKK2 versus AAV5.GFP). No significant effect was found for AVV2.IκBα SR only as a non-specific fusion protein control. AAV.IκBα SR only showed a marginal effect on the clinical course of arthritis. Conclusion We demonstrate that AAV5-mediated IKK2dn gene transfer to the synovium reduces the severity of inflammation in AA rats, when the treatment was started after the onset of disease. In contrast, injection of AAV2.IκBα SR had a poor clinical effect on paw swelling in rats with AA. This could either be due to the dissimi
larities in the mechanisms that these genes use to inhibit NF-κB activation (IKK2 versus IκBα) or to the use of different AAV serotypes as vector (AAV5 versus AAV2). Reference 1. J Adriaensen1, SW Tas1, N Hajji1, A Bakker2, MJ Vervoordeldonk1, PP Tak1

P23 Collagenous repeat containing sequence of 26 kDa protein: a novel mesenchymal gene of cartilage and adipose tissue differen
tiation IH Tarner1, C Büchler2, J Schömerich1, E Neumann1, S Gay2, A Schäffler1, U Müller-Ladner1
1Department of Internal Medicine I, University Hospital Regensburg, Germany; 2Center for Experimental Rheumatology, Department of Rheumatology, University of Zurich, Switzerland Arthritis Res Ther 2005, 7(Suppl 1):P23 (DOI 10.1186/ar1544)
Background Collagenous repeat containing sequence of 26 kDa protein (CORS-26) is a recently discovered novel member of the TNF/t1q/adiponectin superfamily. CORS-26 has been detected in chondrocytes and osteoblasts, but its functional properties are largely unknown. As CORS-26 shows structural analogies to adiponectin, which has been shown to exert proinflamatory and destructive properties in arthritic synovium, the goal of the present study was to examine the expression and regulation of CORS-26 in adipocyte differentiation. Methods Gene expression of 3T3-L1-preadipocytes cultures were examined on the protein and mRNA level by real-time PCR, Western blot, electrophoretic mobility shift assay and luciferase-reporter gene assay. Results CORS-26 showed numerous homologies to adiponectin such as a C-
terminal globular domain and a N-terminal collagen domain. CORS-26 mRNA expression could not be detected in preadipocytes and in early adipocytes after 48 hours of culture. After 4–9 days of adipocyte differentiation, upregu-
lation of CORS-26 mRNA and protein could be detected. CORS-26 promoter activity and mRNA expression could be stimulated by troglitazone and fenofibrate but not by 15-deoxy-prostaglandin J2. In addition, PPARY, but not PPARγ, binds specifically to a promoter response element at position –841/–596. Conclusions CORS-26 appears to be a novel adipokine with strong homolog
es to the other members of the C1q/TNF/adiponectin superfamily, which includes its functional properties that may be as proinflamatory in the arthritic joint as those of adiponectin. P24 Activation of antigen-presenting cells by endogenous retroviral RNA D Moyes1, S Sacre1, N Tempertton1, A Lundberg2, B Foxwell2, P Venables1
1The Kennedy Institute, Imperial College London, UK; 2Wohl Virion Centre, University College London, UK Arthritis Res Ther 2005, 7(Suppl 1):P24 (DOI 10.1186/ar1545)
Background Several studies have linked human endogenous retroviruses (HERVs) with autoimmune disease. We have previously demonstrated that the full-length polymorphic HERV-K113 provirus prevalence is increased in both Sjög
rens’s syndrome (15.6%) and multiple sclerosis (11.9%) compared with the normal UK population (4%). Recent studies have shown that exogenous viral RNA can activate dendritic cells via the TLR7/8-mediated pathway. In this study we investigated the possibility that HERV-K113 RNA sequences are capable of activating both dendritic cells and macrophages. We examine the production of cytokines by both cell types in response to a series of different HERV-K113 RNA species to identify any differences in the profile produced. Methods A clone of the full-length HERV-K113 provirus was digested with restric
tion enzymes to generate different length fragments of the 5′LTR and gag gene for use in vitro transcription, producing single-stranded RNA species. The RNA was treated to remove any residual protein, DNA, lipopolysaccharide or other contami
nants. After quantitation, the RNA was complexed with Lipofectamine 2000 (Invirogo
gen, Paisley, UK) or left uncomplexed before being used to treat cells. Cytokines levels in the cell supernatants were measured by ELISA. Dendritic cells were assayed for tumour necrosis factor (TNF), IL-6 and IP-10, while macrophages were assayed for TNF, IL-6, IL-8 and IL-10. Controls were un-complexed RNA, poly-U synthetic RNA, and the chemical activator of TLR 7 and 8, Resiquimod (R-848). Results Stimulation with R-848 produced TNF, IL-6, IL-8 and IP-10 from macrophages and TNF, IL-6 and IP-10 from dendritic cells (Table 1). Uncom-
plexed RNA did not stimulate cytokine production in any cell type demonstrating a lack of lipopolysaccharide or other contaminant activation of cells. Stimulation of dendritic cells with each of the three complexed RNA species resulted in the pro-
duction of IL-6, TNF and IP-10 (Table 1). Stimulation of macrophages only pro-
duced TNF. Although low levels of IL-6 were detected, there was no increase over control cells (Table 1). Neither IL-8 nor IL-10 was produced in macrophages in response to any of the RNA species. All three RNA species were more active than a poly-U synthetic RNA control. Conclusions The data demonstrate that RNA from HERVs is capable of inducing different cytokines and dendritic cells. The pattern of cytokine expression differs between the two cell types and may reflect different activation pathways in each case. This work demonstrates a possible mechanism of action for HERV induction of an inflammatory response leading to an autoimmune disease.
Cytokine release in response to one species of HERV-K113 RNA from different cells

<table>
<thead>
<tr>
<th>Tumor necrosis factor (ng/ml)</th>
<th>IL-6 (ng/ml)</th>
<th>IP-10 (ng/ml)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Macrophage and K113 RNA</td>
<td>5.46</td>
<td>0.234</td>
</tr>
<tr>
<td>Macrophage and R848 (positive control)</td>
<td>5.78</td>
<td>0.055</td>
</tr>
<tr>
<td>Macrophage and control RNA (negative control)</td>
<td>0.04</td>
<td>0.00</td>
</tr>
<tr>
<td>Dendritic cell and K113 RNA</td>
<td>4.45</td>
<td>3.75</td>
</tr>
<tr>
<td>Dendritic cell and R848 (positive control)</td>
<td>6.49</td>
<td>13.57</td>
</tr>
<tr>
<td>Dendritic cell and control RNA (negative control)</td>
<td>0.095</td>
<td>0.458</td>
</tr>
</tbody>
</table>

Dendritic cell and K113 RNA 4.45 3.75 5.2
Macrophage and K113 RNA 5.46 0.234 0.01
Macrophage and R848 (positive control) 5.78 0.055 0.006
Macrophage and control RNA (negative control) 0.04 0.00 0.0
Dendritic cell and K113 RNA 4.45 3.75 5.2
Dendritic cell and R848 (positive control) 6.49 13.57 5.12
Dendritic cell and control RNA (negative control) 0.095 0.458 0.824

P25
Anti-tumour necrosis factor alpha treatment in patients affected by rheumatoid arthritis with anti-Ro/SSA antibodies

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Background Anti-tumour necrosis factor alpha (anti-TNF-α) treatment could induce the onset of new autoantibodies [1,2] or clinical features of other autoimmune diseases than rheumatoid arthritis (RA) [2].

Aim To analyse the efficacy and safety of anti-TNF-α treatment in six patients affected by RA with anti-Ro/SSA antibodies and to evaluate the clinical and laboratory changes during the treatment.

Patients and methods Anti-nuclear antibodies (A/N) on HEp-2 cells, anti-dsDNA (Farr assay), anticardiolipin (aCL, ELISA) and anti-ENA (CIE) were evaluated before the treatment and every 6–12 months. Anti-Ro/SSA antibodies were confirmed by ELISA, using recombinant 52 and 60 kDa Ro proteins (Pharmacia).

Results Six patients had anti-Ro/SSA antibodies before anti-TNFα treatment. Anti-Ro/SSA was detected in four sera using both CIE and ELISA, while two sera showed anti-60 kDa Ro antibodies only by ELISA. Six patients (mean age, 58 years; standard deviation [SD], 9.8) were affected by long-acting RA (mean duration, 7 years; range, 5–22 years), not responding to common disease-modifying anti-rheumatic drugs (mean, 5 disease-modifying anti-rheumatic drugs; SD, 2.3). All the patients were treated for a mean of 31 months (SD, 20.4 months), four subjects with Infliximab and two with Etanercept. Before the treatment the patients showed active arthritis with a mean of 25.3 tender joints (SD, 2.16), 17.3 swollen joints (SD, 8.6) and Disease Activity Score (DAS) of 5.5 (SD, 1.04); after 6, 12, 18, and 24 months all the patients showed a rapid and sustained improvement with reduction of DAS value (see Table 1). All the patients were affected by Sjögren syndrome (SS), associated to RA, clinically stable during the treatment. One subject was also affected by primary biliary cirrhosis, which remained clinically and histologically stable. Three patients developed anti-dsDNA at low titre after 6 months and a fourth after 12 months of treatment. Only one patient developed skin lesions after 6 months of Infliximab, clinically and histologically similar to subacute cutaneous lupus with IgM deposits at basal membrane. No patients developed aCL, while the titre of anti-Ro antibodies by ELISA was stable during the treatment. One subject, affected by RA and HCV hepatitis, stopped the etanercept treatment due to severe increase of hepatic enzymes.

Table 1
Clinical response to anti-tumour necrosis factor alpha treatment in patients with rheumatoid arthritis and anti-Ro/SSA antibodies

<table>
<thead>
<tr>
<th>Clinical response to anti-tumour necrosis factor alpha treatment in patients with rheumatoid arthritis and anti-Ro/SSA antibodies</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean Disease Activity Score 44</td>
</tr>
<tr>
<td>At onset</td>
</tr>
<tr>
<td>6th month</td>
</tr>
<tr>
<td>12th month</td>
</tr>
<tr>
<td>18th month</td>
</tr>
<tr>
<td>24th month</td>
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</tbody>
</table>

Conclusions Anti-TNF treatment in RA-SS patients with anti-Ro/SSA showed a good and sustained efficacy until the 24th month. Four patients (66.7%) showed anti-dsDNA after 6–12 months, while only one developed subacute cutaneous lupus-like symptoms. No other autoantibodies nor an increase of the anti-Ro titre were observed.

References

P26
Ha-Ras/ERK1-2 pathway is responsible for oxygen species generation in scleroderma fibroblasts

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Background Reactive oxygen species (ROS) are involved in scleroderma (SSc) fibroblast activation, proliferation and type I collagen gene expression [1]. In order to understand the signal transduction pathway involved in ROS generation by SSc fibroblasts, we have assessed the role of Ha-Ras and K-Ras proteins and that of their downstream effectors.

Materials and methods Intracellular ROS were evaluated with 2′,7′-dichlorofluorescein diacetate (DCFH-DA 10 µM). For Ha-Ras and K-Ras protein expression whole cell lysates were immunoprecipitated with specific antibodies and subjected to SDS-PAGE or cells were fixed in paraformaldehyde (4%) and observed by confocal microscopy. SSc skin fibroblasts were transiently transfected with the dominant negative form of Ha-Ras (M17Ras) or with the empty vector using the Effectene Transfection reagents (BioRad).

Results Quiescent SSc fibroblasts contain an altered ratio between the two Ras isoforms showing a selective increase of the mass and the activity of Ha-Ras protein when compared with normal controls. Moreover ERK1-2 are constitutively phosphorylated in quiescent SSc fibroblasts. Inhibition of either Ras, ERK1-2, ROS with specific inhibitor or trasfecting with the negative Ras variant reverse this phenotype back to normal and reduce collagen overproduction by SSc cells.

Conclusions These results suggest that ROS production in SSc fibroblasts is linked and ultimately dependent on increased Ha-Ras signalling via ERK1-2. These events are responsible for the characteristic cellular phenotype of scleroderma fibroblasts and explain some of the clinical features of the disease. Moreover, these data provide evidence for the use of Ras inhibitors in the treatment of the disease.

Reference

P27
Magnetic resonance imaging examinations of the spine in patients with ankylosing spondylitis before and after therapy with the tumor necrosis factor alpha receptor fusion protein etanercept

X Baraliakos1, J Davis2, W Tsuji1, J Braun1

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Objective To assess spinal inflammation by magnetic resonance imaging (MRI) before and after treatment with the tumor necrosis factor (TNF) receptor fusion protein etanercept compared with placebo.

Methods MRI examinations of the lower thoracic and lumbar spine of 40 patients with active ankylosing spondylitis (AS) were performed as part of the recently published randomized controlled trial at four different timepoints: baseline (BL), after 12 weeks (FU1), 24 weeks (FU2) and 48 weeks (FU3). Nineteen patients received etanercept twice weekly, 2 x 25 mg subcutaneously, for 1 year and 21 patients received placebo for 6 months (until FU2) before switching to etanercept. The patients’ (mean age 39.7 years, 75% male, 89% HLA-B27-positive) mean disease duration was 13 years. MRI examinations included T1-weighted sequences before (T1) and after application of gadolinium-diethylene-triamine-pentaacetic-acid (T1/Gd-DTPA) and T2-weighted fat-saturated (T2-FS) sequences. MRI examinations were scored by a modified ASSpMRI score using predefined vertebral units as a basis.

Available online http://arthritis-research.com/supplements/7/S1
Results After 12 weeks, spinal inflammation (T2-FS) regressed by 54% (1.33 mean scoring points per vertebral units at BL and 0.61 at FU1, $P = 0.002$) in the etanercept group, but worsened by 13% in the placebo group (0.94 at BL and 1.08 at TP1, $P = 0.05$). After switching to etanercept, the improvement of patients improved similarly. T1/Gd-DTPA MRI sequences performed equally well. About 60% of all active lesions at BL were detected in the thoracic spine. There were no significant changes in the chronocrical score.

Conclusions Treatment with etanercept of patients with active AS results in regression of spinal inflammation as assessed by spinal MRI. Inclusion of the thoracic spine in MRI examinations of AS patients may be of particular importance.

P28 Two-year follow-up results after re-administration of etanercept in active ankylosing spondylitis

X Baraliakos1, J Brandt1, J Listing2, H Haibel3, HM Rudwaleit2, J Sieper3, J Braun1,3

1Rheumazentrum Ruhrgebiet, Herne, Germany; 2German Rheumatism Research Center, Epidemiology Department, Berlin, Germany; 3Department of Gastroenterology/Rheumatology, Charité, Medical University Berlin, Campus Benjamin Franklin, Germany


Objectives The tumor necrosis factor alpha (TNF-α) receptor fusion protein etanercept has proven short-term efficacy in patients with active ankylosing spondylitis (AS). The results of continuous treatment with etanercept over 1 year were reported previously. Here we report the experience with the second year of follow-up.

Methods Overall, 23 out of 30 AS patients (77%) who had participated in the initial placebo-controlled phase of the trial were included in this 2-year extension, where patients with active disease were treated with etanercept (2 × 25 mg subcutaneously twice a week). Disease-modifying anti-rheumatic drugs and steroids were not allowed. The clinical response was assessed by standard assessment tools for disease activity (Bath AS Disease Activity Index [BASDAI]), function (BASF Functional Index) and mobility (BASF Metrology Index). The primary outcome of this trial was efficacy on disease activity after 2 years of continuous treatment with etanercept in AS patients, compared with patient status at baseline (BL).

Results Of the 30 initial patients, 21 (70%) completed year 2. At week 102, 54% of the patients had maintained a 50% improvement of BASDAI, and 9/21 (43%) were in a state of partial remission according to the ASAS criteria. The mean BASDAI score remained stable (2.6 ± 2.2 at week 54 and 2.7 ± 2.4 at week 102) in the second study year. Similarly, all other clinical parameters showed no change during year 2 with significant improvement compared with BL. Two patients experienced serious adverse events leading to discontinuation of therapy.

Conclusions This study confirms the efficacy and safety of etanercept in the treatment of patients with active AS without simultaneous administration of disease-modifying anti-rheumatic drugs or steroids over 2 years of continuous treatment.

P29 Clinical response to the anti-tumor necrosis factor alpha antibody infliximab in patients with ankylosing spondylitis over 3 years

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1Rheumatology Medical Center Ruhrgebiet, Herne, Germany; 2German Rheumatism Research Center, Berlin, Germany; 3University Medicine Berlin, Campus Benjamin Franklin, Germany


Objective Infliximab, a monoclonal antibody against tumor necrosis factor alpha (TNF-α), is approved in Europe for the treatment of patients with active ankylosing spondylitis (AS) who have responded inadequately to conventional therapy. This report provides analyses from a 3-year extension study, as a follow-up to both the 1-year and 2-year open-label extensions of the original 3-month randomised controlled trial of infliximab in patients with AS.

Methods Of the 49 patients with AS who completed the second year of the study, 46 continued treatment with infliximab 5 mg/kg every 6 weeks through week 156. The Bath AS Disease Activity Index (BASDAI), the Bath AS Functional Index, the Bath AS Metrology Index, patient’s and physician’s global assessment, quality of life (Short Form-36), C-reactive protein, and erythrocyte sedimentation rate were assessed throughout the study period.

Results The improvement of signs and symptoms observed in the majority of the patients during the first and second year was sustained throughout the third year of the study. Forty-three patients (62%) of the 69 patients enrolled at baseline and 93% of the patients who started the third year (complete week 156). A BASDAI 50% improvement was achieved by 28 of 43 patients (65%) at week 156. The scores for other efficacy assessments were similar to the values observed at weeks 54 and 102. Median C-reactive protein levels remained low (1.5 mg/l at week 156). There were no relevant side effects and no discontinuation because of drug-related adverse events during the third year of the study.

Conclusions Patients with AS receiving infliximab for 3 years showed durable clinical response without loss of efficacy. Long-term infliximab treatment was well tolerated by patients in this study.

P30 Clinical response to discontinuation of anti-tumor necrosis factor therapy in patients with ankylosing spondylitis after 3 years of continuous treatment with infliximab

X Baraliakos1, J Listing2, J Brandt1, M Rudwaleit2, J Sieper3, J Braun1

1Rheumazentrum Ruhrgebiet, Herne, Germany; 2German Rheumatism Research Center, Berlin, Germany; 3Chronic Inflammatory Diseases Center, Medical University of Berlin, Campus Benjamin Franklin, Department of Rheumatology, Germany


Objective To analyze the clinical response and the time to relapse after withdrawal of continuous long-term infliximab therapy in patients with ankylosing spondylitis (AS).

Methods After 3 years of infliximab therapy, all AS patients (n = 42) discontinued treatment (TP1) and were visited regularly in order to assess the time to relapse (TP2) for 1 year. Relapse was defined as an increase to a Bath AS Disease Activity Index (BASDAI) value and physician’s global assessment >4 according to the ASAS recommendations.

Results After 52 weeks, 41 of the 42 patients (97.6%) had to be reinfused because of relapse. The mean change of the BASDAI between TP1 and TP2 was 3.6 ± 1.7, and for the physician’s global assessment was 4.4 ± 1.8 (both $P < 0.001$). The mean time to relapse was 17.5 weeks (± 7.9 weeks, range 7–45 weeks). Ten patients (24%) showed a relapse within 12 weeks and 38 patients (90.5%) within 36 weeks. After 52 weeks, only one patient had remained in ongoing remission without anti-tumor necrosis factor therapy. Patients who were in partial remission and those with normal C-reactive protein levels at baseline had longer mean time to relapse after discontinuation. Retreatment with infliximab was safe and resulted in clinical improvement similar to the state before withdrawal in all patients.

Conclusions Discontinuation of long-term therapy with infliximab led to relapse of disease activity in all but one patient after different time periods. Remission and low C-reactive protein levels at the time of withdrawal were associated with longer flare free periods. Retreatment with infliximab was safe and efficacious.

P31 Radiographic progression in patients with ankylosing spondylitis after 2 years of treatment with the tumor necrosis factor alpha antibody infliximab

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1Rheumazentrum Ruhrgebiet, Herne, Germany; 2German Rheumatism Research Center, Berlin, Germany; 3Rheumatology, Charité, Campus Benjamin Franklin, Berlin, Germany


Background Anti-tumor necrosis factor therapy is clinically efficacious in patients with active ankylosing spondylitis (AS) and leads to improvement of spinal inflammation, as assessed by magnetic resonance imaging. It is unclear whether anti-tumor necrosis factor therapy has influence on chronic spinal changes in AS.

Objective To analyze the effect of infliximab on the radiographic course of AS over 2 years.

Methods Complete sets of lateral radiographs of the cervical and the lumbar spine were available from 82 patients from two sources: 41 patients (group 1) had been treated with infliximab (5 mg/kg/6 weeks) as part of a recent randomized controlled trial, and 41 patients (group 2) were part of the early German AS cohort (GESEPIC), without controlled interventions. Radiographs were performed at baseline and after 2 years and were scored by the modified SASSS.

Results Patients in the infliximab group were older, had a longer disease duration and more radiographic damage at baseline. The mean modified SASSS change was 0.4 (± 2.7) and 0.7 (± 3.4) for group 1 and group 2, respectively ($P = 0.05$). Radiographic damage at baseline was a predictor for more radiographic progression. Patients with baseline damage who were treated with infliximab showed a trend for less radiographic progression. There were no correlations between clinical parameters and radiographic progression.

Conclusions AS patients treated with infliximab showed somewhat less radiographic progression after 2 years. Patients with prevalent radiographic damage are prone to develop more damage over time. Infliximab may decelerate radiographic progression in such patients. Larger studies are needed to prove that anti-tumor necrosis factor therapy inhibits structural damage.

Acknowledgement This abstract is eligible for application for a postgraduate student fellowship.
P32
Oxygen radical production determines chondrocyte death and regulates matrix metalloproteinase-mediated matrix degradation during interferon gamma-accelerated immune complex arthritis
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Objective In earlier studies we found that FcγRII determines chondrocyte death and matrix metalloproteinase (MMP)-mediated cartilage destruction during interferon gamma (IFN-γ)-regulated immune complex (IC)-mediated arthritis [1]. As binding of ICs to FcγRII leads to oxygen radical production, we now investigate the contribution of oxygen radicals to induction of both parameters of cartilage destruction using P47phox knockout mice. These mice have a defect in NADPH oxidase activation and fail to produce oxygen radicals.

Methods IFN-γ was expressed in knee joints of P47phox−/− and their wildtype (WT) controls by local injection of adenoviral IFN-γ constructs. One day thereafter, a passive IC-mediated arthritis was induced. Chondrocyte death and MMP-mediated cartilage destruction were measured in various layers of the knee joint using histology of total joint knees. Neutrophiles induced by MMPs were detected using immunolocalisation and anti-VDPN antibodies. Synovium was isolated and mRNA levels (MMPs/ tissue inhibitors of metalloproteinases [TIMPs]) were determined using quantitative RT-PCR.

Results High levels of IFN-γ were found 1 day after injection of the IFN-γ adenoviral construct in knee joints of P47−/− and WT controls, and resulted in a high and comparable upregulation of FcγRII up to day 7 in both groups. Induction of IC-mediated arthritis in FcγRII-deficient knee joints resulted in prominent but comparable joint inflammation both at day 3 and 7. At day 7, macrophages formed the dominant cell type. When compared with WT controls, RNA levels of MMP-3 and MMP-13, which are crucial in cartilage destruction within this model, were ele-
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Background For functional annotation, similarity-based approaches [1] do not take into account all the information from comparative and evolutionary biology. They do not differentiate between orthologs and paralogs among homologs and, furthermore, the closest BLAST is often not the nearest neighbour [2]. Phylogenetic approaches taking into account duplication and speciation events are neces-
sary to solve these problems. But they do not blend any data from transcriptional behaviour. Nevertheless, orthologs can have very similar ‘molecular function’ but undergo a different ‘macroscopic function’ because of a transcriptional shift.

Results Growing data for gene expression profiling are available in various databases concerning normal or pathological tissues (Expressed Sequence Tags [ESTs] from NR, TIGR, GeneNete, Gepis, etc.). Some works recently examined the cor-
relation between evolution (duplication and speciation) of genes and expression divergence within and between species [3,4], and some examine the expression profile between orthologous genes in sequenced species [5].

Methods We performed a phylogenetic analysis of a protein family, using EST databases. This allowed us to enlarge the dataset of species containing homologs and consequently to improve the reconstruction of the genes’ evolu-
tionary history. We then extracted all the transcriptional data contained in EST databases, to decipher the gene expression pattern. Because gene annotation is currently labour intensive, we used a locally developed platform dedicated to phy-
logenetic annotation (named FIGENIX) [6]. We validated this approach on a family of genes possibly implied in rheumatoid arthritis; the peptidyl arginine deiminase (PADI) genes.

Results We show here a phylogenetic annotation with an enlarged dataset including EST contigs and expression data. It allowed us to integrate more func-
tional data for analysis of a set of genes and permits us to give a transcriptional footprint of the gene. Our analysis showed that the PADI-2 paralog group have kept the ancestral molecular function coupled with a probable ancestral expres-
sion profile. These classified data permitted us to perform an updated footprint of the transcriptional data for each paralog group from this protein family.

Conclusion We believe this method announces a new way to annotate unchar-
acterized ESTs. More than classical phylogeny, it allows highlighting of the tran-
scriptional shift between paralogs, and is thus a good tool to improve annotation. It showed that functional shift can occur in differential tissue expression rather than in biochemical function of the protein.

This method of analysis is at its beginning and has to be extended to all kinds of expression database, including databases where expression data are normalized such as UniGene. In the future it cannot be ignored in annotating new unknown ESTs, underlined by DNA microarray assays for example.


Yanai I, et al.: Genome-wide midrange transcription profiles reveal expression level relationships in human tissue specification. Bioinfor-
matics 2004, in press [E-pub].
Expression of innate immune receptors in the immunopathologic lesion of primary Sjogren’s syndrome: preliminary results

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Background Toll-like receptors (TLRs) have a crucial role in early host defence against invading pathogens. They recognize specific molecular patterns that are present in microbial and viral components, whereas several endogenous molecules seem to be placed among their expanding group of ligands. The CD91 receptor (low-density lipoprotein receptor-related protein [LRP1] or alpha 2-macroglobulin receptor [A2MR]) is a multifunctional receptor that recognizes hsp-chaperoned peptides, which are processed and presented by the MHC class I and MHC class II molecules. So far, there is an increasing evidence that the receptors of innate immunity also play an important role in acquired immunity.

Objective The objective of our study was to evaluate the expression of TLRs and CD91 in minor salivary gland (MSG) biopsy tissues from patients with primary Sjogren’s syndrome (pSS).

Methods At the mRNA level, the expression of TLR2, TLR4, TLR7, TLR8 and CD91 was examined in a non-neoplastic salivary gland epithelial cell line from a patient with pSS by means of RT-PCR. Protein expression of TLR2, TLR4 and CD91 was studied by immunohistochemistry in MSG biopsy tissues from 12 patients with pSS and nine control patients with non-specific sialadenitis.

Results RT-PCR analysis revealed transcriptional activation of TLR2, TLR4, TLR7, TLR8 and CD91 genes in the epithelial cell line of pSS patient. In MSG biopsy tissues, abundant expression of CD91 was observed in ductal cells of both pSS and control tissues, but also in the focal lymphocytic infiltrates of pSS patients. TLR2 and TLR4 protein expression was localized in single, scattered cells, both in pSS patients and, to a lesser extent, in control patients, showing a distinct staining pattern.

Conclusion The presence of CD91 and TLRs in the immunopathologic lesion of Sjogren’s syndrome provides preliminary evidence, suggesting their possible role in innate immune responses within the lesion.

The association of different B27 subtypes with the peptide loading complex

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Background The molecular basis for the strong association of HLA-B27 with ankylosing spondylitis (AS) has not been elucidated. A number of B27 alleles including B*2704 and B*2705 are associated with increased susceptibility to AS; in contrast, the alleles B*2706 and B*2709 are not associated with AS. These alleles differ in amino acid regions that have been shown to influence the interaction with tapasin, an accessory molecule that plays a critical role in incorporating HLA class I into the peptide loading complex (PLC). Our aim was to determine whether B27 subtypes differ in their association with the PLC.

Methods The -221 line that is negative for HLA class I alleles A, B and C was transfected with B*2704, 05, 06 and 09 expression constructs, and stable long-term transfectants with equivalent HLA-B27 expression were selected. The PLC was immunoprecipitated using the anti-TAP antibody 148.3 (provided by R Tampe) and magnetic anti-immunoglobulin microbeads. Non-specific binding of HLA class I was determined by immunoprecipitation with an isotype control mAb. Following reducing SDS-PAGE and western blotting of the eluted proteins, the co-precipitation of HLA-B27 was detected by probing the immunoblots with the anti-HLA class I mAb, HC10, followed by HRP-linked secondary antibodies and visualized using enhanced chemiluminescence. Detection of TAP and tapasin was achieved by stripping bound mAbs and reprobing the immunoblots with an equal amount of anti-TAP mAb and then the PLC was reimmunoprecipitated using the anti-TAP mAb and then the PLC was reimmunoprecipitated with the anti-TAP and anti-mouse IgG mAbs. Following reducing SDS-PAGE and western blotting of the eluted proteins, the co-precipitation of HLA-B27 was detected by probing the immunoblots with the anti-HLA class I mAb, HC10, followed by HRP-linked secondary antibodies and visualized using enhanced chemiluminescence.

Results Only HLA-B*2704, 05 and 09 were found to be readily detectable above background on the immunoblot; suggesting that they were co-precipitated by the anti-TAP mAb and therefore incorporated into the PLC. Despite expressing equivalent quantities of HLA class I heavy chain to the other B27 subtypes, HLA-B*2706 was unique in that it was not detectable above background levels. The inability to detect B*2706 was not due to different efficiencies in immunoprecipi-
P38
Differential survival of leucocyte subsets by syngeneic, bone marrow and skin fibroblasts: site-specific rescue of CD4+ T cells versus activation-induced rescue of neutrophils
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Background Chronic inflammatory disease is characterised by predilection for certain sites, the molecular basis of which remains obscure. We investigated the role that fibroblasts play in governing the survival (persistence) as well as the type of infiltrate (predominantly neutrophil versus lymphocyte) using a leucocyte–fibroblast co-culture model. We used matched syngeneic, bone marrow and skin fibroblasts to test the hypothesis that a fibroblast-derived, stromal area post code identifies microenvironments that can support differential leucocyte accumulation.
Methods Matched syngeneic (SFb), bone marrow (BMFb) and dermal fibroblast (DFb) lines were established from eight patients satisfying ACR criteria for rheumatoid arthritis undergoing total hip or knee arthroplasty. Activated peripheral blood CD4+ T cells prepared by negative depletion and neutrophils prepared by density gradient centrifugation were co-cultured with fibroblasts. Survival, apoptosis and proliferation were assessed using total cell counts and active caspase 3 staining (T cell) or tUNOD staining (neutrophils).
Results Site-specific survival of CD4+ T cells was observed in all eight sets of matched samples: at 3 days, DFb maintained better T cell survival than culture in medium alone (40 ± 1.2% [mean ± standard error] compared with 25.4 ± 1.4% (P < 0.05)). However, both SFb and BMFb maintained even better T cell survival compared with DFb: 58.8 ± 1.2% (P < 0.001 versus DFb) and 51.4 ± 2% (P < 0.05 versus DFb). Fibroblast pre-activation with a wide range of proinflammatory signals had no effect on differential survival. T-cell survival was partially reconstituted by medium from T cell:fibroblast co-cultures and reduced by 50% in the presence of transwells suggesting that T cell:fibroblast interactions are necessary for increased survival. Unlike the case for T cells, resting fibroblasts did not enhance neutrophil survival. However pre-treatment of all fibroblasts with tumour necrosis factor alpha significantly increased neutrophil survival: SFb 51.2 ± 6.1%, BMFb 51.1 ± 5.5%, DFb 50.6 ± 4.7%, versus control 16.2 ± 3.3%, P < 0.001. Fibroblast conditioned media reconstituted the survival effect, indicating that a soluble survival factor(s) as opposed to cell–cell contact mechanism is involved in neutrophil survival.
Conclusions Fibroblasts differentially regulate leucocyte subset survival in both a site-dependent and activation-dependent manner. Our results provide an alternative explanation for site-specific differences in the pattern of T-cell and neutrophil accumulation in different chronic inflammatory diseases.
P39
Regulatory T-cell defect in the arthritis-susceptible DBA/1 mouse
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Background DBA/1 mice are susceptible to collagen-induced arthritis and to low-grade spontaneous inflammatory arthritis in elderly males. CD4+CD25+ T cells have been implicated in the suppression of arthritis in the susceptible DBA/1 strain [1,2] and in patients with rheumatoid arthritis [3]. We have studied the function of the CD4+CD25+ T-cell subset in DBA/1 and arthritis-non-susceptible C57Bl/6 male mice.
Methods The frequencies of CD4+CD25+ and CD4+ T cells were assessed in lymph nodes and the spleen of DBA/1 and C57Bl/6 mice by FACs analysis. Spleens were harvested from adult male DBA/1 and BALB/c mice. CD4+CD25+ and CD4+CD25- T cells were purified using Miltenyi reagents and a VarioMACS. Proliferation assays in response to either Concanavalin A (1 µg/ml) or soluble anti-CD3 (0.1–10 µg/ml) were performed using 5 µg CD4+CD25+ cells with 1:5 irradiated adherent splenocytes as antigen-presenting cells. Co-culture of CD4+CD25+ and CD4+CD25- T cells in a 1:1 ratio was used to assess suppression. CD4+CD25+ T cells were used as responders and CD4+CD25- T cells, as targets. Target cells were 51Cr labelled and effector cells were added at either 1:1, 2:1, 4:1, 8:1, 16:1 and 32:1 ratios. Target cells were harvested from inflamed sites such as the rheumatoid synovium. We have found that, although chronic TNF attenuates TCR expression and TCR-proximal signalling, IL-2 expression is suppressed regardless of whether cells are stimulated via the TCR, or with phorbol ester and calcium ionophore to activate the MAPK and NFAT pathways directly. Suppression therefore occurs independently of TCR-proximal effects of TNF [1,2].

P40
Heme oxygenase 1 regulates osteoclastogenesis
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Heme oxygenase 1 (HO-1) plays an important role in vascular disease, transplanta- tion and inflammation. In animal models of acute and chronic inflammation, induction of HO-1 has anti-inflammatory and cytoprotective properties. Since inflammation is an important trigger of osteoclastogenesis, we hypothesized that HO-1 might play a role in osteoclastogenesis.
When HO-1 was induced by hemin in vitro, a significant dose-dependent inhibitory effect on osteoclastogenesis was observed. Hemin primarily inhibited differentiation of mononuclear osteoclast precursors to osteoclasts. These effects were based on a downregulation of the expression of c-fms and RANK, the receptors for mono- cyte-colony stimulating factor and RANKL, whereas MAP kinase, NF-κB or Akt sig- nalling were not affected. In vivo, HO-1 induction prevented endotoxin-induced calvarial bone resorption. Furthermore, assessment of synovial tissue from rheuma- toid arthritis (RA) patients showed expression of HO-1 in monocytes and fibro- blasts, whereas osteoclasts were rarely HO-1 positive. To further assess the role of HO-1 activity in RA patients, we correlated the presence of local bone erosions with serum bilirubin levels. We observed significant higher bilirubin levels in non- erosive than in erosive RA patients. Thus, an increase of HO-1 expression is anti- osteoclastogenic in vitro and might protect from increased bone resorption in vivo.
Acknowledgement This study was supported by the START price of the Aus- trian Science Fund (G5).
P41
How does tumour necrosis factor uncouple T-cell receptor- induced IL-2 gene expression in murine T cells?
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Background T cell receptor (TCR)-induced IL-2 expression is suppressed at the level of mRNA and protein following chronic culture of T cells with tumour necro- sis factor (TNF) at picomolar concentrations, an effect that is reversible upon removal of TNF. This TCR hyporesponsiveness is reminiscent of that of T cells recovered from inflamed sites such as the rheumatoid synovium. We have found, that although chronic TNF attenuates TCR expression and TCR-proximal sig- nalling, IL-2 expression is suppressed regardless of whether cells are stimulated via the TCR, or with phorbol ester and calcium ionophore to activate the MAPK and NFAT pathways directly. Suppression therefore occurs independently of TCR-proximal effects of TNF [1,2].


Available online http://arthritis-research.com/supplements/7/S1
mRNA stability assay Actinomycin D was added and cells harvested over a further 4-h time-course. Total RNA was extracted and probed for IL-2 mRNA by ribonuclease protection assay.

Transcription factor regulation Whole cell lysates were probed for NF-κB and IκB family proteins by immunoblot.

Chromatin remodelling Nuclei were isolated and subjected to limited nucleosome digestion. DNA was extracted and quantitative analysis of target sequences within pII-2 carried out by real-time PCR. An increase in the threshold cycle (Ct) of a target sequence PCR product from activated cells was indicative of stimulation-induced chromatin remodelling.

Results IL-2 mRNA induced via TCR was unstable (t1/2 < 30 min), while PMA and ionomycin stabilised IL-2 mRNA strongly (t1/2 > 2 hours). However, the initial rate of decay was similar in control and TNF-treated cells, suggesting that reduced expression in TNF-treated cells was not due to decreased stability of IL-2 mRNA. c-Rel, IκB and IκBε were regulated differently in control and TNF-treated cells: expression of IκBε was comparably enhanced, while that of c-Rel and IκBβ was attenuated in TNF-treated cells. These altered responses may affect the ability of TNF-treated cells to remodel pII-2 productively through NFκB consensus binding upon cell stimulation [4]. This hypothesis is now being tested by CHART-PCR.

Conclusions Chronic culture of murine T cells in TNF does not alter the stability of IL-2 mRNA induced via TCR, or by PMA and ionomycin, in those cells. However, altered regulation of NF-κB expression and activity in TNF-treated cells may contribute to poor inducibility of IL-2 through effects on stimulus-induced changes in chromatin conformation across pII-2.

References

P42
The invasiveness of fibroblast-like synoviocytes is of relevance for the rate of joint destruction in patients with rheumatoid arthritis and is a patient characteristic

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Objective Rheumatoid arthritis (RA) is characterized by inflammation of synovial joints and degradation of these joints. Fibroblast-like synoviocytes (FLS) are thought to play a rule, because they can invade normal human cartilage in SCID mice [1] and matrigel in vitro [2]. This study was undertaken to investigate the association of these in vitro characteristics with the disease characteristics in patients with RA.

Methods Synovial tissue samples of 72 RA and 50 osteoarthritis patients were obtained; from seven patients with RA, samples of different joints were collected. The FLS invasiveness in Matrigel matrix was studied; the intra-individual and inter-individual differences were compared. The radiological scores of the X-rays of the hands and feet of the patients with the FLS that exhibit the most extreme differences in in vitro ingrowth (most invasive and least invasive FLS) were determined with the Sharp–van der Heijde method to determine the relationship between in vitro invasion data and clinical data.

Results FLS from patients with RA are more invasive than FLS from patients with osteoarthritis (P < 0.001). The intra-individual variation in FLS invasion was much less than the inter-individual variation (P = 0.028; mean difference ± standard deviation, 1204 ± 926 and 3476 ± 2367 for intra-individual and inter-individual variation, respectively), showing that the level of FLS invasion is a patient characteristic. The mean Sharp score of X-rays of the hands and feet of the patients with the most invasive disease (n = 8) was 22.3 ± 0.6, whereas for the patients with the least invasive disease (n = 8) it was 7.6 ± 0.5. This difference was significant by t-test (P < 0.001).

Conclusion The in vitro behaviour of FLS is a patient characteristic given the small intra-individual variation, and is highly correlated with the rate of joint destruction in patients with RA. This suggests that the ex vivo invasive behaviour of FLS from patients with RA is of relevance for the rate of joint destruction in patients with RA.

Acknowledgements TCAF and AHMvdH-vM contributed equally to this work.

P43
A role for IL-7 in regulating CD4+CD25high regulatory T cells

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Background Despite the accumulation of evidence that CD4+CD25high regulatory T cells play an important role in the prevention of autoimmune disease, little is known about how they are regulated in vivo. There are thought to be at least two mechanisms for the generation of regulatory T cells: naturally occurring CD4+CD25high regulatory T cells derive from the thymus, and peripherally-induced regulatory cells arise under tolerogenic conditions. Recently, cytokine activation requirements for CD4+CD25high regulatory T-cell function were associated with IL-7, as well as IL-2 and IL-4. We examined a cohort of patients with rheumatoid arthritis whose disease was well controlled, and where we had previously shown that heterogeneous circulating levels of IL-7 positively correlated with thymic activity, to investigate the role of IL-7 on the function of CD4+CD25high T cells.

Methods Peripheral blood samples were taken from patients with rheumatoid arthritis whose disease was well controlled. Serum IL-7 levels were measured by ELISA. Quantification of the CD4+CD25high T-cell subset was performed using flow cytometry. Thymic activity was evaluated by real-time PCR quantification of T-cell receptor excision circles in CD4+ T cells. Thymidine incorporation assays were used to assess the response of CD4+CD25high T cells to IL-7 stimulation, and also their ability to suppress the proliferation of CD4+CD25− T cells in response to phytohaemagglutinin in co-culture.

Results Circulating levels of IL-7 positively correlated with the frequency of circulating CD4+CD25high T cells (n = 47, R = 0.647, P < 0.0001). This appeared to result from an increased production of these cells by the thymus. High levels of circulating IL-7 in vivo were associated with increased suppressor functions of CD4+CD25high T cells in vitro (n = 5, mean 79% suppression by cells from patients with high IL-7 levels, and 39% suppression by cells from patients with low IL-7 levels). In patients with low circulating IL-7 levels, adding exogenous IL-7 to co-cultures appeared to increase suppression.

Conclusions Our data suggest that IL-7 has a role in regulating CD4+CD25high T-cell number and function. Circulating IL-7 levels are low in active rheumatoid arthritis, and this may be a contributory factor to the reduced size and suppressor function of the CD4+CD25high regulatory T-cell population in this disease.

P44
Results of the Consensus Finding Study Group on Autoantibodies (March 2003–March 2004)

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The European Consensus Finding Study Group on Autoantibodies is currently formed by 43 European laboratories involved in the field of serological diagnostics in rheumatic diseases. The aim of this group is to work towards achieving common consensus in this field: a laboratory result should be the same, wherever the result is obtained.

The Steering Committee of the Consensus Finding Study Group tested 24 candidate sera that had been contributed by the participating laboratories. Ten sera were selected for the annual serum round. This year, special emphasis was put on anti-DNA antibody testing. For this purpose four sera were included that contained different specificities of anti-DNA (Table 1). The remaining six sera were positive for a variety of autoantibodies (Table 1).
**Table 1**

<table>
<thead>
<tr>
<th>Serum</th>
<th>Detected antibodies</th>
<th>Comments</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>dsDNA</td>
<td>Only <em>Crithidia luciliae</em> positive</td>
</tr>
<tr>
<td>2</td>
<td>SS-A 52 kDa + 60 kDa, SS-B</td>
<td>Good consensus</td>
</tr>
<tr>
<td>3</td>
<td>SS-A 52 kDa, SCL-70</td>
<td>SS-A 60 kDa only found by minority</td>
</tr>
<tr>
<td>4</td>
<td>PR-3 ANCA</td>
<td>Very few incorrect results</td>
</tr>
<tr>
<td>5</td>
<td>SS-B</td>
<td>SS-A found by ELISA, counterimmunoelectrophoresis and immunoblot mostly negative</td>
</tr>
<tr>
<td>6</td>
<td>U1-snRNPs, A and C protein</td>
<td>70K negative, good consensus</td>
</tr>
<tr>
<td>7</td>
<td>Centromere (CENP-B)</td>
<td>Good consensus</td>
</tr>
<tr>
<td>8</td>
<td>ssDNA</td>
<td>Perfect consensus</td>
</tr>
<tr>
<td>9</td>
<td>dsDNA</td>
<td>No consensus</td>
</tr>
<tr>
<td>10</td>
<td>dsDNA</td>
<td>Good consensus</td>
</tr>
</tbody>
</table>

For the first time, a dedicated computer program was used to allow more easy data entry and statistical analysis. Next to the 10 sera, a CD-ROM containing 20 Hep-2 cell staining patterns was dispatched to the participating laboratories. The CD-ROM also contained the spreadsheets to be filled in by the participants. Results were returned by 38 out of 43 participating laboratories. The data were discussed at a satellite meeting during the 24th European Workshop on Rheumatology Research in Berlin and were published on the website of the Sanquin Blood Supply Foundation in Amsterdam (via a link distributed to the participants). In depth analysis of individual results compared with the consensus were sent to the participants.

In general, the participants reached a high degree of consensus for most of the samples. The results for anti-dsDNA were very promising. A perfect consensus was reached for the absence of dsDNA antibodies in an anti-ssDNA specific serum (serum B). The absence of false positive results showed that assays measuring anti-dsDNA antibodies have been improved such as to exclude detection of anti-ssDNA. Serum 9 was obtained from a rheumatoid arthritis patient who had been treated with anti-tumour necrosis factor alpha (Infliximab) and developed anti-ssDNA antibodies, yet showed no clinical signs of systemic lupus erythematosus. Using different assays, divergent results were obtained. Most laboratories found anti-dsDNA antibodies by the indirect immunofluorescence technique (substrate *Crithidia luciliae*), whereas anti-ssDNA ELISAs were negative. For this sample most (commercial) Farr assays showed positive reactions. Detailed analysis of the serum in Amsterdam showed the presence of low avidity IgM and IgG antibodies to dsDNA. In order to understand the cause of the discrepancies the influence of choice of assay will be studied in more detail. Divergent results, depending on the method for detection, were also found for antibodies to SS-A. Obviously, ELISA-based techniques were more sensitive. Unfortunately, most ELISAs do not distinguish between anti-SS-A 52 and anti-SS-A 60 antibodies. The clinical relevance of the lower limit of detection has to be established in the future. We will include a more detailed method analysis in the next rounds.

There was general agreement among the participating laboratories that these Consensus Rounds should be continued, including the Hep-2 cell pattern recognition CD-ROM effort. It was decided to focus next round on anti-phospholipid antibodies. For information about the study group please contact Ruud Smeenk {r.smeenk@sanquin.nl}.

### P45

**Effects of overexpression of PAD4 enzyme in mouse synovium**

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**Background** Autoantibodies directed against citrullinated proteins (e.g. anti-CCP) can be detected in rheumatoid arthritis (RA) patients with very high specificity. The antibodies are present already years before the first clinical symptoms and their presence predicts the development of erosive disease. Citrullinated proteins, the target of anti-CCP antibodies, are formed by post-translational deamination of arginine residues, catalyzed by peptidylarginine deiminase enzymes (PADs). PAD enzymes are expressed by cells present in the inflamed joints of RA patients. These data are the basis of our hypothesis that protein citrullination by PAD is intimately involved in the development of RA.

**Objective** To investigate the effect of PAD4 overexpression in synovium of naive mice and in mouse models of arthritis.

**Methods** An adenoviral delivery tool for local expression of mouse PAD4 was successfully constructed. Using this adenoviral construct, PAD4 overexpression was effectuated in cells present in the synovial cavity after intrarticular injection. Effects of PAD4 overexpression in mice with or without co-induction of arthritis (streptococcal cell wall arthritis) were investigated using routine scoring of arthritic features (e.g. swelling) and histology. The presence of citrulline-specific antibodies was measured by ELISA using a synthetic citrullinated peptide (CCP1) and a noncitrullinated control peptide.

**Results** In all naive mice (C57/B16, n = 12) we were able to effectively overexpress PAD4 in the synovial tissue, lasting at least 1 week. This overexpression resulted in the generation of citrullinated proteins in vivo. In mice receiving a control adenovirus no citrullinated proteins were observed. The overexpression did not induce inflammation. Similar experiments in streptococcal cell wall (SCW)-induced mice (C57/B16 + SCW, n = 8) showed a prolonged expression of citrullinated proteins when the knees were preloaded with PAD4 (compared with control adenovirus-treated SCW mice, n = 8), but this did not affect the level of inflammation or tissue damage. Overexpression of PAD4 did not lead to the production of citrulline-specific autoantibodies in these mice.

**Conclusion** Adenoviral expression constructs can successfully be used to introduce PAD enzymes in mouse synovium. Overexpression of PAD4 results in the production of synovial citrullinated proteins, but did not cause additional inflammation in mice nor did it cause an immune response to citrullinated proteins. Generating anti-CCP-positive mice will be crucial in studying the effect of specific immune complexes on arthritic phenomena in mouse models of arthritis.

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### P46

**Long-term survival after lymphocytotoxic monoclonal antibody therapy for rheumatoid arthritis**

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**Background** In the early 1990s, we used the monoclonal antibody alemtuzumab (MabCampath, Schering AG, Berlin, Germany) to treat patients with refractory rheumatoid arthritis. This treatment provided temporary relief of symptoms but was associated with long-term lymphopenia, particularly of T lymphocytes [1]. We continue to follow these patients to exclude any adverse effects of their long-term lymphopenia.

**Objective** The objective of the current study was to compare 10-year mortality in this patient cohort with mortality in a control patient cohort.

**Methods** Fifty-three rheumatoid arthritis patients that received alemtuzumab (median dose, 172 mg; range, 1–420 mg) between 1991 and 1994 (cases) were followed up, compared with 37 among the controls. This provided a mortality rate of 0.045 deaths per person per year for the cases and 0.041 deaths per person per year for the controls. This was not statistically significant (log-rank test, P = 0.73) but it did affect the level of significance the inclusion of cases and controls. In mice receiving a control adenovirus no citrullinated proteins were observed. The overexpression did not induce inflammation. Similar experiments in streptococcal cell wall (SCW)-induced mice (C57/B16 + SCW, n = 8) showed a prolonged expression of citrullinated proteins when the knees were preloaded with PAD4 (compared with control adenovirus-treated SCW mice, n = 8), but this did not affect the level of inflammation or tissue damage. Overexpression of PAD4 did not lead to the production of citrulline-specific autoantibodies in these mice.

**Conclusion** Adenoviral expression constructs can successfully be used to introduce PAD enzymes in mouse synovium. Overexpression of PAD4 results in the production of synovial citrullinated proteins, but did not cause additional inflammation in mice nor did it cause an immune response to citrullinated proteins. Generating anti-CCP-positive mice will be crucial in studying the effect of specific immune complexes on arthritic phenomena in mouse models of arthritis.

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The persistence of abnormal T-cell differentiation patterns predicts relapse in rheumatoid arthritis patients with controlled disease

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Background We previously demonstrated abnormal T-cell differentiation in rheumatoid arthritis (RA) and hyperproliferation of T cells in relation with inflammation. However, it is still not clear whether these T-cell dysfunctions are a primary feature of RA or are only secondary to inflammation. We therefore analysed RA patients in clinical remission in whom systemic inflammation was controlled.

Methods Patients were defined as in remission when they had controlled disease, with no change of activity for at least 6 months, C-reactive protein below 15, no swollen or tender joints and on stable treatment. Relapse was defined as a change in disease activity sustained for at least 3 months, requiring or not a change in treatment. Flow cytometry was used to assess T-cell differentiation pattern in controls (n = 23), active RA (n = 28) and remission (n = 34). CD4+ T-cell proliferation assay in response to mitogen, IL-2, and antibody stimulation in eight paired blood samples for active and remission disease. Statistical analysis was used to seek clinical and laboratory correlate to differentiation abnormalities.

Results The abnormal differentiation patterns observed in active disease were maintained in remission. The first inflammation-associated subset was persistent. The second atypical subset was never observed in health, poorly represented in active disease but largely accumulated in remission. The hyperproliferation associated with the first subset was lost in remission and was therefore driven by inflammation. The second atypical subset was associated with profound hyporesponsiveness in both active and remission disease. Relapse occurred in 13 out of 32 patients within 12 months of follow-up. Relapse was associated with a higher frequency of the inflammation-related cells (P = 0.017). We proceeded to a complete analysis of factors that could predict relapse. Only rheumatoid factor positivity (P = 0.033) and possibly having nodules (P = 0.079) were associated with relapse. Using a regression analysis revealed that the frequency of inflammation related cells was highly significant in predicting relapse, being correct in 78% of cases (P = 0.025). Neither the presence of rheumatoid factor or nodule improved this model.

Conclusions These results suggest that the hyper-reactivity of the inflammatory subset is associated with disease activity; however, its persistence in the absence of inflammation suggests a primary defect possibly in activation-induced cell death. The second subset appear fairly inactive, but more work is necessary to fully characterise these cells. Its complete absence in health and accumulation in disease remission also suggests a primary defect in T-cell differentiation pathways in RA.
P50
Identification of the EGF-TM7 receptor EMR2 and its ligand dermatan sulphate in rheumatoid synovial tissue
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Introduction EMR2 is a member of the EGF-TM7 family closely related to CD97. Chondroitin sulphates have recently been identified as ligands for EMR2 and CD97. Chondroitin sulphates have been implicated in the pathogenesis of rheumatoid arthritis (RA). The objective of this study is to determine the expression of EMR2 and the distribution of EMR2 and CD97 ligands in RA synovial tissue.
Methods Synovial tissue samples were obtained by arthroscopy from patients with RA (n = 19), inflammatory osteoarthritis (n = 13), and reactive arthritis (n = 13). Immunohistologic staining was performed with EMR2 mAb and stained synovial tissue sections were analysed by digital image analysis. Co-expression of EMR2 with lineage and activation markers was determined by double immunofluorescence microscopy. To evaluate the expression of EMR2 and CD97 ligands in RA synovium, binding assays using fluorescent beads loaded with EMR2-Fc or CD97-Fc constructs were performed.
Results EMR2 expression in the synovial sublining was significantly higher in RA compared with disease controls. Most EMR2-positive cells were macrophages and dendritic cells, expressing co-stimulatory molecules and tumour necrosis factor alpha. Dermatan sulphate was shown to be the ligand of the largest isoform of EMR2 and CD97 in rheumatoid synovium. In addition, the smaller isoforms of CD97, but not EMR2, bound CD55 on fibroblast-like synoviocytes.
Conclusion The EGF-TM7 receptor EMR2 and CD97 are abundantly expressed on myeloid cells in synovial tissue of RA patients where they encounter their ligands dermatan sulphate and CD55. These interactions might facilitate the retention of activated macrophages in the synovium.

P51
Prevalence and specificity of autoantibodies to defensins in sera of patients with systemic autoimmune diseases
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Background Defensins are small positively charged peptides (29–47 amino acids) that are abundant in leukocytes and play a role in host defense against bacteria and viruses. There are two categories of defensins: A-defensins are that are highly conserved among species and play a role in host defense against bacteria and viruses. There are two categories of defensins: A-defensins are secreted from human neutrophils, and B-defensins are produced from the epithelial cells. Each peptide contains six cystein amino acid residues, connected with disulfide bonds. The physicochemical properties of defensins are similar with the properties of another molecule, B2-glycoprotein I (B2-GPI), the major target of the autoantibodies found in the sera of patients with antiphospholipid syndrome (APS).
Objective We investigated whether sera from patients with APS as well as primary Sjogren Syndrome (pSS), systemic lupus erythematosus (SLE), and rheumatoid arthritis (RA) contain autoantibodies that react with defensins.
Methods We synthesized the linear peptides NH2-ACYPVRPPACAGGERRYTGQYOGRLWAFCC-OH and NH2-GIGDPVTLCKSAIGCHVFPQPRYKQXGTGLGPTKC-CKKP-OH, corresponding to the amino acid sequences of the mature forms of A1 (defA1) and B2 (defB2) defensins, respectively. These peptides were oxidized, in CKKP-OH, corresponding to the amino acid sequences of the mature forms of A1 (defA1) and B2 (defB2) defensins, respectively. These peptides were oxidized, in order for the disulfide bonds of the native molecules to be created, and subsequently were lyophilized. The peptides were dissolved in water and they were tested in ELISA experiments against sera from patients with APS (n = 24), pSS (n = 24), SLE (n = 16), and RA (n = 8). Additionally, sera from normal individuals were tested. Homologous inhibition experiments were performed in order to examine the specificity of the immune response against defensins.
Results None of the tested sera reacted against the defA1. Sera from patients with systemic autoimmune diseases contained autoantibodies to defB2 as follows: 21% of patients with APS and 25%, 31%, and 12% of the sera from the patients with pSS, SLE, and RA, respectively, gave a positive reaction against the same peptide. The normal sera reacted with the peptides at all. In the inhibition experiments the defB2 peptide, when it was used as soluble inhibitor, inhibited the binding of the antibodies at the plate-bound defB2 by 64%.
Discussion Defensins are components of the innate immunity and share common physiochemical properties with the B2-GF1 protein. A rather small proportion of sera from patients with systemic autoimmune diseases contain antibodies that react specifically with the defB2 peptide. The presence of these autoantibodies is not disease specific and their pathogenic significance, if any, remains to be elucidated.

P52
Tumor necrosis factor alpha reverses the immunosuppressive properties of mesenchymal stem cells in collagen-induced arthritis
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Background Mesenchymal stem cells (MSCs) are bone-derived progenitor cells widely investigated for their potential of differentiation towards multiple lineages, such as osteocytes and chondrocytes. Recently, we and others showed that MSCs exhibit immunosuppressive properties inducing in vivo tolerance of T lymphocytes towards allogeneic cells. Moreover, these cells can be easily genetically modified to express ectopic molecules, such as anti-inflammatory cytokines.
Objective Here, we investigated whether naïve and IL-10-expressing MSCs could display an inhibitory effect towards self-reactive T lymphocytes in vitro and have a biological effect in the murine model of collagen-induced arthritis (CIA).
Methods We used the murine C3H10T1/2 cell line (C3 MSCs) in the CIA murine model of RA. We injected various doses of MSC at immunization or at boost and evaluated the clinical and immunological parameters. Immunosuppressive properties of MSC were determined in vitro in mixed lymphocyte reactions.
Results We evaluated the potential immunosuppressive role of MSCs in the CIA model and showed that MSCs did not display any benefit whatever the day of cell injection (day 0 or day 21) and the numbers of MSCs (105 or 4 x 105). Both clinical and immunological analysis argued for the accentuation of the Th1 helper response. Using luciferase-expressing MSCs, we were unable to detect labeled cells in the articular environment of the knee, suggesting that worsening of the symptoms was unlikely due to the homing of MSCs in the joints. Experiments in vitro showed that addition of tumor necrosis factor alpha was sufficient to reverse the immunosuppressive effect of MSCs on T-cell proliferation and this observation was associated with an increase of IL-6 secretion.
Conclusion Here, we demonstrated that the immunosuppressive properties of MSCs did not provide any clinical benefit in CIA. Our data suggest that environmental parameters, in particular inflammation, may influence the immunosuppressive properties of MSCs.

P53
Neutralizing IL-17 during re-activation of experimental arthritis prevents joint inflammation and bone erosion by decreasing RANKL and IL-1
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Background Rheumatoid arthritis is characterized by an intermittent course of the disease with alternate periods of remission and relapse. T cells, and in particular the T-cell cytokine IL-17, are expected to play an important role in the flare-up of arthritis.
Objective To study the role of T-cell IL-17 in flare-up of experimental arthritis.
Methods Antigen-induced arthritis was induced in C57Bl/6 mice by immunizing and boosting with mBSA/ complete Freund’s adjuvant, and subsequent intra-articular injection of 60 µg mBSA. At week 4 of arthritis, 2 µg mBSA was injected into the articular joint to induce a flare-up of the smouldering inflammation. To study the role of IL-17 in this flare-up, neutralizing rabbit-anti-mouse-IL-17 antibodies (or control antibodies) were injected 2 hours prior to antigen rechallenge. Results Quantitative PCR at various time points after arthritis induction showed that IL-17 mRNA expression was already upregulated at day 1, increased even more at day 2 and day 7, and clearly diminished at day 21. After antigen rechallenge, IL-17 mRNA expression rapidly increased, peaking at 4 hours with a 250-fold upregulation compared with naive mice.
Neutralizing IL-17 significantly prevented joint swelling, as measured by 99mTc uptake at day 1 (Fig. 1a). Arthritis knee joints were isolated at day 4, and histological analysis showed significantly suppressed joint inflammation (Fig. 1b) and cartilage proteoglycan depletion in the anti-IL-17-treated group. Blocking IL-17 also clearly protected arthritic mice against bone erosions (Fig. 1c). IL-17 mRNA expression rapidly increased, peaking at 4 hours with a 250-fold upregulation compared with naive mice.
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P54

Functional Toll-like receptor 9 modulates the activity of bone marrow B cells isolated from rheumatoid arthritis patients

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Background Toll-like receptors (TLRs), a family of pathogen recognition receptors, represent an important component of the innate immune system that also contributes to the development of acquired immunity. TLR9 expressed in the cytoplasm of several cell types including B cells, and recognize and are activated by unmethylated CpG-rich, pathogen-derived DNA sequences. This CpG stimulation triggers B-cell proliferation and promotes Th1 response. Moreover, DNA containing CpG-rich motifs, acting as polyclonal stimuli, participates in the maintenance of serological memory by human memory B cells. Recent data indicate that bone marrow in rheumatoid arthritis (RA) patients may actively participate in the pathogenesis of RA as a secondary lymphoid organ via overproduction of proinflammatory cytokines and a site of effective antigen presentation.

Objective To test the hypothesis that RA bone-marrow-derived B cells express functional TLR9.

Methods Bone marrow mononuclear cells (BMMC) were isolated from RA bone marrow samples obtained during joint replacement surgery. The expression of TLR9 protein on B lymphocytes, gated as CD19-positive cells in BMMC preparation, was assessed by intracellular staining and flow cytometric analysis. BMMC were stimulated in vitro with agonistic (CpG-ODN) or control (GpC-ODN) oligodeoxynucleotides (15–30 μg/ml). In blocking experiments chloroquine (2–3 μg/ml) was added to the culture 50 min before stimulus. The expression of activation markers CD86 and CD54 on B lymphocytes (CD19+) were analyzed after 48 and 72 hours in culture using flow cytometry. Ki-67 and CFSE staining (flow cytometry) was applied to evaluate B-cell proliferation after 72 and 120 hours of culture with oligodeoxynucleotides. The concentrations of oligodeoxynucleotides and chloroquine used in experiments were not toxic to BMMC as judged by colorimetric lactate dehydrogenase assay. The presence of bacterial DNA in bone marrow plasma and BMMC was evaluated by DNA extraction and PCR amplification. Primers used for PCR recognize highly conserved regions of the eubacterial 16S-ribosomal RNA gene.

Results RA bone-marrow-derived B lymphocytes express TLR9 protein that could be detected via intracellular staining and flow cytometric analysis. Importantly, these TLR9 are functional. CpG-ODN, but not control GpC-ODN, in a dose-dependent manner enhanced the expression of activation markers (CD86 and CD54) on B cells in BMMC cultured in vitro. The specificity of CpG-ODN triggered expression of CD86 was confirmed in experiments where cells cultured in the presence of chloroquine, a known inhibitor of TLR9-triggered signal transduction, failed to respond to CpG-ODN. Moreover, CpG-ODN triggers bone marrow B-cell proliferation in vitro, as judged by enhanced expression of proliferation marker Ki-67 and a diminished level of CFSE dye. Interestingly, our preliminary data indicate the presence of bacterial DNA in several samples of bone marrow tissues isolated from RA patients. We could amplify DNA encoding bacterial 16S-ribosomal RNA in one bone marrow plasma and three BMMC out of five analysed samples.

Conclusions Our results indicate that CpG oligodeoxynucleotides, the potent agonists of TLR9, modulate the activity of B cells from bone marrow of RA patients via induction of costimulatory and adhesion molecules (CD86, CD54) expression, and via cell proliferation. Thus, our data suggest that bone marrow of RA patients may represent an important secondary lymphoid organ that actively participates in the pathogenesis of RA.

P55

BiP induces IL-4-dependent regulatory T cells

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Background Previously we have described the stress protein BiP as a putative autocrine/IgG regulating cytokine in RA [1]. The administration of BiP intravenously (i.v.) prior to induction of collagen-induced arthritis (CIA) resulted in almost complete amelioration of disease [1]. Our studies now indicate that BiP has several immunomodulatory actions including the skewing of T-cell differentiation towards Th2 [2].

Aim This study focused on the therapy of CIA and investigated subcutaneous administration of BiP in comparison with intravenous administration and whether adoptive transfer of BiP-treated cells could successfully inhibit the onset of disease. Finally, IL-4 knockout mice were used to determine the importance of the T cell in the therapeutic role of BiP.

Methods CIA was induced in DBA-1 mice by injection of bovine collagen type II (CII) in complete Freund’s adjuvant followed by a booster injection in incomplete Freund’s adjuvant at day 21. At the first appearance of swollen joints, the mice were injected subcutaneously (s.c.) with BiP, a control protein, BSA or vehicle control (PBS). Disease progression was followed by measurement of swollen joints. At termination, splenocytes and draining lymph node cells were removed and T-cell cytokine secretion was assessed. Mixed spleens and lymph nodes from groups of DBA-1 mice that had been immunized s.c. with BiP or BSA (200 μg), or i.v. with BiP or BSA (10 μg), were collected 12 days after immunization. Cell cultures (2.5 × 10^6 cells/ml) were set up with 20 μg of the respective protein (BiP or BSA) for 5 days. Cells were then washed and injected intraperitoneally into DBA-1 mice (20 × 10^6 cells/mouse) that had received the first CII immunization 24 days previously. DR1-/- IL-4 knockout mice, (n = 20) developed by backcrossing C57Bl/6 IL-4-/- mice to DR1+/- mice, were immunized with CII, and on day 24 after immunization were given 10 μg BiP i.v. Wild-type HLA-DR1+/- transgenic mice (n = 20/group) were administered 10 μg BiP or PBS i.v.

Results Administration i.v. or s.c. of BiP significantly reduced (P < 0.05) the incidence and severity of CIA when given at the onset of disease. A lower incidence of arthritis was also recorded from groups of mice treated with BiP s.c. and i.v. (37.5% and 64%, respectively) as compared with 100% recorded from the control group by day 70. T cells removed from mice that had been treated with BiP via both routes were shown to secrete IL-4 in response to CII, results indicated upregulation of IL-5 and IL-10 production from BiP-treated groups compared with the articular control group. In the adoptive transfer studies the mice receiving subcutaneous BiP-primed cells had a significant suppression of arthritis by day 48, and by day 66 in those receiving intravenous BiP-primed cells, compared with mice that had received BSA-primed T cells (P = 0.05). When the IL-4-/- mice were scored for disease severity the IL-4-/- mice treated with BiP were no different from wild-type mice treated with PBS whereas wild-type mice treated with BiP had a significant suppression of arthritis (P ≤ 0.05, Students t-test).
Conclusion These findings suggest that treatment of CIA with BIP is mediated at least in part by induction of IL-4-dependent regulatory T cells.

References

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P56
High-dose chemotherapy and syngeneic stem cell transplantation in a patient with refractory rheumatoid arthritis: poor response associated with persistence of synovial abnormalities
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Background High-dose chemotherapy (HDC) and stem cell transplantation (SCT) is an experimental treatment option for patients with refractory rheumatoid arthritis (RA). The re-infusion of stem cells with a possible intrinsic cell defect may be the cause for disease relapse despite increased sensitivity to disease-modifying anti-rheumatic drugs (DMARDs). This can be avoided by a syngeneic transplantation with healthy stem cells from an identical sibling.

Objectives We treated a 44-year-old woman, who had seropositive, erosive RA, with HDC and syngeneic SCT from her healthy identical twin sister. The patient had undergone multiple joint operations and had become refractory to conventional DMARDs, etanercept and infliximab.

Methods Outcome measures were DAS 28, rheumatoid factor titer (lgM), need for DMARD therapy and synovial inflammation for which tissue was obtained at baseline, 2, 3 and 6 months through knee arthroscopy. Stem cells from the donor were mobilized with filgrastim and collected by leukapheresis on day –1 and 0. Before conditioning, infliximab, methotrexate and prednisone were discontinued and the patient was discharged on day 14 without joint complaints. After 1 month disease activity flared accompanied by an acute phase response. Despite maintenance therapy with 10 mg prednisone and re-institution of methotrexate up to 22.5 mg/week she had continued active disease up to 1 year after SCT (Fig. 1). Synovial biopsies at all timepoints showed a marked infiltration of neutrophils and plasmacells, even 2 months after HDC. Immunohistological staining showed infiltration of activated T cells (CD8+), B cells (CD19+) and plasma cells (CD138+). Discussion HDC and syngeneic SCT did not result in remission of RA. The persistence of RF, anti-CCP (gG) and plasma cells in the synovial tissue suggests host plasma cells were not eradicated by cyclophosphamide, nor replaced by donor plasma cells (rheumatoid factor and anti-CCP negative).

P57
Expression of IL-18 in muscle tissue of patients with treatment-resistant idiopathic inflammatory myopathies
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Background Idiopathic inflammatory myopathies, myositis, are characterized by infiltrates of T lymphocytes and macrophages in muscle tissue. Some patients with myositis are very resistant to immunosuppressive treatment. Thus new therapies are urgently required. An increased knowledge of the key molecular mechanisms in myositis would be important for development of new targeted therapies for these patients. IL-18 is a pleiotropic cytokine with proinflammatory and immunoregulatory effects. It has been shown to play an important pathogenic role in various autoimmune disorders (e.g. rheumatoid arthritis and Sjögren’s syndrome). Whether IL-18 has a role in disease mechanism in myositis is not known.

Objective To study the expression of IL-18 in muscle tissue of patients with idiopathic inflammatory myopathies.

Methods Thirteen treatment-resistant patients, six polymyositis, four dermatomyositis, one juvenile dermatomyositis, and two inclusion body myositis with signs of active muscle inflammation, were included in our study. Muscle biopsies were investigated by immunohistochemistry using monoclonal antibodies against IL-18.

Results Intracellular IL-18 expression was detected in all patients with polymyositis, dermatomyositis, and inclusion body myositis with signs of active muscle inflammation, were included in our study. Muscle biopsies were investigated by immunohistochemistry using monoclonal antibodies against IL-18.

Conclusion This is the first study to demonstrate IL-18 expression at the protein level in muscle tissue from patients with idiopathic inflammatory myopathies. This was a consistent finding in mononuclear inflammatory cells in all three subsets of patients with treatment-resistant disease. These results suggest that IL-18 could have a role in the immunopathogenesis of myositis.

P58
Evaluation of chondrocyte micromass culture for the study of cartilage degradation
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Background An understanding of the mechanisms involved in cartilage degradation that occur in rheumatoid arthritis and osteoarthritis is essential for the development of treatments to block disease progression. Culturing chondrocytes to synthesize a cartilage matrix would ideally provide a cartilage matrix of consistent composition that would reproducibly respond to different stimuli. When cultured in monolayers, chondrocytes convert to a fibroblastic morphology and gradually lose their native phenotype, no longer able to synthesize type II collagen and aggrecan. However, when chondrocytes are cultured at a high density in the presence of growth factors, the chondrocytes regain their native phenotype and maintain a cartilage morphology [1].

Objective To optimise the culture conditions for chondrocyte micromass synthesis of matrix components, and to evaluate the response of the culture to cytokine stimulation by measuring the degradation of matrix components.

Methods Chondrocytes extracted from bovine nasal cartilage were passaged several times to produce substantial cell stocks. Harvested cells were resuspended at 2 × 106 cells/ml and seeded in the centre of each well of a 48-well plate (20 μl/well). Cultures were maintained in a serum-free medium with or without ITS (insulin, transferrin and selenium), ascorbic acid, and transforming growth factor-β (TGF-β) and dexamethasone (DEX). Cultures were maintained in a serum-free medium with or without ITS (insulin, transferrin and selenium), ascorbic acid, and transforming growth factor-β (TGF-β) and dexamethasone (DEX).
growth factor beta 1 (TGFβ1) for 14–21 days. Histological analysis of the micromass cultures examined the presence of proteoglycans and type II collagen. The effects of cytokine stimulation with IL-1, oncostatin M (OSM) and the combination of both cytokines on matrix degradation were tested by analysing proteoglycan and collagen release. Collagenase activity was measured by bioassay. Results Both ITS and ascorbic acid were necessary for maximum collagen incorporation into micromass cultures. Collagen and proteoglycan incorporation increased with increasing TGFβ1 concentration and increasing culture duration, maximum incorporation detected when TGFβ1 was used at 30 ng/ml and cultures were maintained for 21 days. Histology showed that both proteoglycans and type II collagen were present throughout the chondrocyte micromass matrix. When micromass cultures were stimulated with IL-1, OSM and IL-1/OSM for 14 days, proteoglycan release was greater compared with control, but there was no difference for collagen release (see Fig. 1). Active collagenase levels were negligible, although high levels of pro-collagenase were detected.

Conclusion The chondrocyte micromass cultures synthesized a matrix that contained proteoglycan and type II collagen. The micromass culture may serve as a good model for studying proteoglycan but not collagen degradation.

Reference


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**P59**

A link between complement activation and anti-SSA in immune complex-induced cytokine production in systemic lupus erythematosus

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Background We have earlier shown that polyethylene glycol (PEG)-precipitated immune complexes (IC) from systemic lupus erythematosus (SLE) patients can induce IL-10 and IL-6 production from peripheral blood mononuclear cells. SLE is associated with IC-induced classical complement activation. Autoantibodies together with autoantigens released from apoptotic cells partly explain the IC formation. We therefore wanted to investigate how complement activation and levels of autoantibodies correlate to the amount of circulating IC and IC-induced cytokine production.

Others have previously shown an inverse correlation between IL-10 and IL-12 in SLE and we have shown that the degree of complement activation affects IC-induced IL-10 and IL-12 in different ways. A second aim was to investigate the effect of the SLE IC on the production of IL-10 and IL-12.

Methods In total 195 SLE samples were investigated. Levels of autoantibodies (anti-nuclear antibodies, anti-DNA, SSA, SSB, RNP and Sm) were known for 116/195 samples. In a first study we investigated 19 patients with paired serum samples obtained at different occasions and mostly showing activation of the classical complement pathway. Here we primarily wanted to evaluate the effect of disease activity on IC-induced cytokine production. In a second study 78 samples with normal classical complement function and known autoantibody status were studied. Samples were PEG-precipitated and 10% PEG precipitates were added to serum-free cultures of normal peripheral blood mononuclear cells, and the levels of IL-10, IL-6 and IL-12p40 were measured in the supernatants after 20 hours. Classical complement pathway function, levels of C2, C3 and circulating IC were measured in all samples.

Results In paired analysis, increased complement activation (lowered classical function and raised C3d/C3 ratio) was associated with increased IL-10 production (P = 0.046). For IL-6 there was a parallel but non-significant trend. Decreased C3 levels were also associated with increased IL-12 production (P = 0.03). When investigating these complement-activating sera in cross-section we found increased IL-10 levels in ENA+ (P = 0.03) and DNA+ samples (P = 0.046) compared with ENA- and DNA- samples with the largest impact of anti-SSA/SSB (P = 0.02). The same pattern was found for IL-6. In sera with normal complement levels there was no association between anti-body status and IL-10 production, but IL-12 levels were increased in ENA+ cultures (P = 0.01) and linked to anti-SSA/SSB (P < 0.0001). There was no association to anti-DNA.

Circulating IC in serum and PEG IC-induced IL-10 production correlated in samples from active SLE (r = 0.55, P = 0.003), and we therefore used circulating IC as a surrogate marker for IC-induced IL-10 production in statistical evaluation of all sera with known antibody status. In analysis of variance with circulating IC as the dependent variable we found a strong interaction between decreased complement function and the occurrence of ENA, especially anti-SSA (complement P < 0.0001, anti-SSA P = 0.0001, interaction P = 0.002). Anti-DNA showed no association.

Conclusion We have found a link between classical complement activation, levels of circulating IC and induction of the cytokines IL-10, IL-6 and IL-12 with strong interaction between complement activation and presence of autoantibodies, notably anti-SSA. We hypothesize that, in quiescent SLE, autoantibodies circulate in monomeric form. In active SLE apoptotic cells release SSA forming IC with circulating anti-SSA, with subsequent induction of cytokines like IL-10. PEG-precipitated SLE IC induce the production of IL-10 and IL-12 with parallel patterns depending on complement and autoantibodies. Inverse regulation of IL-10 and IL-12 in SLE therefore does not seem to depend on SLE-specific IC.

**P60**

The value of serum type II collagen epitope measurement in assessing early clinical response to treatment with anti-tumour necrosis factor alpha therapy in rheumatoid arthritis

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Introduction Current guidelines on the use of anti-tumour necrosis factor alpha (anti-TNF-α) therapies in rheumatoid arthritis (RA) recommend a 3-month trial of the drug before a clinical assessment of treatment efficacy can be made. The serum level of the type II collagen propeptide, C2C, is specific for the destruction of type II collagen by the collagenases MMP-1, MMP-8 and MMP-13. Previously we have shown that the ratio of C2C/CPII is increased in osteoarthritis and correlates with cartilage destruction. The current pilot study assessed the utility of serum measurement of C2C and CPII in predicting early response to treatment with anti-TNF-α therapy in a group of 20 RA patients.

Method Twenty patients were assessed before commencement of either infliximab (n = 8) or etanercept (n = 15) therapy, and at 1-month and 3-month time-points after therapy was commenced. Measurements of 28 swollen and tender joint counts for DAS82 score, erythrocyte sedimentation rate (ESR) and C-reactive protein (CRP) were taken at the time of each assessment. Additional serum was collected for measurement of CPI and C2C by ELISA. The change in serum levels of ESR, CRP, C2C, CPII and a ratio of C2C:CPII between 0 and 1 month was calculated, and then correlated with clinical outcomes at 3 months to assess their predictive value, using the Spearman Rank Correlation Coefficient.

Results The median DAS82 score fell from 6.20 to 3.74 following 3 months of treatment (P = 0.0004, Wilcoxon Sign Rank Test). The change in C2C:CPII at 1 month of therapy was more closely associated with the change in swollen joint count at 3 months (P = 0.16) than either CRP (P = 0.62) or ESR (P = 0.94). The change in C2C:CPII at 1 month was more closely associated with tender joint count at 3 months (P = 0.19) than either the ESR (P = 0.59) or CRP (P = 0.52). One-month changes in C2G and CPII when used individually were not predictive of swollen joint count at 3 months (P = 0.55 and P = 0.74, respectively) or tender joint count at 3 months (P = 0.4 and P = 0.8, respectively).

Conclusion The ratio of C2C:CPII appears to offer a better method of predicting early response to biological therapy than the standard acute phase markers CRP.

**Figure 1**

Cytokine Stimulated Release of Chondrocyte Micromass Matrix Components

<table>
<thead>
<tr>
<th>% Release</th>
<th>Control</th>
<th>IL-1</th>
<th>OSM</th>
<th>IL-1/OSM</th>
</tr>
</thead>
<tbody>
<tr>
<td>Proteoglycan</td>
<td>50%</td>
<td>60%</td>
<td>70%</td>
<td>80%</td>
</tr>
<tr>
<td>Collagen</td>
<td>30%</td>
<td>40%</td>
<td>50%</td>
<td>60%</td>
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</tbody>
</table>

The effect on proteoglycan and collagen release when bovine nasal chondrocyte micromass cultured for 14 days in serum-free medium supplemented with 25 ng/ml transforming growth factor beta 1 and then stimulated for 14 days with IL-1 (1 ng/ml), oncostatin M (OSM) (10 ng/ml) and IL-1/OSM combination (1/10 ng/ml). A significant difference with control was identified by Student's t test, *** P < 0.005.
and ESR. Measurement of the C2C2/CPII ratio may more closely reflect cartilage changes in RA through measurement of both the synthesis and destruction of type II collagen. A further trial with larger patient numbers is required to fully assess the utility of this measure in predicting outcome to therapeutic intervention in the treatment of RA.

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Oncostatin M in rheumatoid arthritis: a key cytokine acts synergistically with other proinflammatory cytokines to promote human cartilage loss

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Introduction Oncostatin M (OSM), an IL-6 type cytokine, is raised in the rheumatoid arthritis (RA) joint and correlates with markers of inflammation and cartilage destruction. This study explores the mechanistic role of OSM in cell adhesion, angiogenesis and matrix degradation.

Methods Microvascular endothelial cells (EC), primary RA synovial fibroblasts (SFC), synovial explant culture and RASF/C normal cartilage co-cultures were stimulated with OSM (20 ng/ml) ± IL-1 (5 ng/ml). Cell proliferation, cell adhesion molecule expression, tubule formation, cell migration and matrix degradation were assessed by proliferation, flow cytometry, matrigel angiogenesis and ELISA assays.

Results OSM stimulated EC/RASF (basal = 0.9/0.56 to 1.56/1.94; P < 0.05, day 4) alone but demonstrated a synergistic effect in the presence of IL-1 (P < 0.01). OSM and IL-1 increased intercellular adhesion molecule expression, with no effect on vascular cell adhesion molecule or platelet endothelial cell adhesion molecule. OSM had an additive effect with IL-1 on intercellular adhesion molecule expression (P < 0.05). OSM increased EC tubule formation (basal = 20 ± 1.5 to 47 ± 3.7; mean ± standard error, P < 0.01), and increased EC migration (basal = 1.26 ± 0.11 to 1.87 ± 0.187; P < 0.05). OSM synergistically increased TIMP-1 production in EC, SFC and synovial explants in the presence of IL-1, with no effect on u-PA or urokinase (type plasminogen activator) receptor expression. OSM and IL-1 stimulated MMP-1 and MMP-13 expression in cartilage and SFC alone (P < 0.05) but had a significant threefold synergistic induction when cultured together (P < 0.01). Cartilage sections stained with safranin-O demonstrated almost complete depletion of proteoglycan expression in RASF/C/cartilage co-cultures following 4 weeks incubation with IL-1/OSM. This was reflected in the supernatants where IL-1 and OSM together synergistically increased GAG release from a basal level of 3.5–9.1 (µg GAG/mg cartilage weight) compared with either IL-1 or OSM alone.

Conclusion OSM plays a critical role in RASF/C activation and cartilage invasion, also promoting angiogenesis. Its ability to act synergistically with other proinflammatory cytokines such as IL-1 further supports a key role for OSM in RA.

P63

Influence of HLA-DR genes on the production of rheumatoid arthritis-specific autoantibodies to citrullinated fibrin

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Rheumatoid arthritis (RA), a chronic inflammatory joint disease, develops in patients expressing particular HLA-DR alleles. RA patients’ sera contain antibodies to a post-translationally modified form of fibrin on which arginyl residues are transformed in citrulline.

We tested whether HLA-DR alleles influence the production of anti-citrullinated fibrin antibodies in RA patient sera and whether the replacement of arginyl residues by citrullyl residues on fibrin peptides could modify their binding to RA-associated HLA-DR molecules and their recognition by T cells in RA patients and controls.

We found that RA-associated HLA-DR alleles are also associated with presence of anti-citrullinated fibrin antibodies in RA patient sera. Multiple peptides from the alpha and beta chain of fibrin are capable to bind many HLA-DR alleles. RA-associated HLA-DR alleles are good fibrin peptide binders. However, citrullination does not influence fibrin peptide binding to HLA-DR or fibrin peptide recognition by T cells.

Finally, peripheral blood T cells that recognize native or citrullinated fibrin peptides are common in RA patients and very uncommon in normal controls. These results suggest that citrullination of fibrin has nothing to do with peptide/HLA-DR/T cell interaction and is merely involved in the definition of B-cell epitopes.

P62

Methotrexate, through adenosine release, downregulates tumor necrosis factor alpha-induced synovial fibroblast IL-15 expression and proliferation

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Background Tumor necrosis factor alpha (TNF-α) is found at high concentrations in the rheumatoid joint and induces upregulation of synovial fibroblast IL-15, a cytokine known to induce fibroblast proliferation through an autocrine loop. The mechanism of action of low-dose oral methotrexate (MTX) is not well understood. By inhibiting AICAR transformylase, MTX has been described to induce the extra-cellular release of the potent anti-inflammatory autacoid adenosine.

Objective To test the effect of MTX on TNF-α-induced synovial fibroblast IL-15 expression and proliferation.

Methods Synovial fibroblasts (Sfib) isolated from surgical specimens of rheumatoid arthritis (RA) patients (n = 10) were cultured in six-well plates. Sfib were stimulated with 10 ng/ml TNF-α and pretreated for 2 hours with medium or MTX at varying doses (0, 0.01, 0.1, 1, 10 µM) in the presence or absence of adenosine deaminase, DPCPX (adenosine A1 receptor antagonist) or DMX (adenosine A2 receptor antagonist). Surface and intracellular IL-15 protein were determined by immunofluorescence and flow cytometry. IL-15 mRNA was measured by real-time quantitative RT-PCR in a LightCycler instrument (Roche). Sfib proliferation was evaluated using the alamar blue bioassay.

Results TNF-α induced an upregulation of intracellular and surface IL-15 protein expression and of IL-15 mRNA, together with an increased Sfib proliferation rate. Sfib proliferation was significantly inhibited by a neutralizing anti-IL15 monoclonal antibody but not by an isotype control antibody. In the presence of MTX, TNF-α-induced IL-15 upregulation and Sfib proliferation were reduced by 40–85% in a dose-dependent manner. Adenosine deaminase reversed the effects of MTX as did addition of DMX but not DPCPX 1 hour prior to MTX.

Conclusion MTX interferes with TNF-α-induced synovial fibroblast IL-15 upregulation and proliferation. This effect seems to be mediated through adenosine release and adenosine A2 receptor engagement. This may be a mechanism by which MTX controls the aggressive behavior of synovial fibroblasts in RA.

Acknowledgements This work was supported by Ministerio de Educación y Ciencia Programa Ramón y Cajal (EM) and Ministerio de Educación y Ciencia grant SAF 2003-01670 (EM and MG).

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Bone marrow as a secondary lymphoid organ: mature T-cell subsets in bone marrow from rheumatoid arthritis and osteoarthritis patients

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Introduction Recent data indicate that bone marrow plays an important role not only as a primary lymphoid organ responsible for haemopoiesis, but also as a secondary lymphoid organ with capability of antigen presentation exceeding that of lymph nodes. Although in chronic inflammatory/immune disease, like rheumatoid arthritis (RA), bone marrow participates in the initiation and/or perpetuation of the disease, there is little information about the real number of lymphocyte subpopulations in the bone marrow of these patients and how they can be modulated by T-cell growth factors. IL-15 acting through IL-15 receptors (including high-affinity IL-15R alpha chain) is a key cytokine influencing the development of natural killer cells in bone marrow, and proliferation and maintenance of the memory CD3+ cell pool. However, there is no information about the levels of IL-15 in bone marrow.

Objectives To compare the real cell numbers within lymphocyte subsets in bone marrow isolated from RA and osteoarthritis (OA) patients. To measure the levels of soluble IL-15 and surface-expressed IL-15R alpha in bone marrow plasma and cells, respectively. To analyze the presence of memory and actively proliferating T cells in the bone marrow.

Available online http://arthritis-research.com/supplements/7/S1
Methods
Bone marrow samples, obtained from RA and OA patients (mean age 53.1 ± 10.6 years and 54.3 ± 13.6 years, respectively) undergoing joint replacement surgery, were diluted four times in heparinized PBS. Bone marrow plasma samples were obtained by centrifugation and levels of IL-15 were measured using specific ELISA. The real number of lymphocytes stained for CD3+ and CD19+ were counted in the presence of TruCount beads using flow cytometry. Surface-expressed IL-15R was done on cells separated by gradient centrifugation, acid wash of surface-bound IL-15 and flow cytometric analysis. Surface expression of CD45RO was evaluated by flow cytometry. Cell proliferation was measured by intracellular expression of Ki-67.

Results
There were twice as many T (CD3+) cells in RA in comparison with OA bone marrow (6.1 ± 2.8 versus 3.2 ± 1.6 cells × 10^6/mg bone marrow, P = 0.008). In contrast, only 42% of B (CD19+) cells present in OA were present in RA bone marrow (2.0 ± 0.9 versus 0.85 ± 0.3 cells × 10^6/mg bone marrow, P = 0.02). Interestingly, both CD3+CD4+ and CD3+CD8+ cells obtained from RA patients expressed a significantly higher level of CD45RO (P = 0.002 and P = 0.001, respectively), measured as the mean fluorescence intensity, than in OA. In addition, there was a tendency (although not statistically significant, P = 0.08) for a higher percentage of CD3+CD8+CD45RO+ cells in bone marrow from RA patients in comparison with OA patients (38.7% versus 28.1%). Interestingly, lymphocytes isolated from RA patients expressed a significantly higher level of surface IL-15R alpha chain (P = 0.01), indicating their activation status. Cells isolated from RA bone marrow bound significantly more K-67 than cells isolated from OA bone marrow, indicating that RA cells proliferated more vigorously. There were elevated levels of IL-15 in RA bone marrow plasma from RA in comparison with OA patients (1304.5 ± 956.3 pg/ml and 760 ± 238.7 pg/ml, respectively, P = 0.01).

Conclusion
Lymphocytes obtained from RA patients expressed higher levels of IL-15R alpha chain and proliferated more rapidly than lymphocytes obtained from OA patients. It is likely that locally overproduced IL-15 is responsible for the elevated number of T cells in RA bone marrow. Higher density of CD45RO+ memory marker expressed on T cells from RA patients further supports the role of IL-15 as a known growth factor for memory T cells. A significantly lower B-cell number in RA than in OA suggests that these cells actively emigrate from RA bone marrow to peripheral blood and affected joints. Distinct subpopulations of mature lymphocytes present in bone marrow from RA and OA patients indicate that the bone marrow acts as a secondary lymphoid organ that actively contributes to the pathogenesis of RA.

P65
Signaling pathways involved in TRAIL-induced rheumatoid arthritis synovial fibroblast proliferation
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Tumor necrosis factor alpha-related apoptosis inducing ligand (TRAIL) is a pro-apoptotic factor that can also induce cell proliferation. The role of TRAIL in rheumatoid arthritis (RA) is still unclear. Previously, we reported that TRAIL induces RA fibroblast-like synoviocytes (FLS) proliferation. We now investigate the intracellular mechanisms involved in TRAIL-induced cell proliferation. Therefore, we tested the effect of TRAIL on signaling pathways including MAP kinases (p38 and ERK1/2) and PI3 kinase/Akt, known to control cell proliferation. For all these experiments, the concentration of TRAIL used to stimulate cell was 0.5 nM. TRAIL induced p38 MAP kinase but with a lower intensity in comparison with tumor necrosis factor alpha (TNF-α) (n = 3). TRAIL also induced ERK1/2 and Akt phosphorylation in RA FLS in a time-dependent manner, showing maximum activation between 5 and 10 min by western blot (n = 3). This kinetic and intensity of ERK and Akt activation were similar to positive control TNF-α (n = 3). The transfection factor NF-kB plays a major role in cell survival and is activated by MAP kinases and Akt. When NF-kB is activated, it translocates from the cytoplasm to the nucleus. We examined NF-kB translocation into the nucleus of RA FLS following TRAIL stimulation using immunofluorescence. RA FLS treated with TRAIL did not induce a nuclear uptake of NF-kB (n = 3). The percentages of RA FLS positive NF-kB translocation was increased from 4.3 ± 0.9% to 8.7 ± 2.3% when stimulated with TRAIL. For the positive control IL-1β, this percentage increased to 97.9 ± 1.1%. This result was confirmed by western blot. To determine the implication of MAP kinases and PI3 kinase/Akt in TRAIL-induced proliferation, we therefore tested different specific signaling inhibitors including PI3 kinase inhibitor LY294002, ERK1/2 inhibitor PD98059, and p38 inhibitor SB203580. RA FLSs were incubated with the specific inhibitors at different concentrations. MeSO vehicle control for 1 hour and were then stimulated with TRAIL. Proliferation was measured according to the level of incorporated thymidine. ERK 1/2 inhibitor PD98059 and p38 inhibitor SB203580 significantly downregulated TRAIL-induced proliferation in a dose-dependent manner (n = 3). PI3 kinase inhibitor LY294002 almost completely blocked proliferation promoted by TRAIL. These results highlight the main role of Akt in TRAIL-mediated proliferation.

P66
Local IL-18 gene transfer prevents severe joint destruction in murine collagen-induced arthritis by induction of IL-4 and osteoprotegerin
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Introduction
IL-18 is a member of the IL-1 family of proteins that exerts proinflammatory effects and is a pivotal cytokine for the development of T-cell-mediated immune responses. IL-18 can promote both the Th1 and Th2 pathways. Recent studies indicated IL-18 as an important stimulator of chronic inflammation in human diseases such as rheumatoid arthritis, Crohn’s disease and several allergic disorders.

Objective
To investigate the aggravating effect of local IL-18 overexpression on both joint inflammation and joint destruction in murine collagen-induced arthritis.

Methods
Collagen-induced arthritis was induced in DBA-1 mice by intradermal injection of 100 µg bovine type II collagen in FCA. At day 21 the mice were boosted with 100 µg type II collagen. IL-18 gene transfer was performed on day 21, with a particular injection of 1 × 10^6 pfu AdIL-18 injected with 1 × 10^6 pfu AdSfl70.3. Histopathology was examined at days 5 and 12 after AdIL-18 injection. Bone destruction was investigated using X-ray analysis. In addition, both systemic and local cytokine levels were determined in sera and patellar washouts, using a multiplex bead array (Luminex Technology). Osteoprotegerin levels were examined by ELISA.

Results
Here we report that overexpression of IL-18 in knee joints of collagen type II primed DBA-1 mice resulted in aggravation of joint inflammation. Enhanced influx of proinflammatory cells, predominantly polymorphonuclear cells, was seen already at day 5 in both synovial tissue and the joint cavity. At day 12 enhanced severe joint inflammation was seen in the AdIL-18 injected knee joint, whereas the AdSfl70.3-injected or saline-injected mice showed modest joint inflammation. Of high interest, although severe joint inflammation developed after IL-18 gene transfer, no signs of joint destruction were noted at day 12 after IL-18 overexpression. Histopathological and X-ray analysis revealed that both cartilage and bone destruction were completely prevented after intra-articular IL-18 exposure during collagen-induced arthritis. In addition, we found that local overexpression of IL-18 resulted in elevated levels for IL-4 in both serum (29 ± 14 versus 4 ± 3 pg/ml) and in synovial tissue washouts (1240 ± 220 versus 24 ± 27 pg/ml) when compared with AdSfl70.3. Remarkably high levels of osteoprotegerin were found in synovial tissue washouts at day 12 after IL-18 gene transfer compared with AdSfl70.3 vector (1570 ± 270 versus 210 ± 20 pg/ml). Moreover, local IL-10 levels were strongly enhanced whereas IL-15 levels were significantly reduced after IL-18 gene transfer.

Conclusion
The present study clearly demonstrated that local IL-18 overexpression exacerbates joint inflammation, but prevents development of severe cartilage and bone destruction. High levels of both IL-4 and osteoprotegerin indicate establishment of a non-destructive type 2 inflammation. These data suggest that IL-18 may have a dual role in chronic destructive arthritis and that therapies based on local IL-18 blockade might be inadequate in rheumatoid arthritis.

P67
Gene expression profiling provides a link between high inflammatory synovitis and myofibroblast-like synoviocytes
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Objective
The molecular pathogenesis of rheumatoid arthritis (RA) is still poorly understood. Given the heterogeneity in gene expression patterns and cellular distribution between RA synovial tissue, we determined whether this variability is also reflected at the level of fibroblast-like synoviocytes (FLS) cultured from those synovial tissues.

Methods
Gene expression profiles in FLS from 19 RA synovial tissues were analyzed using cDNA microarrays and hierarchical cluster analysis. To validate the subclassification, we performed prediction analysis and principal component
P68
Anakinra (Kineret) in psoriasis and psoriatic arthritis: a single-center, open-label, pilot study.
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Background Both gene and protein expression of IL-1 are highly upregulated in skin and synovium of patients with psoriatic arthritis (PsA) and psoriasis. IL-1 is known to play a key role in keratinocyte activation, matrix metalloproteinase upregulation, differentiation of osteoblast precursors into mature osteoblasts, angiogenesis and the development of erosive disease. Thus, the purpose of the study is to assess the effects of IL-1 inhibition on the clinical features of psoriasis and PsA disease activity, on synovial and cutaneous immunohistochemistry and on magnetic resonance imaging (MRI) features of an affected knee joint.
Methods To date, eight PsA patients (six male and two female, average age 41 years [22–61 years]) with active skin and joint disease have been enrolled for treatment over 12 weeks with 100 mg anakinra daily by subcutaneous injection. Physical examination, patient and physician global assessment of disease activity (on a scale of 0–3), tender and swollen joint scores, erythrocyte sedimentation rate, C-reactive protein and PASI scores were performed at all visits. Plain X-rays of hands, wrists, knees and feet were performed at baseline. A biopsy of a psoriatic plaque, multiple arthroscopic synovial biopsies and a MRI scan of an inflamed knee joint were performed at baseline and week 12. HAQ scores, patient assessment of disease activity and pain using visual analogue scales were obtained at weeks 0 and 12. PsA-QoL were calculated at weeks 0 and 12. The primary endpoint was the proportion of patients who met the Psoriatic Arthritis Response Criteria (PsARC) at 12 weeks.
Results Seven patients completed the study. One male patient was non-compliant and dropped out of the study protocol and subsequently withdrew before completion of the study. Baseline physical examination revealed psoriasis and active synovitis in all patients. Three of the seven patients (43%) met the PsARC at week 12. Mean HAQ scores improved from 1.23 (0.75–1.9) to 0.96 (0.25–1.6), while mean PsA-QoL scores changed from 22/46 (9–41) to 20/46 (5–40). Other relevant data are presented in Table 1.
Conclusion This ongoing study has shown anakinra to be of modest benefit in patients with PsA. Further patient recruitment, MRI assessment and immunohistochemical analysis of tissue samples is ongoing.

Table 1 (abstract P68)

<table>
<thead>
<tr>
<th>Patient assessment of disease activity (0–3)</th>
<th>Physician assessment of disease activity (0–3)</th>
<th>Tender joint score (0–78)</th>
<th>Swollen joint score (0–76)</th>
<th>Patient assessment of disease activity on VAS</th>
<th>Patient assessment of pain on VAS</th>
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<td>4.5% (0–8)</td>
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</table>
Methods The presence of TR2, TR3, TR4 and TR7 in synovial tissue, from RA patients, osteoarthritis patients and healthy controls was studied with immunohistochemistry techniques. Furthermore, monocyte-derived dendritic cells from RA patients and healthy controls were cultured for 6 days and subsequently stimulated via specific TLR pathways; TR2 (pam3cys), TR3 (poly(I:C)), TR4 (LPS) and TR7 (R848). We determined the expression of cell surface markers (CD14, CD80, CD83, CD86, MHC1 and MHCII) by flow cytometry and tumour necrosis factor alpha, IL-6, IL-10 and IL-12 production was measured by multiplex cytokine bead arrays.

Results TR2, TR3, TR4 and TR7 expression was markedly increased in synovial tissue from RA patients, compared with synovial tissue from osteoarthritis patients and healthy controls. After stimulation via specific TLR pathways, flow cytometry showed a clear DC maturation upon stimulation via all TLR pathways without any difference between RA cells and cells from healthy controls. However, cytokine production by DC from RA and controls was clearly different. RA DC produced increased levels of the proinflammatory cytokines tumour necrosis factor alpha and IL-6 upon stimulation of TR2 or TR4. In contrast, such differences were not noted after TR3 and TR7 stimulation. Triggering of TR3 and TR7 pathways resulted in increased production of IL-12, which was equal between RA and control DC. Intriguingly, simultaneous stimulation of TR3/4, TR3/7 and TR4/7 pathways resulted in a marked synergy with respect to the production of proinflammatory mediators.

Conclusion These results point out that despite a comparable DC phenotype, RA cells produce higher cytokine levels upon stimulation of TR2 and TR4 compared with healthy controls. The combination of specific TLR stimulations resulted in a distinguished synergy in cytokine production. Here, we postulate the hypothesis that the persistence of viral material in synovial tissue triggers the TR3 and TR7 pathways, which subsequently results in inflammation and release of endogenous ligands, resulting in TR4 stimulation that leads to a vicious circle of synovial inflammation.

P71

Post-transcriptional regulation of proinflammatory cytokines in arthritis using gene delivery of AU-rich element binding factors

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Background Monocytes and macrophages are abundant in rheumatoid synovial tissue and play a major role in the pathogenesis of rheumatoid arthritis (RA) by secreting proinflammatory cytokines such as tumour necrosis factor alpha (TNF-α). An innovative approach is based on the regulation of mRNA stability and degradation, which constitute a critical step in the control of gene expression rather than neutralization of the downstream protein. Stability and degradation of TNF-α mRNA are regulated by cis-acting sequences as AU-rich elements (AREs). Tristetraprolin (TTP), a class of Cys-Cys-Cys-His (CCCH) zinc finger proteins, was identified as the critical TNF-α ARE-binding protein. Importantly, TTP knockout mice develop inflammatory arthritis, dermatitis and myeloid hyperplasia, prevented by anti-TNF-α antibodies. A recent study suggested that a low TTP/TNF-α RNA expression ratio could indicate failure of RA patients to produce adequate amounts of TTP in response to increased TNF-α production. Our aim is to investigate the therapeutic potential of gene expression of ARE-binding elements for anti-TNF-α therapies.

Methods We used the THP1 human monocyte cell line known for a high lipopolysaccharide (LPS)-induced TNF-α secretion. An expression vector containing TTP gene driven by the CMV promoter was constructed. TTP expression was evaluated by western blot following transfection by electroporation (320 nV). The secretion of TNF-α by THP1 was assessed by ELISA before and after TTP transfection (1 µg/10⁶ cells), following LPS stimulation (50 ng/ml).

Results A significant decrease in TNF-α expression was observed in the TTP-transfected THP1 cells, compared with a GFP mock control. This suppression increased over time and lasted at least 48 hours after LPS stimulation (23% at 3 hours and 37% at 24 hours).

Conclusion These preliminary results support an important role of TTP in regulating TNF-α in monocytes and might be the new target for gene delivery in an anti-TNF-α strategy in RA. In vitro evaluation of this strategy in experimental models of RA will be tested.

P72

Arthroscopic lavage with methylprednisolone is superior compared with either treatment alone in patients with inflammatory arthritis of the knee: a randomized prospective trial

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Background Patients with recurring or persisting inflammatory arthritis of the knee despite anti-rheumatic therapies are frequently treated with intra-articular steroid injections. Lavage of a rheumatic joint may also be beneficial by removing synovial debris and proinflammatory substances from the joint. Only uncontrolled studies have been performed so far and none of these has studied local synovial features.

Objectives To compare the therapeutic effect of three local interventions: arthroscopic lavage with steroid application (AL + st), arthroscopic lavage with placebo (AL + pl) and needle biopsy with steroids (NB + st, as a representative of joint injection). To study synovial tissue biopsies for predictive factors for the response to local therapy.

Methods Arthroscopic lavage with 1 l saline was performed under local anaesthesia using 2 troocharts. At the end of the procedure 80 mg methylprednisolone or placebo was instilled. Needle biopsy was performed under local anaesthesia with 1 trochar and instillation of 80 mg methylprednisolone. In all patients synovial tissue specimens were obtained and histologically analyzed. Kaplan–Meier curves were constructed depicting the time until recurrence of arthritis. Cumulative incidences of recurrence were used to calculate relative risks (RRs) between treatment groups.

Results Seventy-eight patients were equally randomized over the three interventions. AL + st was the best therapy with a median time until recurrence of 0.58 years, followed by NB + st (0.23 years) and AL + pl (0.08 years) (Fig. 1). The RR for recurrence compared with AL + st was 2.0 for NB + st (P = 0.03) and 4.7 for AL + pl (P < 0.001). Synovial tissue analysis showed a relation between infiltrating lymphocytes and outcome of AL + st; RR = 2.7 (P = 0.01) in patients with less infiltrating lymphocytes. The opposite was found for fibrosis; RR = 2.9 (P = 0.03) in patients with more fibrosis.

Figure 1

Kaplan–Meier curves for the time until recurrence of arthritis.

Conclusion Joint lavage preceding steroid injection had a marked effect on time until recurrence when compared with joint lavage or steroid injection alone. The clinical effect was correlated with the presence of a lymphocytic infiltrate and the absence of fibrosis.

P73

Phenotypic, genotypic and functional characterization of mesenchymal stem cells from synovial membrane compared with bone marrow

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Department of Immunologie/Rhumatologie, Lapeyronie Hospital, Montpellier, France


Objective Mesenchymal stem cells (MSC) are progenitor cells of mesodermal lineages that are present in different tissues such as the fat pads and the bone
marrow (BM) but also in the cartilage and the synovial membrane (SM). The aim of this study was to better characterize BM-derived and SM-derived MSC and discriminate between the two tissue sources.

**Methods**

BM-MSC and SM-MSC were compared for the expression of cell surface markers and induction of MHC class I and II molecules by interferon (IFN)-γ, IFN-β and IFN-α. Functional characterization was assessed through their differentiation potential towards chondrocytes and osteoblasts using quantitative RT-PCR, and their immunosuppressive properties by mixed lymphocyte reaction and indoleamine 2,3-dioxygenase activity. Using macroarray technology, the expression of 268 genes was monitored in four samples from BM-derived and SM-derived MSC.

**Results**

BM-derived and SM-derived MSC were shown to express CD44, CD73, CD90 and CD105 in the same range and to respond to IFN stimulation. We showed that IFN-γ, IFN-β and IFN-α are able to stimulate the expression of MHC class I in BM-MSC, as well as in SM-MSC. Furthermore, the macroarray analysis shows a statistically significant discrimination between BM-derived and SM-derived MSC, in particular immunosuppressive cytokine as IL6 and IL8 were upregulated in synovocytes compared with BM-MSC. Validation in terms of specific proteins is being undertaken.

**Conclusion**

Altogether, the data indicate that BM-MSC and SM-MSC shared multiple phenotypic and functional properties. However, the genomic signature permits one to discriminate the MSC originating from the two different tissues.

### P74

**Proinflammatory role for AT1 receptors in the rat synovium**

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The increasing recognition that angiotensin II (Ang II) has proinflammatory roles supportive of chronic inflammation and of the recent development of selective Ang II type 1 receptor antagonists in experimental arthritis suggests both an important role for Ang II in arthritis, and a novel therapeutic approach to discriminate between the two tissue sources.

**Methods**

BM-MSC and SM-MSC were compared for the expression of cell surface markers and induction of MHC class I and II molecules by interferon (IFN)-γ, IFN-β and IFN-α. Functional characterization was assessed through their differentiation potential towards chondrocytes and osteoblasts using quantitative RT-PCR, and their immunosuppressive properties by mixed lymphocyte reaction and indoleamine 2,3-dioxygenase activity. Using macroarray technology, the expression of 268 genes was monitored in four samples from BM-derived and SM-derived MSC.

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**Conclusion**

Altogether, the data indicate that BM-MSC and SM-MSC shared multiple phenotypic and functional properties. However, the genomic signature permits one to discriminate the MSC originating from the two different tissues.
S30

P76 Sustained downregulation of the TCRζ chain defines a transition from antigen mode to inflammation mode during terminal T-cell differentiation
Z Zhang, M Panesar, P Amjadi, A Foey, S Owen, F Dazzi, FM Brennan, AP Cope
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The molecular events that define early phases of activation and differentiation of effector T cells have been well characterised. Those events regulating terminal differentiation and effector function of chronically activated T cells at sites of inflammation, on the other hand, are less well understood. Using in vitro and in vivo models, we have explored the effects of the chronic inflammatory process on T-cell differentiation by investigating how tumour necrosis factor (TNF) regulates T-cell activation and effector responses. These studies have revealed that TNF-stimulated T cells resemble those derived from inflamed synovial joints since they express cell surface activation antigens, but are profoundly hyporesponsive to TCR engagement. Studies with mouse T cells suggest that this may be explained, at least in part, by the fact that TNF selectively targets the expression of the TCRζ chain. Loss of TCRζ expression perturbs the assembly, expression and stability of the TCR/CD3 complex leading to attenuation of membrane proximal tyrosine phosphorylation, intracellular calcium mobilisation and the transcription of cytokine genes upon TCR engagement, when compared with untreated T cells. We have begun to investigate whether TCRζ expression could be used as a ‘biomarker’ for chronically activated, hyporesponsive T cells in human peripheral blood. Using a FACS-based assay, we have identified subsets of CD3+ T cells expressing low levels of TCRζ (hereafter termed TCRζdim) cells in the peripheral blood of healthy donors, as well as patients with inflammatory arthritis. In vitro studies of peripheral blood lymphocytes from healthy donors define not only antigen-dependent downmodulation of TCRζ expression, which is transient, but also more sustained downregulation, which may arise through antigen-independent mechanisms. Experiments reveal that, when compared with TCRζbright cells, the TCRζdim population is enriched for cells expressing effector memory cell surface markers. While TCRζdim cells are hyporesponsive to TCR engagement, they retain effector potential, since a significant proportion are capable of producing TNF-α and interferon gamma upon stimulation with phorbol ester and calcium ionophore. In contrast, the TCRζbright subset is enriched for IL-10 producers. Furthermore, TCRζdim T cells are capable of activating monocytes through cell contact-dependent mechanisms. Together these data suggested that TCRζdim T cells may represent a subset of circulating effector memory cells in vivo. Finally, we observed that TCRζdim T cells are enriched in inflamed joints of patients with inflammatory synovitis. Treatment of rheumatoid arthritis patients with anti-TNF (infliximab, 3 mg/kg) leads to significant accumulation of TCRζdim T cells in peripheral blood of a subset of patients. Indeed, the extent of accumulation at 14 weeks after starting treatment predicts the DAS28 clinical response at 30 weeks. We propose that sustained downregulation of the TCRζ chain defines a checkpoint where intracellular signals driving T-cell differentiation and effector responses switch from antigen mode to inflammation mode, where effector function may be largely antigen independent. As such this cell subset may represent a valid therapeutic cellular target.

Acknowledgments This work was funded by the Wellcome Trust and the Arthritis Research Campaign UK.

P77 Rheumatoid synovial fibroblasts activate endothelial cells and promote neutrophil recruitment in a flow based multicellular model of the rheumatoid pannus
E Smith1, F Lally1, A Filer2, M Stone1, J Shaw1, GB Nash3, CD Buckley2, GE Rainger1
1Department of Physiology, The Medical School, University of Birmingham, UK; 2Department of Rheumatology, The Medical School, University of Birmingham, UK; 3Respiratory and Inflammation Research, AstraZeneca, Alderley Park, UK
In rheumatoid arthritis, leucocytes are recruited from the blood by vascular endothelial cells (EC) and accumulate in stromal tissue forming ectopic leucocyte aggregates that contribute to soft tissue remodelling and bone destruction. The signals that regulate the process of chronic leucocyte recruitment into the diseased joint are poorly defined; however, it is probable that cells of the tissue stroma that have undergone a disease-specific transition in phenotype contribute to inflammation by the inappropriate production of proinflammatory cytokines and chemokines [1,2]. Here we have used a novel co-culture model [3] to monitor the role of stromal cells in regulating the quality and quantity of leucocytes that enter the synovium. We tested the hypothesis that fibroblasts from the rheumatoid joint, but not fibroblasts from normal tissue (skin), have the ability to drive inflammation by activating EC and promoting the recruitment of neutrophils. EC were established in co-cultured with fibroblasts from the synovium (SF) or skin (R) of RA patients on the opposite sides of porous transwell membranes. After 24 hours of EC conditioning, co-cultures were incorporated into a parallel plate leucocyte adhesion assay and the ability of EC to recruit flowing neutrophils determined. Neutrophils adhered efficiently to EC co-cultured with 5 x 105 SF (88 ± 12/mm100 cells perfused) but not to EC co-cultured with SF (12 ± 9/mm100 cells perfused). Anti-CD18 and anti-CD11b antibodies markedly decreased neutrophil adhesion, and an anti-CD18 antibody (the β2 integrin) abolished neutrophil recruitment. The antibody blockade of the neutrophil chemokine receptor CXCR2 but not CXCR1 also abolished neutrophil recruitment. Supemantants collected from cocultures of EC/SF, but not from SF cultured alone, activated EC to support neutrophil adhesion, indicating the presence of a soluble activating factor(s) generated exclusively in co-culture. EC/SF co-culture supernamantants also contained a high concentration of IL-6 (2925.2 ± 521.2 pg/ml), and both IL-6 and neutrophil adhesion were reduced in a dose-dependent manner by the inclusion of hydrocortisone in the co-culture medium. An anti-IL-6 antibody also abolished neutrophil adhesion.

We propose that in the rheumatoid synovium, a previously unsuspected process of cross-talk involving IL-6 signalling occurs between synovial fibroblasts and vascular EC resulting in the upregulation of adhesion molecules and chemokines that support neutrophil recruitment. The observation that neutrophil adhesion in this coculture system can be inhibited by anti-IL-6 neutralising antibodies or hydrocortisone suggests that this novel in vitro model of the synovium faithfully mimics important in vivo processes involved in leucocyte accumulation within the synovium. It also suggests that this new model can act as a useful screen for novel anti-inflammatory therapies in rheumatoid arthritis.

References

P78 Impaired early B-cell tolerance in patients with rheumatoid arthritis
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Purpose Autoantibody production is a characteristic of most autoimmune dis-

cases including rheumatoid arthritis (RA), but the stage of B-cell development at which B-cell tolerance is broken remains unknown. We previously established in healthy donors that most autoreactive B cells in RA evade one or both of these checkpoints. In addition, analysis of the antibody repertoire in RA might lead to potential insights about the mechanisms that may explain loss of B-cell tolerance.

Methods We obtained peripheral blood from four patients with clinically and serologically documented active RA, who had not yet received steroids, disease-modifying anti-rheumatic drugs or biologic therapy, or who had been off such regimens for at least 4 months. Isolating their peripheral B cells, we sorted, cloned and expressed in vitro antibodies from single new emigrant (CD19+CD10-IgM+CD27-) and mature naive (CD19+CD10-IgM-IgG-IgA-IgD+) B cells. In total, we examined by ELISA the specificity of 232 recombinant antibodies.

Results The antibody sequences in two of the patients showed a significant increase in the proportion of 11 amino-acid long CDR3s in Igk chains (previously described in RA synovium and blood), while the other two patients demonstrated an increase in Jk1 usage along with a shift towards more downstream Vk segments. This skewed lgt repertoire suggests that receptor editing, one of the mechanisms that ensures B-cell tolerance, is defective in those two patients. Despite the different antibody sequence patterns of our RA patients, all four patients showed significantly increased proportions of polyreactive antibodies in the new emigrant compartment (23.1% versus 8.2% in controls, P = 0.0094), autoreactive antibodies in the mature naive compartment (45.3% versus 20.4% in controls, P = 0.0001), and anti-CCP antibodies in both compartments (13.8% versus 9% in controls, P = 0.019). This demonstrates that autoreactive B cells in RA patients fail to be removed at both checkpoints of early B-cell tolerance.
Conclusions RA patients exhibit defective central and peripheral B-cell tolerance, which may favor the development of autoimmunity. We have also identified two distinct groups of RA patients based on their antibody sequences that suggest divergent mechanisms within the RA population – yet lead to a common phenotype.

P79 Characterization of the IL-12 family of cytokines in human dendritic cells infected with live Chlamydia trachomatis MK Matyszak, JGH Gaston University of Cambridge Clinical School, Department of Medicine, Addenbrooke’s Hospital, Cambridge, UK

Introduction Chlamydia trachomatis (CT) is a clinically important pathogen. In 2–5% of cases, infection results in the development of reactive arthritis. We have previously shown that human dendritic cells (DC) can be readily infected with live CT following in vitro exposure [1]. Infected DC efficiently process chlamydia and present chlamydial antigens to both CD4+ [1] and CD8+ T cells [1,2]. Infected DC also produce a number of cytokines including IL-12 and tumour necrosis factor alpha but not IL-10 [1]. The production of IL-12 following infection gives DC the ability to stimulate Th1 responses to chlamydia. Here we have investigated production of another two cytokines from the IL-12 family – IL-23 and IL-27 – by DC infected with live CT. The results were compared with those obtained following DC activation with other inflammatory stimuli.

IL-23 is a heterodimer composed of p19 and p40 subunits, where the p40 subunit is encoded by the IL-12 p40 gene. IL-23 has been implicated in the development of inflammatory arthritis. IL-27 is a heterodimer between the p28 and Epstein–Barr virus-induced protein 3 (EBI3) subunits. The main function of IL-27 is to regulate T-helper cell responses. We previously showed that human dendritic cells (DC) can be readily infected with live CT. The results were compared with those obtained following DC infection giving DC the ability to stimulate Th1 responses to chlamydia. Here we have investigated production of another two cytokines from the IL-12 family – IL-23 and IL-27 – by DC infected with live CT. The results were compared with those obtained following DC activation with other inflammatory stimuli.

Results We showed that infection of DC with live CT resulted in the upregulation of message for all four subunits studied (p19, p40, p28, EBI3). The message was detected at 18 and 24 hours post infection. LPS-activated DC upregulated p28, p40, and EBI3. There was no p19 message at either 18 or 24 hours post stimulation. The main subunit upregulated following IFN-γ activation was p28 and there was no detectable p19 mRNA at any of the times studied. Interestingly, there was also no expression of p19 when immature DC were exposed to heat-killed CT, Exposure of DC to heat-killed CT did, however, upregulate p28, p40 and EBI3. A small amount of EB3 message was detected in immature DC, but on none of the other subunits studied.

Conclusion Whereas activation of DC with LPS, IFN-γ and heat-killed CT stimulates production of IL-27, these stimuli are insufficient to induce p19 upregulation, and in consequence IL-23 production. However, infection of DC with live CT resulted in the production of mRNA for both IL-23 and IL-27. This study highlights important differences in immune responses following exposure to live and heat-killed CT.

References


P80 NK cell status and IL-10-dependent therapeutic effect of NK cell stimulation on collagen-arthritids in DBA/1 mice

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Background and objectives Defective NK cell function has been linked with autoimmunity. Both the number of NK cells and their functional capacity of releasing interferon gamma (IFN-γ) and IL-4 after TCR ligation are for instance impaired in NOD mice developing diabetes, in mice developing a model of multiple sclerosis and also in humans with autoimmune diseases. To investigate the NK cell role in rheumatoid arthritis, we studied their quantitative and qualitative profile in collagen-induced arthritis (CIA) DBA/1 susceptible mice, and we tested whether NKT stimulation with their synthetic ligand alpha-galactosylceramide (α-GalCer) was therapeutic in CIA.

Methods The number of NK cells in the liver was determined by flow cytometry with an anti-TCRβ or empty or α-GalCer-loaded CD1 tetramer. CIA was induced by immunization of DBA/1 mice with collagen II (CII) in adjuvant, and with a boost 21 days later. α-GalCer (4 μg) was administered at the same time of the first immunization. In one experiment, one group of mice was also treated with an anti-CD4 receptor antibody. Specific CD4+ cells from lymph node (LN) response were monitored by immunizing mice with 75 μg CII in adjuvant in hind paws. Some mice were administered 4 μg α-GalCer in the CII/adjuvant mixture at the same time. Nine days after immunization, CD4+ cells were purified from LN and cultured with CII and antigen-presenting cells. Proliferation was measured after 3 days by measuring BrDU incorporation, and IL-4, IL-10 and IFN-γ levels were assessed by ELISA in the supernatants.

Results The number of NK cells among leucocytes in the liver of DBA/1 mice was comparable to what is generally observed in C57Bl/6 and suggest a normal quantitative profile of NK cells in DBA/1 mice. In contrast, in vivo NK cell function was altered in DBA/1 mice since stimulation with α-GalCer (4 μg intraperitoneally) led to decreased IL-4 and IFN-γ levels in the serum 2 hours after the injection, as compared with C57Bl6 mice (693 ± 154 pg/ml versus 1557 ± 137 g/ml IL-4 [P<0.01] and 2077 ± 378 versus 4005 ± 581 IFN-γ [P<0.02]). Treatment of CIA with α-GalCer at day 9 induced a clear-cut diminution of clinical (ANOVA test, P=0.0001) and histological scores (1.9 ± 0.4 versus 1.85 ± 0.24, P<0.005) of arthritis, as compared with the control group. Importantly, treatment of mice with an anti-IL-10 receptor abrogated the protective effect of α-GalCer. The α-GalCer-induced protection was associated with the ability of LN CD4+ cells from CIA-immunized and α-GalCer-treated DBA/1 mice to secrete larger amounts of IL-10 upon in vitro restimulation with CII, while IL-4 and IFN-γ levels were not affected. CIA-induced proliferation was slightly reduced in LN CD4 cells from CIA-immunized and α-GalCer-treated DBA/1 mice as compared with controls.

Conclusion These findings raise the possibility that NKT stimulation might induce a shift toward an anti-inflammatory Th2 status and could be used therapeutically to treat chronic autoimmune arthritis.

P81 Distinct patterns of RANKL/osteoprotegerin system modulation through anti-tumour necrosis factor and corticosteroid therapy in rheumatoid arthritis synovium

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Background Anti-tumour necrosis factor (TNF) therapy with both etanercept and infliximab decreases radiographic progression of patients with rheumatoid arthritis (RA), while the effect of local corticosteroid injections, a routine adjuvant treatment in arthritis, on bone metabolism is still debated. Thus, we investigated the effect of both anti-TNF and local corticosteroid therapy on synovial expression of osteoprotegerin (OPG) and receptor activator of NF-κB ligand (RANKL). Methods OPG and RANKL were evaluated by immunohistochemistry in serial synovial biopsies obtained from 18 RA patients before and after 8 weeks of treatment with etanercept (nine patients) or infliximab (nine patients). Eighteen additional patients with arthritis that received a local corticosteroid injection were evaluated before and after 2 weeks of the injection. Biopsies were evaluated by double-blind semi-quantitative analysis and image analysis. In the in vitro effect of TNF antagonists and corticosteroids (dexametasone) on RANKL/OPG expression in osteoblasts was evaluated by western blot. Statistical analysis was performed using the Wilcoxon’s signed-rank test followed by Bonferroni correction.

Results OPG was present in all biopsies with a characteristic pattern restricted mainly to the endothelial cells and few mononuclear cells. RANKL was present mainly in the T-cell area and to a lesser extent on some endothelial cells, but absent in other mononuclear cells. Treatment with both infliximab and etanercept induced a similar synovial OPG expression pattern. Neither infliximab nor etanercept induced RANKL expression following 8 weeks of treatment. The RANKL/OPG ratio decreased following therapy in both groups, the effect being more pronounced in the responders as compared with non-responders to therapy. Local corticosteroid treatment resulted in a similar change of the RANKL/OPG ratio through a different mechanism, with a significant decrease of the synovial RANKL and no changes in the OPG expression. In vitro both TNF antagonists and corticosteroids mimicked the in vivo effect inducing a decrease in the RANKL/OPG ratio in TNF-primed osteoblasts.
Conclusion Therapy with both TNF antagonists and local corticosteroids modulates the RANKL/OPG system, inhibiting bone destruction through distinct mechanisms. Thus, association of these two therapies may be beneficial in preventing bone erosions in RA.

P82

IL-1-driven cartilage and bone destruction are dependent on Toll-like receptors (TLR) 4, but not TLR2

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1Department of Rheumatology, VU University Medical Center, Amsterdam, The Netherlands; 2Department of Pathology, Vrije Universiteit Medical Center, Amsterdam, The Netherlands; 3Department of Pathology, Vrije Universiteit Medical Center, Amsterdam, The Netherlands; 4Department of Immunopathology, Sanquin-Research, Amsterdam, The Netherlands Arthritis Res Ther 2005, 7(Suppl 1):P82 (DOI 10.1186/ar1603)

Background: Rheumatoid arthritis (RA) is an autoimmune disease characterized by systemic, chronic joint inflammation. In spite of great efforts, the etiology of RA has not been completely elucidated to date. Toll-like receptors (TLRs) belong to the family of pattern recognition receptors and are involved in both innate and adaptive immune responses against microorganisms via recognition of pathogen-associated molecular patterns. In addition, TLRs have been reported to recognize several endogenous ligands, which are generated under stress conditions and cartilage damage. Triggering of TLRs results in the release of various proinflammatory cytokines such as IL-1β and tumor necrosis factor alpha. IL-1β is one of the crucial cytokines in the pathogenesis of RA and is involved in Th1-mediated processes and cartilage and bone destruction. Therefore, TLRs may potentially be involved in either initiation or chronicity of arthritis.

Objective: To study the contribution of TLR4 and TLR2 in IL-4 driven joint inflammation, cartilage destruction and bone erosion.

Methods CSTBL/6 wild-type (WT), BL/6 TLR2 knockout (KO), CSTBL/10 WT and BL/10 TLR4 KO mice were intra-articularly injected with 3 x 106 PFU mouse IL-1β adenovalar vector (Adml1-β) or control vector (AdSde70-3). Inflammatory cell infiltration, cartilage proteoglycan (PG) depletion and cartilage and bone destruction were microscopically examined 7 days after virus injection. Results: Prolonged expression of IL-1β in mice knee joints induced a severe arthritis in WT animals, exhibiting pathophysiologic changes resembling those in human RA. High amounts of inflammatory cells, predominantly polymorphonuclear cells, were present in the knee joint cavities of both WT and KO mice. Severe PG depletion, cartilage destruction and bone erosion were observed in WT mice, which did not differ from those in TLR2-deficient mice. Interestingly, in TLR4-deficient mice, cartilage PG depletion and destruction were significantly reduced. TLR4-KO mice showed also a marked reduction in bone erosion compared with WT mice, although this reduction was not significant.

Conclusion: These data strongly suggest that TLR4 is involved in IL-1β-driven pathologic processes. Both cartilage and bone destruction were reduced in TLR4 KO mice, although joint inflammation was comparable with WT mice. This indicates the involvement of potential TLR4 ligands, generated by IL-1β-induced cartilage degradation, in chronic RA. Our data point out that TLR4 may be a novel therapeutic target in the treatment of RA.

Acknowledgements Supported by the Dutch Arthritis Association. Adml1-β virus was a kind gift from Dr Carl D Richards from the Department of Pathology and Molecular Medicine, McMaster University, Ontario, Canada.

P83

Differential expression of multidrug resistance-related proteins on monocyte-derived macrophages from rheumatoid arthritis patients

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Background: Primary or acquired drug resistance is well recognized as a common cause of treatment failure of patients with cancer. From a rheumatoid arthritis (RA) perspective, the issue of resistance to anti-rheumatic drugs (e.g. disease-modifying anti-rheumatic drugs [DMARDs]) has not received much attention. A possible mechanism of drug resistance is overexpression of multidrug resistance (MDR)-related proteins. The objective of this study was to identify whether various MDR proteins are expressed on macrophages as potential target cells for DMARDs.

Methods: Monocyte-derived macrophages (M) were obtained from 15 RA patients (median age: 56 years, 13 females/two males) and eight healthy controls (median age: 51 years, four females/four males). Monocytes were isolated from peripheral blood mononuclear cells and differentiated into macrophages in the presence of monocyte-colony stimulating factor. Cytosins of MDMs were prepared for immunohistological analysis of the MDR-related proteins: P-glycoprotein, multidrug resistance associated protein (MRP) 1, MRP4, MRP5, breast cancer resistance protein (BCRP) and lung resistance protein (LPR). Staining intensities were scored as follows: (0), negative; (1), weakly positive; (2), positive; (3), strongly positive. The total score is depicted as the summation of percentiles of cells with intensities 0–3.

Results: MDMs of healthy controls and of RA patients stained strongly positive for macrophage markers CD68 and CD54. Except for MRP4, MDR protein expression was observed both in MDMs of healthy controls and RA patients. Results are shown as the median score with ranges (in parentheses) for MDR expression and a statistical evaluation (Mann–Whitney U test) for differential expression (Table 1).

Table 1

<table>
<thead>
<tr>
<th>MDR protein</th>
<th>Rheumatoid arthritis patients (n = 15)</th>
<th>Controls (n = 8)</th>
<th>P value</th>
</tr>
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<tbody>
<tr>
<td>BCRP</td>
<td>1.04 (0.51–2.27)</td>
<td>0.63 (0.44–1.45)</td>
<td>0.043</td>
</tr>
<tr>
<td>LPR</td>
<td>0.87 (0–2.49)</td>
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<td>0.876</td>
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<td>MRP5</td>
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<td>0.238</td>
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<tr>
<td>P-glycoprotein</td>
<td>0.24 (0–1.05)</td>
<td>0.1 (0.05–1.06)</td>
<td>0.813</td>
</tr>
<tr>
<td>MRP4</td>
<td>&lt;0.05</td>
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Conclusions: MDR proteins, known to be involved in conferring drug resistance, are expressed on macrophages of RA patients. Beyond this, there seems to be a trend for a higher expression of MDR proteins on MDM from RA patients compared with healthy controls. Further studies are warranted to assess whether MDR is a clinically relevant issue in daily treatment of RA patients.

Acknowledgement: This study is supported by the Dutch Arthritis Association (Grant NFR-03-I-40).

P84

Inhibition of tumour necrosis factor alpha production by activated T cells of rheumatoid arthritis patients by novel anti-folate drugs: an ex vivo pilot study

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Introduction: The folate antagonist methotrexate (MTX) is the ‘anchor-drug’ in the treatment of patients with rheumatoid arthritis (RA) [1]. The main target of MTX in intracellular folate metabolism is dihydrofolate reductase (DHFR) but several other targets have been described (e.g. thymidylate synthase [TS] and 5-aminoimidazole-4-carboxamide ribonucleotide [AICAR]). At present the exact mechanism of action of MTX in RA still remains elusive [1]. Despite the potent anti-inflammatory capacity of MTX many patients (at least 50%) become resistant to MTX during long-lasting therapy. However, little is known about the mechanisms of resistance against MTX in RA patients [2]. From the field of oncolgy, where MTX is used against haematological malignancies, new anti-folate drugs were developed to circumvent MTX resistance [3]. These new folate antagonists have the following characteristics: are better transporred through the reduced folate carrier, are retained intracellular more efficienly by polyglutamylation via folylpolyglutamate synthetase, and/or have other targets in the folate pathway besides DHFR (e.g. TS).

Objective: To investigate whether two new-generation anti-folate drugs, PT523 (DHFR-inhibitor) and ZD1694 (TS-inhibitor), have equal or better anti-inflammator capacity compared with MTX based on their capacity to inhibit tumour necrosis factor alpha (TNF-α) production by activated T cells.

Methods: Whole blood from 11 RA patients and six healthy volunteers was incubated ex vivo with MTX, PT523, ZD1694 and, as a control, the DMARD sulphasalazine (SSZ) after T-cell stimulation with α-CD3/CD28. Inhibition of TNF-α production was measured after 72 hours by ELISA [4].

The IC-50 values (defined as the drug concentration exerting 50% inhibition of TNF-α production) are used as a value for the anti-inflammatory capacity of the drug (Table 1).

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</tbody>
</table>
Results Both PT523 and D1694 turned out to inhibit TNF-α production by activated T cells much more efficiently than MTX (5–15 times). For comparison, the DMDARD SSZ is effective at much higher concentration (μM range). The inhibition of TNF-α production by the anti-folate drugs does not seem to be a result of (apoptotic) cell death of T cells whereas SSZ induces apoptosis of T cells (data not shown).

Conclusion In an ex vivo setting, two novel anti-folate drugs designed to circumvent MTX resistance proved to be very effective in inhibiting TNF-α production by activated T cells from RA patients and healthy volunteers. Future experiments are designed to evaluate ex vivo anti-folate sensitivity profiles for ‘MTX-responders’ and ‘MTX-non-responders’ to investigate whether these novel generation of anti-folate drugs can be useful in cases of clinical failure on MTX.

References


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P85

Marked expression of IL-1 receptors in cell nuclei and muscle fiber membrane in muscle tissue of patients with idiopathic inflammatory myopathies

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Background In chronic inflammatory diseases, IL-1 is known as an important proinflammatory cytokine inducing the expression of a variety of genes mediating the synthesis of several proteins, which can induce both acute and chronic inflammatory changes. Idiopathic inflammatory myopathies, such as polymyositis and dermatomyositis, are chronic autoimmune muscle disorders characterised by proximal muscle weakness and histopathological signs of patchy distribution of inflammatory cells in the skeletal muscle. Muscle tissue of patients with such myopathies has been shown to have an increased expression of IL-1α and IL-1β; however, the expression and pathophysiological role of IL-1 receptors in muscle tissue from such patients and healthy subjects has not yet been elucidated.

Aim To investigate the expression of IL-1 receptors in muscle tissue from both patients and healthy subjects and to describe whether IL-1 receptors are differentially expressed in symptomatic and non-symptomatic muscle tissue of patients with polymyositis and dermatomyositis.

Method Muscle biopsies from eight patients with polymyositis, three patients with dermatomyositis, and six healthy subjects were included in this study. Muscle biopsies were taken from two different sites, one from a symptomatic muscle and another biopsy from a non-symptomatic muscle. IL-1α, IL-1β, and IL-1RI and IL-1RII expression were investigated by immunohistochemistry. IL-1RI and IL-1RII were also investigated by confocal microscopy.

Results In patients with polymyositis and dermatomyositis, IL-1α was found to be expressed in endothelial cells and inflammatory cells, and significantly increased in symptomatic when compared with non-symptomatic muscle tissue. IL-1α was not expressed in muscle tissue of healthy subjects. In patients, IL-1RI and IL-1RII were strongly expressed in inflammatory cells, endothelial cells, in the membrane of the muscle fiber, as well as in the nucleus of the muscle fiber patients, whereas in muscle tissue of healthy subjects only a scattered pattern of IL-1RI and IL-1RII expression in a few endothelial cells and in a few of nuclei of the muscle fiber could be observed. The membrane and nuclear expression were confirmed by double stainings.

Discussion This is the first study to show the expression of IL-1RI and IL-1RII in the cell nuclei and in the membrane of muscle fibers. Moreover, we have found some marked differences between symptomatic and non-symptomatic muscle tissue of patients and healthy subjects indicating a potentially important role of IL-1 receptors in the pathogenesis of idiopathic inflammatory myopathies.

References


Table 1

<table>
<thead>
<tr>
<th>Drug</th>
<th>Target</th>
<th>Reduced folate (cell uptake)</th>
<th>Polypolyglutamate synthetase affinity (cell retention)</th>
<th>Rheumatoid arthritis patients (n = 11)</th>
<th>Controls (n = 6)</th>
</tr>
</thead>
<tbody>
<tr>
<td>MTX</td>
<td>DHFR</td>
<td>++</td>
<td>+</td>
<td>78 (77) nM</td>
<td>57 (27) nM</td>
</tr>
<tr>
<td>PTS23</td>
<td>DHFR</td>
<td>++</td>
<td>–</td>
<td>5.8 (3.2) nM</td>
<td>6.4 (3.8) nM</td>
</tr>
<tr>
<td>ZD1694</td>
<td>TS</td>
<td>++</td>
<td>++</td>
<td>16 (26) nM</td>
<td>4.8 (3.0) nM</td>
</tr>
<tr>
<td>SSZ</td>
<td>NF+xB</td>
<td>–</td>
<td>–</td>
<td>278 (216) μM</td>
<td>191 (29) μM</td>
</tr>
</tbody>
</table>

Available online http://arthritis-research.com/supplements/7/S1

S33
Effects of anti-rheumatic treatments on the prostaglandin E\textsubscript{2} biosynthetic pathway in synovial tissue and synovial fluid cells from patients with rheumatoid arthritis

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Background Microsomal prostaglandin E synthase (mPGES-1) is upregulated in experimental arthritis and is markedly expressed in synovial tissue from patients with rheumatoid arthritis (RA), suggesting its important role in the pathogenesis of inflammatory arthritis. However, the effects of current anti-rheumatic therapies on mPGES-1 expression have not been examined.

Objective To study the effects of anti-tumour necrosis factor (TNF) alpha blockers and glucocorticoids on prostaglandin (PG) E\textsubscript{2} biosynthesis and mPGES-1 expression in synovial fluid mononuclear cells (SFMC) and synovial tissue from RA patients.

Methods Synovial tissues were obtained from 18 RA patients before and after treatment with TNF-blockers (infliximab and etanercept) and from 16 patients before and after intra-articular injection of steroids. SFMC were obtained from eight RA patients. In vitro effects of TNF-blockers and dexamethasone (Des) on mPGES-1 expression in SFMC were examined by flow cytometry. PGE\textsubscript{2} levels in culture supernatants were determined by enzyme immunoassay. Immunohistological analysis and double immunofluorescence were performed using antibody against mPGES-1, cyclooxygenase (COX) and CD163.

Results Treatment of SFMC with TNF-blockers or Des decreased lipopolysaccharide-induced mPGES-1 and COX-2 expression in CD14\textsuperscript{+} monocytes and PGE\textsubscript{2} synthesis in culture supernatants. Double immunofluorescence revealed that mPGES-1 and COX-2 were co-localized in SFMC and in synovial tissue cells. Local treatment with steroids significantly reduced the mPGES-1, COX-2 and COX-1 expression in synovial tissue. However, neither mPGES-1 nor COX-2 expression in RA synovial tissues were significantly affected by anti-TNF therapy.

Conclusion In vitro, both TNF-blockers and Des suppressed mPGES-1 expression in SFMC. In RA synovial tissue, local steroids but not TNF-blockade downregulated mPGES-1. These data provide support to the use of combination of TNF-blockade and local steroids but not TNF-blockade downregulated mPGES-1 expression in RA synovial tissues were significantly affected by anti-TNF therapy.

Identification of a novel soluble form of the IL-18 receptor accessory protein as an immunomodulator in experimental arthritis

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Background In the inflammatory process preceding erosive arthritis, IL-18 plays an important role. IL-18 is known to regulate immune responses by stimulating Th1 maturation, and signaling is initiated through formation of a trimeric receptor complex, consisting of IL-18 bound to the IL-18R\textalpha and its accessory receptor IL-18R\textbeta.

Objective The aim of this study was to determine the physiological role of a recently described soluble form of the IL-18 receptor accessory protein (sIL-18R\textbeta) in mice.

Methods Mouse sIL-18R\textbeta (genebank accession number AK053176) was cloned from murine lung cDNA and used for the generation of an adenoviral vector (AdSil-18R\textbeta). Expression analysis of the sIL-18R\textbeta and its full-length membrane bound IL-18R\textbeta in different murine tissues was achieved through endpoint PCR. To investigate the in vivo mode of action, sIL-18R\textbeta was systemically overexpressed in collagen type II-immunized male DBA/1 mice. Systemic overexpression was achieved through intravenous injection of 3 x 10\textsuperscript{7} pfu AdSil-18R\textbeta or the control vector (AdLuc) before clinical manifestation of collagen-induced arthritis (CIA). At 1 and 4 days post adenoviral injection, splenocytes were harvested and the cytokine profile in plasma and splenocyte culture supernatants was determined.

Results Short IL-18R\textbeta mRNA was highly expressed in tissue of lymphoid origin, and no expression could be observed in immune privileged organs like the testis, the eye and the brain, suggesting a prominent role in immune regulation. Expression of sIL-18R\textbeta was disease regulated in mice suffering from CIA, whereas the full-length IL-18R\textbeta was not regulated. Splenocytes of sIL-18R\textbeta-treated immunized mice produced significantly less interferon gamma and IL-10 compared with control treated animals. Adenoviral overexpression of the sIL-18R\textbeta before clinical manifestation of CIA significantly aggravated arthritis, which was accompanied by a reduction of circulating IL-10, interferon gamma and a significant increased anti-bovine collagen II IgG\textsubscript{2}.

Conclusion Our results describe the existence of a novel short soluble form of the membrane IL-18R\textbeta, which is mainly expressed in lymphoid tissues. This sIL-18R\textbeta expression appears regulated during CIA. Furthermore, we show that this novel soluble IL-18R\textbeta functions as a putative modulator of IL-18 signaling; aggravating CIA, by modulating T-cell immunity.

Identification of a novel soluble form of the IL-18 receptor accessory protein as an immunomodulator in experimental arthritis

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RL Smeets, OJ Amzt, MB Bennink, WB van den Berg, FAJ van de Loo
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Conclusion Our results describe the existence of a novel short soluble form of the membrane IL-18R\textbeta, which is mainly expressed in lymphoid tissues. This sIL-18R\textbeta expression appears regulated during CIA. Furthermore, we show that this novel soluble IL-18R\textbeta functions as a putative modulator of IL-18 signaling; aggravating CIA, by modulating T-cell immunity.
Hierarchical clustering of differentially expressed genes among doublets of the nine investigated cell populations (w, weeks in culture; res, 3 hours re-stimulated) using Affymetrix Mouse Genome 430A 2.0 Arrays and DNA-Chip Analyzer (dChip).

memory for the expression of distinct genes coding for cytokines, chemokines, adhesion molecules, and so on. This functional memory contributes considerably to the chronicity of inflammation and its eventual refraction to therapy.

Here, we describe the global gene expression profiles of memory for the expression of distinct genes coding for cytokines, chemokines, adhesion molecules, and so on. This functional memory contributes considerably to the chronicity of inflammation and its eventual refraction to therapy.

Figure 1

Conclusions Expression of pre-IL-1α decreased the growth of SaOs-2 cells. Co-transfection of icIL-1Rα1 did not antagonize this effect. These observations suggest that intracellular effects of pre-IL-1α are not necessarily susceptible to inhibition by icIL-1Rα.

P92 Expression of microsomal prostaglandin E synthase-1 in muscle tissue of patients with idiopathic inflammatory myopathies
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Background Microsomal prostaglandin E synthase (mPGES-1) catalyzes the formation of prostaglandin (PG) E2 from cyclooxygenase (COX)-derived PGH2. mPGES-1 is induced by proinflammatory cytokines, such as IL-1β and tumor necrosis factor alpha, and is linked to conditions with high PGF2α biosynthesis and inflammation. A recent study has demonstrated enhanced COX-1 and COX-2 expressions in affected muscle tissues of patients with polymyositis (PM) and dermatomyositis (DM), suggesting their important role in the pathophysiology of these diseases. However, expression of mPGES-1 in muscle tissue has not been investigated.

Objective To study the expression of mPGES-1 in muscle tissue of patients with idiopathic inflammatory myopathies.

Methods Muscle biopsies were obtained from 13 patients with idiopathic inflammatory myopathies (six PM, four DM, one juvenile DM, two inclusion body myositis) and from six healthy subjects. Immunohistochemical analysis was performed using antibodies against mPGES-1.

Results mPGES-1 staining was detected in all patients with PM, DM and inclusion body myositis. Specifically strong intracellular staining was observed in inflammatory cells in infiltrates, in endothelial cells of capillaries, in scattered mononuclear cells and in fibroblast-like cells. In some patients mPGES-1 staining was localized in smooth muscle cells and endothelial cells of large vessels. In healthy subjects, weak mPGES-1 staining was detected only in scattered fibroblast-like cells, in a few mononuclear cells surrounding large vessels and in some capillaries.

Conclusion These results demonstrate the upregulation of mPGES-1 in muscle tissue of refractory patients with idiopathic inflammatory myopathies compared with healthy controls, suggesting a role of mPGES-1 in the pathophysiology of these diseases.

P93 Quantifying the contribution of the second HLA-DRB1 susceptibility allele to the risk of rheumatoid arthritis: a meta-analysis
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Background HLA-DRB1 alleles encoding the shared epitope (SE) susceptibility sequence predispose to rheumatoid arthritis (RA). Having two copies results in the relative risk for RA for individuals having one compared with zero, or two compared with one SE allele; from these, the ratio OR1/0 OR2/1 is calculated.

Methods In a meta-analysis of 44 datasets of case–control studies meeting predefined criteria, the odds ratios OR1/0 and OR2/1 are calculated, as an estimate of the relative risk for RA for individuals having one compared with zero, or two compared with one SE allele; from these, the ratio OR1/0 OR2/1 is calculated.

Results Overall the weighted mean ratio OR1/0 OR2/1 (95% confidence interval) was 0.90 (0.80–1.01). In the 39 studies in which all patients met the ACR criteria for RA, the overall ratio OR1/0 OR2/1 was 0.89 (0.78–1.01; see Fig. 1). In a multiple regression analysis on a group level the ratio OR1/0 OR2/1 was not influenced by racial origin, the frequency of compound heterozygosity (0401/0404 or 0401/0408), the percentage of female or rheumatoid factor-positive patients, disease duration or age at disease onset.

Conclusions The contribution of the second SE allele to RA risk does not differ significantly from that of the first SE allele. This result will help to pool immunogenetic data across populations, resulting in a detailed description of the contribution of immunogenetic factors to RA risk.
Efficient IL-18 and IL-18BPc adenoviral gene transfer to cultured murine submandibular gland epithelial cells and successful murine retrograde submandibular duct cannulation to modulate IL-18 function in the salivary gland of animal models of Sjogren’s syndrome

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Introduction We recently demonstrated that the proinflammatory and immunoregulatory cytokine IL-18 is strongly upregulated in salivary glands (SG) of Sjogren’s syndrome (SS) patients. IL-18 gain or loss of function experiments in animal models of human diseases have provided evidence of the pathogenic role of this cytokine in chronic inflammation. However, in SS the pathogenic relevance of IL-18 in the development of murine autoimmune sialoadenitis has not as yet been evaluated. Here we describe in vitro experiments in which murine SG epithelial cells were tested for transfection efficiency with IL-18 and IL-18BPc AdV gene transfer. In addition, in preparation for in vivo SG modulation of IL-18 function by AdV-mediated gene transfer, we optimised retrograde SG cannulation in mice.

Methods Primary SG ductal epithelial cells (SG-DEC), established from submandibular glands of C57BL/6 mice using the explant outgrowth technique, as well as a murine SG-DEC line were used for AdV transfection. A mIL-18AdV from plasmid IL-18 TG3652 [1] was developed in our laboratory while we used the same mIL-18BPcAdV construct as previously reported [2]. AdVs encoding for LacZ or luciferase were used as controls. All AdVs were incubated at 50 MOI.

Results High efficiency of transfection of cultured murine SG-DEC was obtained with both IL-18AdV (Fig. 1) and IL-18BPcAdV (Fig. 2). Western blot confirmed the presence of protein production detectable as single bands from target-geneAdV but not control-geneAdV transfected SG-DEC. A time-course study demonstrated in vitro gene expression up to 3 weeks after transfection. Feasibility of local SG delivery through retrograde submandibular duct cannulation was demonstrated by injection of trackable compounds.

Figure 1

Figure 2

(a) Expression of murine IL-18 in salivary gland ductal epithelial cells (SG-DEC) transfected with IL-18AdV but not with LacZAdV (b). (c) Beta-galactosidase staining confirmed effective transfection of SG-DEC by LacZAdV.

Conclusions Here we report for the first time evidence of high and sustained efficiency of IL-18 and IL-18BPc AdV gene transfer in murine SG-DEC. In addition, we successfully adapted a cannulation technique previously used in bigger animals for in vivo local delivery of modulatory molecules to murine salivary glands.

Local delivery of IL-18/IL-18BPc adenoviral vectors in vivo in salivary glands of NOD mice and other murine models of SS through retrograde submandibular excretory duct cannulation will provide evidence of a possible pathogenic role of IL-18 in participating in autoimmune sialoadenitis and will establish a rationale for using IL-18 blocking agents as therapeutic tools in SS.

References
immunization with SmD1(83-119). In vitro experiments showed that Tr1-cell-mediated suppression of anti-DNA autoantibody production is dependent on the activity of IL-10 as the addition of neutralizing anti-IL-10 antibodies abrogated this effect. Furthermore, adoptive transfer of SmD1(83-119) reactive Tr1 cells containing lymph node cells delayed the occurrence of anti-DNA autoantibodies in the recipient mice as well. We conclude that high-dose application of SmD1(83-119) induces SmD1(83-119) specific tolerance in NZB/W F1 mice, which is mediated by SmD1(83-119)-reactive Tr1 cells. These results may open new ways for future autoantigen specific cell-based therapies in systemic lupus erythematosus.

References


Acknowledgements RU and JH contributed equally to this work.

P96
Hearing improvement in a variant Muckle–Wells syndrome case in response to IL-1 receptor antagonist

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Background The proinflammatory cytokine IL-1β has been implicated in the pathogenesis of a number of the hereditary periodic fever syndromes. One such syndrome, Muckle–Wells syndrome (MWS), is characterised by the triad of urticaria, progressive sensorineural deafness and systemic amyloid A amyloidosis. Other features include rigors, leucocytosis, raised acute phase reactants and serum amyloid A levels. A number of case reports have recently emerged involving treatment with the recombinant human IL-1 receptor antagonist, Anakinra (Kineret; Amgen, Cambridge, UK) [1–3].

Case report A 59-year-old caucasian female presented with increasingly severe and intractable disease over a 15-year period. In addition to the above features, she also exhibited papilloedema and chronic aseptic meningitis. No other family members were affected. Upon commencing treatment with Anakinra, there was complete resolution of her inflammatory symptoms within 24–48 hours, and rapid normalisation of her C-reactive protein and serum amyloid A levels (from 415.0 mg/l to 12.6 mg/l after 4 weeks of therapy). Her intracranial pressure and CSF white cell counts also returned to normal. Audiometry confirmed a 15–30 decibel improvement in the 250–4000 Hz frequency range in each ear. No mutations of the responsible gene – NALP3/CIA51 on chromosome 1q44 – were demonstrated on her DNA sequencing.

Discussion Our patient is the oldest reported sporadic case of MWS. Heterozygous missense mutations have thus far been reported in only 60% of MWS patients analysed [4]. The confirmed improvements in hearing, intracranial pressure, and CSF white cell counts seen here with Anakinra lend further support to the treatment of the autoimmune inflammatory conditions by targeting IL-1. The pathogenesis of the sensorineural deafness in MWS is uncertain although it is postulated that expression of mutated NALP3/CIA51 in cartilage may have a causative role [3].

References


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P97
The cytokine memory of SmD183-119-autoantigen-specific Th cells of systemic lupus erythematosus patients

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Objective The aim of the study was to analyze the cytokine memory of Th cells derived from systemic lupus erythematosus (SLE) patients and healthy donors for autoantigen-specific T cells by in vitro stimulation with SmD183-119, a common autoantigen in SLE.

Method Autoreactive CD8+ T cells derived from 37 SLE patients and 14 healthy donors were enriched by repetitive ex vivo stimulation of peripheral blood mononuclear cells with SmD183-119. For control, peripheral blood mononuclear cells were stimulated only with IL-2. After two rounds of antigen stimulations, cultures were stimulated with phosphor 12-myristate 13-acetate/ionomycin for intracellular cytokine staining. Frequencies of cytokine-expressing T cells were analyzed and, in SLE patients, compared with disease activities and autoantibody levels.

Results Comparing cultures from SLE patients with those from healthy donors, SLE patients displayed higher frequencies of tumor necrosis factor alpha-positive T cells and the frequencies correlated with disease activity. SmD183-119-induced tumor necrosis factor alpha expression was associated with serum amyloid A levels. The frequencies of IL-10-expressing T cells were lower in cultures from SLE patients. Cultures from patients with high frequencies of IL-10+ T cells revealed low disease activities. SmD183-119-induced increases in IL-10-expressing T cells were associated with low anti-dsDNA and anti-SmD183-119 antibody levels in culture supernatants.

Conclusion The enrichment of SmD183-119-reactive T cells by in vitro cultures showed that cytokine changes specifically occur in lupus patients. The results give insight into the cytokine memory of autoreactive Th cells and their role in lupus pathogenesis.

P98
PTPN22 as a rheumatoid arthritis susceptibility but not severity gene

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Background Due to the complex multigenic nature of rheumatoid arthritis (RA) identification of RA susceptibility and severity genes appears to be more challenging than originally anticipated. Among many recently reported RA susceptibility genes, a missense single nucleotide polymorphism in the protein tyrosine phosphatase PTPN22 appears to be involved in susceptibility to multiple autoimmune diseases including diabetes, systemic lupus erythematosus and Graves disease. Whether this polymorphism is also associated with severity of the phenotype in diseased individuals is not known. PTPN22 encodes a hematopoietic phosphatase also known as Lyp that functions as a negative regulator of T-cell activation via interaction with the c-Src tyrosine kinase Csk and phosphorylation of regulatory tyrosines or other Src family kinases, such as Lck and Zap70. The R620W polymorphism results in substitution of conserved arginine with tryptophan in the proximal SHH-3 binding domain of PTPN22, which is necessary for interaction with Csk. In vitro experiments show that the W620 variant of PTPN22 is less efficiently to Csk, suggesting T cells expressing this allele may be hyper-responsive and more prone to autoimmunity.

Objective To investigate the association of R620W polymorphism with RA in a Dutch Caucasian population and to determine whether this polymorphism associates with a qualitative phenotype of RA (remission versus progression) or a quantitative phenotype (rate of joint damage).

Methods PTPN22 genotyping was performed on DNA from 425 RA and 343 undifferentiated arthritis patients participating in the Leiden Early Arthritis Clinic and over 200 control individuals, both of Dutch Caucasian origin. Samples were genotyped using allele-specific genetic PCR. Disease features were measured as previously published. X-rays were scored every year.

Results We confirmed association of the R620W allele of PTPN22 polymorphism with RA in our Dutch Caucasian population. Minor allele frequencies of 0.07 and 0.12 were found in controls and cases, respectively, with P = 0.008 and an allelic odds ratio of 1.91, 95% confidence interval = 1.18–3.11. Surprisingly, the R620W allele appeared to be a susceptibility gene for undifferentiated arthritis that either progresses or does not progress to RA. PTPN22 status did not influence the disease persistency, as analyzed in the remission versus non-remission group, or the disease severity as determined by analysis of joint damage.

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Available online http://arthritis-research.com/supplements/7/S1
Progression of joint damage (Sharp–van der Heijde units).

Conclusion: Our results suggest that the R620W allele of PTPN22 increases susceptibility to RA but does not confer risk to a more severe disease course either with respect to joint destruction or with respect to disease severity.

P99
Tryptase as a PAR-2 activator in joint inflammation
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Background Protease-activated receptor-2 (PAR-2) is one of a family of G-protein coupled transmembrane receptors activated by proteolytic release of a ‘tethered’ ligand. We previously reported this receptor has a pivotal role in chronic joint inflammation using a PAR-2 ‘knockout’ mouse [1], but the serine protease responsible for its activation remains uncertain.

Objective We investigated whether β-trypsin has proinflammatory actions in the mouse knee and specifically whether a tryptase inhibitor can modulate experimentally induced chronic joint inflammation.

Methods Five micrograms of human β-trypsin was injected into the knee joint cavity of two groups of anaesthetized (Halothane/O₂) C57BL/6J mice and PAR-2 gene disrupted mice (PAR-2–/–) but is virtually absent in PAR-2 gene disrupted (PAR-2–/–) mice but is virtually absent in PAR-2 gene disrupted (PAR-2–/–) mice. The activity of tryptase was assayed by comparing caliper measurements of knee joint diameter pre-injection and post-injection. Chronic monoarthritis was induced using the emulsion. In a parallel group of mice, 50 µg of the tryptase inhibitor 4-amidino phenyl pyruvic acid (APP) was co-administered with the FCA/methycellulose emulsion. Intra-articular injection of Freunds complete adjuvant (FCA) (in 5% methycellulose). In

Results Intra-articular injection of β-trypsin resulted in rapid joint swelling in wild-type mice that was completely abrogated in PAR-2–/– mice (Fig. 1a), suggesting that tryptase-mediated inflammatory actions require functional PAR-2.

Conclusion: The present study indicates that SLE-SS and the SLE-noSS patients are immunogenetically dissimilar, whereas there is an apparent close immunogenetic relationship between SLE-SS and pSS patients. Furthermore, our data corroborate that the synergistic interactions between distinct pairs of alleles in the DR or the DQ locus confer higher relative risk for these diseases and for distinct clinical manifestations than each of these alleles individually. In pSS patients, the DRB1*0301-*1104 heterozygote genotype, whereas SLE-SS patients had an increased frequency of the genotypes DQA1*0101-DQB1*0602 with regulatory associations with proteins than single alleles. The absence of PAR-2 increases frequency of the DRB1*1501-DQA1*0102-DQB1*0602 haplotype. In SLE-SS patients, positive associations of the DQB1*0201 allele with anti-dsDNA (strong) and of DQA1*0501 with anti-La/SSB (marginal) were observed. In SLE-noSS, DQB1*0301-DQB1*0602 was strongly positively associated with intestinal lung disease. DQB1*0301-DQB1*0602 with central nervous system involvement, DQA1*0501 with serositis and DRB1*1501 with anti-dsDNA, whereas DQB1*0301 homozygosity demonstrated a significant protective effect for glomerulonephritis. In pSS patients, the DRB1*0301-DQA1*0104 and DQB1*0201- *0301 genotypes were strongly positively associated with purpura, DQB1*1104- *1501 with arthritis, DQB1*0201-*0502 with renal tubular acidosis, DQB1*0301 homozygosity with lymphadenopathy, DQA1*0501 homozygosity with low C4 and DRB1*0301 allele with anti-La/SSB, low C4 and cryoglobulinemia. In these patients, the extended haplotype DRB1*0301-DQA1*0105-DQB1*0201/ DRB1*1104-DQA1*0501-DQB1*0301 associated strongly with the occurrence of low C4, anti-La/SSB and purpura.

Conclusions The present study indicates that SLE-SS and the SLE-noSS patients are immunogenetically dissimilar, whereas there is an apparent close immunogenetic relationship between SLE-SS and pSS patients. Furthermore, our data corroborate that the synergistic interactions between distinct pairs of alleles in the DR or the DQ locus confer higher relative risk for these diseases and for distinct clinical manifestations than each of these alleles individually. In pSS, the presence of the extended haplotype DRB1*0301-DQA1*0501-DQB1*0201/ DRB1*1104-DQA1*0501-DQB1*0301 appears to associate with adverse predictors for lymphoma development.

P101
Specific inhibition of FoxO transcription factors in rheumatoid arthritis synovial tissue
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Background Phosphorylation-dependent inactivation of FoxO transcription factors by the proto-oncogene product protein kinase B (PKB) plays a central role in promoting cellular survival, proliferation, and activation mediated by PI3-kinase. PI3-kinase-dependent activation of PKB has been observed in rheumatoid arthritis synovium.

arthritus (RA) synovial tissue, and blocking PKB activation has a protective effect in animal models of arthritis. However, the molecular mechanisms by which activation of PKB promotes arthritis have not been elucidated.

**Objectives**

To determine whether FoxO transcription factors (FoxO1, FoxO3a, and FoxO4) are specifically inactivated in RA synovial tissue, to identify cell types in RA synovial tissue in which FoxO proteins are inactivated, and to identify inflammatory stimuli relevant to RA that inactivate FoxO transcription factors in cultured RA fibroblast-like synoviocytes (FLS) in vitro.

**Methods**

Expression and PKB-dependent phosphorylation of FoxO1, FoxO3a, and FoxO4 were determined using specific antibodies in immunohistochemical and computer-assisted quantitative digital analysis of synovial tissue sections obtained from 12 RA and nine osteoarthritis (OA) patients. Double labelling with cell-specific antibodies was performed to identify FoxO expression and inactivation in specific cell populations. In vitro, cultured RA (n = 3) and OA (n = 2) FLS were stimulated with tumour necrosis factor (TNF) alpha, transforming growth factor (TGF) beta, or soluble CD154 prior to lysis and detection of FoxO phosphorylation by immunoblotting. FLS proliferative responses to these stimuli were determined in the presence and absence of the PI3-kinase inhibitors 3,4-difluorophenylalanin (DRO) or wortmannin (WMN).

**Results**

Phosphorylated inactive FoxO1, FoxO3a, and FoxO4 were observed in both RA and OA synovial tissue. Inactivation of FoxO1, FoxO3a, and FoxO4 was restricted to FLS, T lymphocytes, and synovial macrophages, respectively. Inactivation of FoxO1 and FoxO4 was significantly enhanced (P < 0.05) in RA synovial tissue compared with OA synovial tissue. No significant differences in the inactivation of T lymphocyte FoxO3a were observed between RA and OA synovial tissue. In vitro, PKB3-dependent inactivation of FoxO1 was observed in RA FLS following stimulation with TNF, TGF, and soluble CD154. Inactivation of FoxO1 was not sufficient to promote FLS proliferation, as only TNF and TGF but not soluble CD154 stimulated PI3-kinase-dependent FLS proliferation. Our studies demonstrate that inactivation of FoxO1 and FoxO4 is enhanced in RA compared with OA, provide the first (patho)physiological evidence of FoxO4 inactivation in vivo, and suggest important roles for FoxO1 and FoxO4 in maintaining, respectively, FLS and macrophage activation and survival in RA synovial tissue.

**P102**

Quantitative and qualitative analysis of CD4+CD25+ regulatory T cells in systemic lupus erythematosus patients

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CD4+CD25+ regulatory T cells (Treg) that specialize in the suppression of immune responses play a critical role in the regulation of peripheral immune tolerance and thus might be critically involved in the pathogenesis of autoimmune diseases. As for systemic lupus erythematosus (SLE), however, data concerning Treg are so far limited. We therefore initiated detailed quantitative and qualitative analysis of naturally occurring CD4+CD25+ Treg from SLE patients as compared with healthy controls. FACs analysis revealed increased proportions of CD4+CD25+ Treg, as well as activated CD4+CD69+ T cells, among peripheral blood mononuclear cells in SLE patients as compared with healthy controls. Ongoing experiments aim to analyze the capacity of purified CD4+CD25+ Treg to suppress the proliferation of autologous or allogeneic T cells. Preliminary results indicate a tendency towards a reduced suppressive capability of CD4+CD25+ Treg in SLE patients as compared with healthy controls. Additional experiments will determine the statistical significance of this observation and will correlate quantitative and/or qualitative defects of Tregs in SLE patients with clinical data. Finally, this study will also allow one to experimentally abrogate potential defects of Treg in SLE patients. This might provide the basis for new therapeutic concepts in the treatment of SLE and other autoimmune diseases.

**P103**

HSP70/J-protein chaperone machines: expression analysis in granulocytes

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Background: Polymorphonuclear leucocytes (PMNLs) represent the first line of defense in innate immunity. PMNLs are the predominant cell type accumulating in the synovial fluid of rheumatoid arthritis (RA) patients and play a crucial role in the development of tissue damage. Unstimulated PMNLs are postmitotic terminally differentiated cells whose default setting is death by apoptosis. Pathogens or inflammation induce a profound transcriptional and translational activity. Abrupt expression of the proliferation of autologous or allogeneic T cells. Preliminary results indicate a tendency towards a reduced suppressive capability of CD4+CD25+ Treg in SLE patients as compared with healthy controls. Additional experiments will determine the statistical significance of this observation and will correlate quantitative and/or qualitative defects of Tregs in SLE patients with clinical data. Finally, this study will also allow one to experimentally abrogate potential defects of Treg in SLE patients. This might provide the basis for new therapeutic concepts in the treatment of SLE and other autoimmune diseases.

**P104**

Genotype-dependent NOS-3 expression and rheumatoid arthritis

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The –786C/C-variant of the endothelial nitric oxide synthase nos-3 gene has been shown to be associated with coronary artery disease because of a blunted inducibility of gene expression [1]. IL-10, a cytokine involved in Th1/Th2 cell differentiation, is a new stimulus for NOS-3 expression [2].

We therefore address the question whether IL-10-induced NOS-3 expression is decreased in individuals with the –786C/C genotype and, if so, whether a Th1-mediated disease like rheumatoid arthritis is associated with this genotype. Endothelial cells were isolated from an umbilical cord vein of known genotype and cultured as described [1]. The expression of NOS-3 was analysed by real-time semi-quantitative RT-PCR [1]. Genotyping was performed as described elsewhere [1]. Patients met the revised criteria of the ACR for the classification of rheumatoid arthritis, and donated blood samples after informed consent.

Primary human umbilical vein endothelial cells with the –786C/C genotype did not respond with an increase in NOS-3 expression to IL-10 incubation (5 ng/ml). This defect could be repaired after pre-incubation of the cells with a decoy oligonucleotide (10 µmol/l) directed against the C-variant of the promoter. Among 587 patients with rheumatoid arthritis tested, incidences for the –786C/C genotype were significantly higher than in the general population (17% versus 7%). In conclusion, NOS-3 is one mediator of anti-inflammatory IL-10 action. Individuals with the –786C/C nos-3 genotype have an increased risk for the development of rheumatoid arthritis. This might be due to the IL-10 insensitivity of the C-variant of the promoter.
S40
Arthritis Res Ther 1

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P105
Anti-high-density lipoprotein antibodies and lipoprotein characteristics in systemic lupus erythematosus-related cardiovascular disease
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Background The risk of cardiovascular disease (CVD) in systemic lupus erythematosus (SLE) is exceedingly high. Previously, a lupus pattern of dyslipidemia has been described (raised triglycerides, and low high-density lipoprotein [HDL]) and we recently reported that these lipid abnormalities were associated with tumor necrosis factor (TNF) activity. Methods Twenty-three women (52 ± 8.2 years) with SLE and a history of CVD (SLE cases) were compared with 26 age-matched women with SLE and no clinical manifestations of CVD (SLE controls) and 26 age-matched healthy women (controls). Lipoprotein-related measurements included lipoprotein particle size determination by use of NMR spectroscopy and affinity of low-density lipoprotein (LDL) to proteoglycans. Antibodies against apolipoprotein A1 (apoA1) in HDL and TNF was between SELISA. Common carotid intima-media thickness was measured by B-mode ultrasound as a surrogate measure of atherosclerosis. Results Anti-apoA1 were raised in SLE cases as compared with SLE controls (P = 0.03) and controls (P = 0.001), and in SLE controls as compared with controls (P = 0.01). Among SLE cases, anti-apoA1 was associated with TNF (P = 0.01). Small dense LDL were more common among SLE controls and controls than in SLE cases (P = 0.036 and 0.086, respectively). Small HDL was more common among controls than in SLE cases and SLE controls (P = 0.001). LDL association with proteoglycans did not differ between groups Activity in the TNF system was significantly associated with triglycerides and negatively with HDL (P < 0.01). Conclusion SLE-related dyslipidemia showed a surprising pattern with large LDL and HDL rather than small; that is, not an expected 'atherogenic' lipid profile. Anti-apoA1 antibodies where strongly associated with CVD in SLE. Whether they may play a pathogenic role (e.g. by inhibiting anti-inflammatory properties of HDL) is presently under investigation.

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P106
Discrepancy between jun/fos proto-oncogene mRNA and protein expression in the rheumatoid arthritis synovial membrane
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Protein/mRNA expression of cjun, junB, junD, and cfos, levels of the mRNA-stabilizing protein HuR were assessed in synovial membranes (SM) from patients with rheumatoid arthritis (RA), osteoarthritis (OA), joint trauma (JT), or postmortem normal controls (NC) using ELISA western blotting and real-time RT-PCR. Protein expression for Jun/Fos proto-oncogenes was significantly increased (JunB and JunD) or numerically increased (cJun and cFos) in RA SM compared with OA, JT, and NC. In contrast, jun/fos mRNA expression was significantly decreased (cJun and junB) or numerically decreased (JunD and cFos) in RA and OA compared with JT or NC. Protein expression levels of AUFL were comparable among the different groups. For TTP and HuR, interestingly, significantly increased protein expression was observed in RA and OA SM compared with either JT or NC. Discrepancies between the mRNA and protein expression for several jun/fos genes suggest broad alterations of post-transcriptional processes in the RA SM. Whereas increased levels of mRNA-stabilizing TTP may contribute to the low levels of jun/fos mRNA, abundant mRNA-stabilizing HuR may augment translation of the remaining mRNA into protein. As a consequence, both increased expression of AP-1-dependent target genes by the activating transcription factors cJun/cFos and modified binding activity of the resulting AP-1 complexes via the action of deactivating JunB and JunD may contribute to the pathogenesis of RA.

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P107
Distinct biological properties of human mesenchymal stem cells from different sources
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Background Mesenchymal stem cells (MSCs) have been isolated from different tissues/organs, but it is not clear whether they possess distinct biological properties. We have previously characterized MSCs from the adult human synovial membrane (SM), which can differentiate at the single cell level to cartilage, bone, adipocytes, and skeletal muscle [1–3]. We have also reported that cells isolated from the adult human peritoneum (P) are chondrogenic in vitro [4]. In the present work, we show that expanded periosteal cells are multipotent. We then compare the chondrogenic and osteogenic potentials of P-MSCs with those of SM-MSCs. Methods MSC populations were enzymatically released from the SM and peritoneum of four adult human donors. To test multipotency, P-MSCs were subjected to in vitro differentiation assay or injected to regenerating tibials anterior surface to induce cartilage formation of nude mice. In vitro chondrogenesis was then evaluated by measuring the mRNA expression of cartilage proteoglycans and by quantification RT-PCR for chondrocyte markers. To investigate bone formation in vivo, MSCs were seeded into Collagraft scaffolds and implanted under the skin of nude mice. Bone formation was assessed by histology and the human origin investigated by in situ hybridization for human ALU genomic repeats and by RT-PCR for bone markers using primers specific for human cDNA. Results P-MSCs underwent chondrogenesis, osteogenesis, and adipogenesis in vitro as well as myogenesis in vivo. Multipotency was inherent at the single cell level. P-MSCs were compared with SM-MSCs from the same donors in the capacity to form cartilage in vitro and bone in vivo. Under our experimental conditions, SM-MSCs displayed greater chondrogenic potential than P-MSCs with MSCs contents of cartilage-specific proteoglycans and higher expression levels of mature chondrocyte markers. For bone formation, engraftment of P-MSCs and SM-MSCs into Collagraft was comparable and either MSC population survived long term in vivo (20 weeks). Histologically, no bone was evident at 4 weeks. At later time points (8–20 weeks), abundant bone formation was detected consistently in all periosteal samples. In contrast, bone was rarely observed, and in small amounts, in the synovial samples, with most human cells contributing to a fibrous-like tissue. In all cases, bone was mostly of human origin. As evaluated by quantitative RT-PCR, the expression levels of human OC, normalized for human beta-actin, were significantly higher in the periosteal samples than in the synovial ones. Bone was neither retrieved in empty Collagraft scaffolds nor in Collagraft scaffolds seeded with human dermal fibroblasts used for a cell negative control. Conclusions Expanded P-MSCs can differentiate to cartilage, bone, adipocytes, and skeletal muscle. Importantly, SM-MSCs displayed a greater chondrogenic potential in vitro than P-MSCs. By contrast, P-MSCs formed bone in vivo consistently and reproducibly as opposed to SM-MSCs. Our results suggest that MSCs derived from different tissue have distinct biological properties, thereby pointing to a need for development of quality controls for MSC preparations in clinical settings.

References

P108
Regulation of T-cell differentiation by IL-4R α-chain single nucleotide polymorphisms
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Chronic inflammation in rheumatoid arthritis (RA) is mediated by repeatedly activated proinflammatory Th1 cells. In contrast, Th2 cells that might downmodulate the...
chronic autoimmune response are rarely found in RA. It has been previously documented that RA T cells are severely impaired in their ability to differentiate into Th2 effectors while exerting enhanced Th1 differentiation. The mechanisms underlying this functional abnormality, however, have not been delineated. As IL-4 is a most critical determinant in regulating immune responses by promoting Th2 cell development and inhibiting Th1 cell differentiation, we analyzed the role of single nucleotide polymorphisms (SNPs) in the IL-4 receptor (IL-4R) α-chain, which is critical for binding of IL-4 and for IL-4 signal transduction, in the differentiation of human T cells. Three hundred and sixty-one healthy individuals were genotyped by allele-specific PCR for the two IL-4R α-chain SNPs that are located in functionally important regions of the IL-4R α-chain — the IL-4SNP and the Q51R SNP551 in the IL-4-binding and STAT6-binding domains, respectively. Naïve and memory CD4-positive T cells were isolated from the peripheral blood of individuals who were homozygous for either allele at SNP50 and SNP551, and were primed for 5 days with mAbs to CD28 and/or CD3 in the presence or absence of exogenous IL-4. The phenotype of the resulting differentiated effector cells was then analyzed by flow cytometric analysis of cytoplasmic cytokines. The SNP551 alleles did not affect T-cell differentiation. In contrast, the inhibitory effect of IL-4 on Th1 cell differentiation was significantly diminished in CD4 T cells that were homozygous for the mutated allele at SNP50 (SOV) as compared with those with the wild type allele (ISO). Likewise, the augmenting effect of IL-4 on Th2 cell differentiation was enhanced on T cells that were homozygous for the wild-type allele as compared with T cells expressing the mutant allele. These data indicate that the mutant allele of the IL-4R α-chain at SNP50 is associated with a decreased T-cell response to IL-4. To delineate a potential mechanism of different responses to IL-4 in the cells expressing different alleles of the IL-4R, T cells form individuals who were homozygous for either the wild-type or the mutant allele at SNP50 were primed with different stimuli — IL-4 and analyzed by flow cytometry for phosphorylated STAT6. Whereas STAT6 concentrations were not different between T-cell expressing ISO or SOV, STAT6 phosphorylation in response to IL-4 stimulation was significantly reduced in T cells expressing the SOV allele compared with T cells expressing ISO. Thus, the SOV SNP50 allele of the IL-4R α-chain might regulate T-cell differentiation by diminishing T-cell responses to IL-4, resulting in a reduced STAT6 phosphorylation and subsequently in diminished Th2 cell differentiation. The SOV SNP50 allele might thereby contribute to the development of unbalanced Th subset activation, as characteristic for autoimmune diseases, such as RA.

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P109 Role of IL-10 as a susceptibility factor for rheumatoid arthritis and cardiovascular disease

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IL-10 polymorphisms, which are located in functionally important regions of the IL-10 gene (ISOV SNPs 50 and 551), have been associated with RA. In a case-control study of 284 RA patients and 568 healthy controls, we observed that the IL-10 promoter polymorphism (P = 0.021). In conclusion, this genetic basis of IL-10 secretion and the functionality of IL-10 promoter polymorphisms, we used the technique of allele-specific transcript quantification to characterise the ratio between two alleles of the IL-10 gene in 15 healthy heterozygous individuals. We identified two groups whereby five healthy donors exhibited a 1:1 ratio whereas seven exhibited a ratio > 1 (P < 0.0017) [2]. Donors heterozygous for haplotype IL-10.2 were only prevalent in the group with higher allelic expression ratios. The G allele of the IL-10 promoter single nucleotide polymorphism –2849 tags this haplotype, providing functional evidence that different allelic transcription partly explains the constant association found with cardiovascular disease in late life.

In conclusion, this study provides evidence that IL-10 haplotypes dictating production of IL-10 are involved not only in conferring susceptibility to RA, but also in risk for cardiovascular death in old age.

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P110 Regulation of myeloid cell function and MHC class II expression by tumor necrosis factor

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Neutralizing agents to tumor necrosis factor (TNF) are the most successful treatment option for individuals with rheumatoid arthritis (RA). In fact, tumor necrosis factor (TNF) neutralization and subsequent inhibition of antigen-presenting myeloid cells in rheumatoid arthritis (RA) provides a 50% lower IL-10 production than controls (P < 0.0017) [2]. Donors heterozygous for haplotype IL-10.2 were only prevalent in the group with lower allelic expression ratios. The G allele of the IL-10 promoter single nucleotide polymorphism –2849 tags this haplotype, providing functional evidence that different allelic transcription partly explains the constant association found with cardiovascular disease in late life.

In conclusion, this study provides evidence that IL-10 haplotypes dictating production of IL-10 are involved not only in conferring susceptibility to RA, but also in risk for cardiovascular death in old age.

Available online http://arthritis-research.com/supplements/7/S1
Methods Activation of H-Ras, K-Ras, and N-Ras homologs in RA SF T lymphocytes were determined by activation-specific GTPase precipitation and immunoblot analysis. T-lymphocyte intracellular ROS production was measured by FACS-based analysis of DCF oxidation. Control, active Ras, and RapGAP constructs were introduced into human Jurkat T cells and healthy donor peripheral blood T lymphocytes by electroporation and nucleofection techniques, respectively. For ROS analysis, cells were cotransfected with RFP to detect transfected cells. For static adhesion assays, a luciferase reporter plasmid was used to detect transfected cells: cells were allowed to adhere to immobilized fibronectin or recombinant human intracellular adhesion molecule, non-adherent cells washed off, and adherent cells quantitated by luciferase assays. In some experiments, cells were preincubated with the pharmacological inhibitors BAPTA-AM, LY294002, and DPI, indicating a calcium-sensitive hydrogen peroxide source of ROS that does not require a functional NADPH oxidase. These results are consistent with our previous observations in purified RA SF T lymphocytes. In contrast, N-Ras, but not H-Ras or K-Ras, induced integrin-dependent adhesion in Jurkat T cells and peripheral blood T lymphocytes. N-Ras-induced adhesion was sensitive to LY294002, indicative of PI3-kinase signaling. Additionally, inactivation of Rap1 with RapGAP had no effect on N-Ras-induced adhesion. This represents the first (patho)physiological signaling pathway by which integrins can be activated independently of Rap1. Our results suggest that selective targeting of H-Ras and N-Ras may allow specific modulation of T-cell ROS production and integrin activation in RA T lymphocytes.


P112 Requirement of IL-17 receptor signaling in resident synoviocytes for development of full blown destructive arthritis E Lubberts1,2, P Schwarzenberger2, W Huang3, JR Schum1, JJ Peschon3, WB van den Berg1, JK Koilis2
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Chronic arthritis is characterized by persistent joint inflammation and concomitant joint destruction. IL-17 is a novel proinflammatory T-cell cytokine suspected to be involved in inflammatory and autoimmune diseases such as rheumatoid arthritis. Here, we report that IL-17 receptor (IL-17R) signaling is required in resident synovial cells for full progression of chronic synovitis and bone erosion. Repeated injections of Gram-positive bacterial cell wall fragments (SCW) directly into the knee joint of naive IL-17R-deficient (IL-17R–/–) mice had no effect on the acute phase of arthritis but prevented progression to chronic destructive synovitis as was noted in wild-type (wt) mice. Micro-array analysis revealed significant down-regulation of leukocyte-specific chemokines, selectins, collagenase-3, and IL-1 in the synovium of IL-17R–/– mice. Bone marrow (BM) chimeric mice revealed the need for IL-17/IL-17R signaling in resident synovial cells for development of full blown synovitis. Chimeric mice of host wt and donor IL-17R–/– BM cells developed destructive synovitis in this chronic relapsing SCW arthritis model similar to wt → wt chimeras. In contrast, chimeric mice of host IL-17R–/– and donor wt BM cells were protected from full blown destructive arthritis similar to IL-17R–/– → IL-17R–/– chimeras. These data strongly suggest T-cell IL-17→IL-17R signaling in resident synovial cells to be a pivotal mechanism through which an acute macrophage-driven joint inflammation progresses into a chronic destructive synovitis. Prevention of local synovial IL-17→IL-17R signaling warrants consideration as a therapeutic target in chronic destructive arthritis.

P113 Different molecules at the surface of stimulated T cells induce IL-1β, tumour necrosis factor and IL-1RA in human monocytes D Burger, N Molnari, L Gruaz, JM Dayer Division of Immunology and Allergy, Clinical Immunology Unit, Faculty of Medicine, University Hospital, Geneva, Switzerland Arthritis Res Ther 2005, 7(Suppl 1):P113 (DOI 10.1186/ar1634)

Imbalance in cytokine homeostasis is thought to play an important part in the pathogenesis of chronic inflammatory diseases such as rheumatoid arthritis. We demonstrated that T cells might exert a pathological effect through direct cellular contact with monocyte-macrophages, inducing a massive upregulation of IL-1β and tumour necrosis factor (TNF) [1]. We showed that this mechanism that might be relevant to chronic inflammation is specifically inhibited by high-density lipoproteins (HDL) [2]. Like many other stimuli, besides proinflammatory cytokines, the contact-mediated activation of monocytes induces the production of cytokine inhibitors such as IL-1Ra. HDL inhibited the production of IL-1β and TNF but not that of IL-1Ra induced in monocytes activated by membranes isolated from stimulated T cells to mimic cellular contact. This was also the case in peripheral blood mononuclear cells stimulated by either phytohaemagglutinin or tetanus toxoid. Similarly, IL-1Ra mRNA expression was not inhibited contrary to IL-1β and TNF mRNA. This demonstrates that different molecules at the surface of stimulated HUT-78 cells are involved in the induction of IL-1β, TNF and IL-1Ra in monocytes, IL-1β and TNF being activated by HDL-specific ligand(s). Separation of CHAPS-solubilized membrane molecules by liquid isoelectric focusing showed that two activity peaks were present; one activating IL-1β, TNF and IL-1Ra production, the other inducing the production of IL-1Ra in the absence of IL-1β and TNF. Further isolation of these two types of factor by gel filtration demonstrated that factor(s) inducing IL-1β, TNF and IL-1Ra displayed a M, around 40,000 kDa, whereas factors inducing IL-1Ra only displayed M, around 70,000 kDa and 30,000 kDa. Thus different factors are expressed at the surface of stimulated T cells that differentially trigger the production of proinflammatory and anti-inflammatory factors, and are differently affected by HDL.


P114 Infliximab treatment does not induce apoptosis in peripheral blood mononuclear cells up to 24 hours after initiation of treatment in rheumatoid arthritis patients CA Wijbrands, P Reinders-Blankert, P Klarenbeek, TJM Smeets, MJ Vervoordeldonk, PP Tak Clinical Immunology and Rheumatology, Academic Medical Center/University of Amsterdam, The Netherlands Arthritis Res Ther 2005, 7(Suppl 1):P114 (DOI 10.1186/ar1635)

Background Apoptosis of peripheral blood T lymphocytes from patients with Crohn’s disease has been described after in vitro activation followed by incubation with infliximab. These ex vivo data raised the question of whether in vivo treatment of rheumatoid arthritis (RA) with the chimeric tumour necrosis factor alpha antibody, infliximab, causes apoptosis in peripheral blood mononuclear cells. This study was designed to detect the early effects of infliximab treatment on apoptosis in peripheral blood of patients with RA.

Methods Ten patients with active RA (Disease Activity Score [DAS 28] ≥ 3.2) received 3 mg/kg infliximab intravenously in combination with methotrexate (mean dose of 25 mg weekly). All 10 patients underwent blood sampling before, 1 hour after and 24 hours after the administration of infliximab. Apoptosis was determined using double staining with annexin-V, as an early marker of apoptosis, and 7-amino-actinomycin D (AAD) to exclude necrotic cells from this population. Peripheral blood erythrocytes were lysed and the mononuclear cells were incubated with the different antibodies. The percentages of annexin-V-positive and 7-AAD-negative monocytes and lymphocytes were analyzed by flow cytometry. For statistical analysis, a paired t test was used to compare the percentages of apoptotic cells 1 hour and 24 hours after treatment with those at baseline.

Results All samples were analyzed for the presence of and change in apoptosis. At baseline, the median percentage of apoptotic monocytes/myeloid cells was 0.90% (range 6.23–0.19); 1 hour after treatment, the median percentage was 0.56% (range 2.90–0.32) and 24 hours after treatment the median percentage was 0.21% (range 2.90–0.00). In the lymphocyte population, the median percentage of apoptotic cells was 0.98% (range 2.15–0.00) at baseline as compared with 0.52% (range 6.30–0.00) 1 hour after treatment and 0.39% (range 2.85–0.00) 24 hours after infliximab administration.

Conclusions In this in vivo study we found no statistically significant increase from baseline in the percentage of apoptotic monocytes or lymphocytes in the peripheral blood of RA patients at 1 hour or 24 hours after infliximab treatment.

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P115 Resistance of rheumatoid arthritis synovial fibroblasts to p38 MAP-kinase inhibition of pro-destructive functions mediated by tumor necrosis factor alpha/tumor necrosis factor receptor-1

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Objectives In rheumatoid arthritis (RA), tumor necrosis factor (TNF) alpha is a major inducer of the proinflammation/pro-destructive functions of synovial fibroblasts (SFB). These effects are predominantly mediated via the TNF receptor-1 (TNFR1). In addition to the NF-κB pathway, the p38 MAP kinase seems to play a central role for the underlying signal transduction. In the present study, RA-SFB were compared with osteoarthritis (OA)-SFB concerning the TNF-α/TNFR1/2-induced secretion of IL-6, IL-8, PGE2, and matrix metalloproteinase-1/tissue inhibitor of matrix metalloproteinase-1 (MMP-1/TIMP-1), as well as the sensitivity to p38 MAP-kinase inhibition.

Methods Early-passage (second) RA-SFB and OA-SFB were analyzed for TNF-α expression by FACS. The cells were then stimulated with TNF-α (10 ng/ml) or agonistic anti-TNFR1 (HTR-9) or anti-TNFFR2 monoclonal antibodies (UTR-1; 10 μg/ml) each with/without inhibition of the p38 kinase by SB203580 (1 μM). Secretion of IL-6, IL-8, PGE2, MMP-1, and TIMP-1 was evaluated by ELISA.

Results RA-SFB and OA-SFB both expressed TNFR1 and TNFR2 on their surface, without significant differences between the two groups. Secretion of IL-6, IL-8, PGE2, and MMP-1, but not TIMP-1, was significantly augmented by stimulation of RA-SFB and OA-SFB with TNF-α. Except for PGE2 (induced via both TNFRs), these effects were exclusively mediated via the TNFR1. Inhibition of p38 kinase reduced the secretion of IL-6 and PGE2 significantly and equally well in RA-SFB and OA-SFB. However, the secretion of MMP-1 was significantly suppressed only in OA-SFB, whereas RA-SFB were insensitive to the inhibition of MMP-1 secretion by p38 inhibition.

Conclusion In early-passage RA-SFB and OA-SFB, TNF-α-induced proinflammation/pro-destructive functions are predominantly mediated by TNFR1. Strikingly, RA-SFB are partially resistant to the suppression of pro-destructive MMP-1 by p38 MAP-kinase inhibition. The underlying structural or functional alterations of the p38 MAP kinase in RA-SFB may contribute to the pathogenesis and/or therapeutic sensitivity of RA.

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P116 Patterns of gene expression in rheumatoid arthritis synovial tissue: inter-patient variability greater then intra-patient variability in a small study

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Background The synovial membrane is not entirely homogeneous, leading to a local variability within a joint. Synovial tissue can be retrieved from patients in a number of ways (e.g. open surgery, blind needle biopsy, and arthroscopy), and the analysis of its gene expression is important for understanding the functional differences within a joint.

Aim To study inter-patient versus intra-patient variability in gene expression in rheumatoid arthritis (RA) synovial tissue.

Patients and methods Orthopaedic samples Three synovial biopsies were taken from three RA patients (patients 1–3) at joint replacement surgery. All nine biopsies were divided into three, creating nine samples from each joint, and a total of 27 samples.

Arthroscopic samples Two to four synovial biopsies were sampled at arthroscopy from four RA patients (patients 4–7) with an inflamed knee joint. Multiple samples were taken from different sites in all patients.

Handling of synovial tissue and microarray analysis All samples were snap frozen and stored at −80°C. Following RNA extraction (at 4°C), reverse transcription, cDNA amplification and labelling, each sample was hybridised in duplicate against a reference, on a CDNA array locally produced, representing 18,139 unique genes. After data filtering, genes were defined as differentially expressed (DE) if they had a B score > 0 and a fold change > 2. Several hierarchical clusterings were performed to obtain an overview of the data. DE genes in the samples were used to compare the variation between samples from one biopsy, the variation between biopsies from one joint and the variation between biopsies from different patients. Clustering also allowed comparisons between the sampling techniques.

Results In the orthopaedic subset, variation between samples within one biopsy (patients 1–3) was between 1.2% and 6.7% of analysed genes. The amount of DE genes between biopsies was between 1.2% and 5.9%. Hierarchical clustering of biopsies showed more similarities within a patient than between patients, except for one biopsy. One biopsy from patient 1 clustered with biopsies from patient 2 because the other two biopsies from patient 1 had higher fat cell content (confirmed microscopically) than any of the other biopsies. This was confirmed by gene expression profiles with activity in the fatty acid and lipid metabolism. When these genes were removed from the analysis, the samples clustered perfectly according to patient. The analysis of the arthroscopic subset (patients 4–7) showed a variation of DE genes between biopsies of 0.3–1.6%, and a perfect matching in cluster analysis with all biopsies from the same patient clustering together, without any further labouiring with data.

Table 1

<table>
<thead>
<tr>
<th>Patients</th>
<th>Average sample weight (mg)</th>
<th>Total RNA yield (mg)</th>
<th>RNA yield per milligram of tissue (mg)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Patients 1–3</td>
<td>32.9</td>
<td>14,808</td>
<td>502</td>
</tr>
<tr>
<td>Patients 4–7</td>
<td>19.0</td>
<td>9834</td>
<td>407</td>
</tr>
</tbody>
</table>

Conclusions This study shows that inter-patient variability is greater than intra-patient variability in gene expression, in RA synovial tissue. We found that one biopsy is enough to represent one patient as they clustered nicely together, with one exception, which was related to high content of fat cells in the biopsy. Variability is in the same order of magnitude in samples close to each other as compared with those further apart within the same patient.

P117 Association of FCGR2A and Fc gamma receptor haplotypes with Spanish polymyalgia rheumatica and giant cell arteritis

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Background Polymyalgia rheumatica (PMR) and giant cell arteritis (GCA) are two inflammatory diseases that are thought to arise from a complex interaction between multiple genetic factors and environmental triggers. We have previously demonstrated an association between the Fc gamma receptor (FcγR) genetic locus on chromosome 1q22-23 and rheumatoid arthritis, and have now extended our study to include other inflammatory/autoimmune diseases.

Methods The FCGR2A-131HR, FCGR3A-158FIV and FCGR3B-NA1/NA2 functional polymorphisms and a novel FCGR2B 3′-UTR polymorphism were examined for association with PMR (n = 89) and GCA (n = 83) in two well-characterised clinical cohorts from Northern Spain. In view of the close molecular proximity between FCGR2A, FCGR3A, FCGR3B and FCGR2B we have examined FcγR haplotypes for association with rheumatoid arthritis. Pairwise disequilibrium coefficients (D′) were initially calculated in 115 matched controls. The EHPlus program was used to estimate haplotype frequencies for patients and controls and to determine whether significant linkage disequilibrium was present. A likelihood ratio test was performed to test for differences between the haplotype frequencies in cases and controls. A permutation procedure implemented in this program enabled 1000 permutations to be performed on all haplotype associations to assess significance.

Results There was borderline linkage disequilibrium between FCGR2A and FCGR3A (D′ = −0.313, P = 0.03) with more significant disequilibrium between FCGR2A and FCGR3B (D′ = −0.646, P = 0.0001). There was a significant difference in the FCGR2A allele (P = 0.03) and genotype frequencies (P = 0.03) with GCA compared with controls. Specifically, there was an increase in the FCGR2A-131HR genotype in both the PMR (odds ratio [OR] = 2.15; 95% confidence interval [CI] = 1.0–4.7, P = 0.04) and GCA (OR = 2.53, 95% CI = 1.3–5.1, P = 0.01) populations compared with controls.

Increased homozygosity for the FCGR2A/FCGR3A 131R/158B haplotype was associated with 25% of PMR (OR = 4.20, 95% CI = 1.3–13.1, P = 0.01) and 24% GCA (OR = 4.46, 95% CI = 1.5–3.3, P = 0.004) individuals. Logistic regression analyses suggested that both FCGR2A and FCGR3A contributed to GCA susceptibility. In addition, homozygosity for the
FCGR3A/FCGR3B 158F-NA2 haplotype was found in 25% controls compared with 44% GCA subjects (OR = 2.35, 95% CI = 1.0–5.7, P = 0.06). Logistic regression analyses suggested that FCGR3A was the most important site contributing to GCA susceptibility. A subgroup of GCA patients who had experienced visual symptoms was examined. Homozygosity was seen in 25% controls, 27% GCA without eye involvement and 63% GCA with visual manifestations (OR = 0.83, 95% CI = 0.9–3.89, P < 0.08). For each haplotype logistic regression analyses suggested FCGR3A was the most important site.

Conclusions We have demonstrated that FCGR2A may contribute to the ‘susceptibility’ of PMR and GCA in this Spanish population. The increased association of this haplotype suggests the presence of additional genetic polymorphisms in linkage disequilibrium with this haplotype that may contribute to the risk, in a mouse model of systemic lupus erythematosus. FCGR3A haplotypes may define a subpopulation of individuals at higher risk of vascular occlusion. These findings may ultimately provide new insights into disease pathogenesis.

Acknowledgement This work was funded by The Health Foundation.

P118 Noggin haploinsufficiency influences severity of arthritis in different mouse models
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Introduction The severity and outcome of chronic arthritis is determined by the balance between destructive and homeostatic or anabolic molecular signaling pathways. Increasing evidence suggests a role for embryonic signaling pathways essential for development and growth, in the maintenance of tissue homeostasis and in the induction of repair. Unintely or inappropriate activation of such pathways may also have a role in the progression of some diseases. Bone morpho-genetic proteins (BMPs), originally identified as protein factors that induce a cascade of endochondral bone formation, have critical functions in cell proliferation, differentiation, adhesion and death. We have previously identified different BMPs in patients with chronic arthritis [1]. In this study, we evaluate the effect of shifting the balance in BMP signaling by reducing endogenous levels of noggin, a BMP antagonist, to study a mouse model of ankylosing spondylitis in the absence of a specific genetic mutation.

Materials and methods Heterozygous mice with a targeted inactivation of the noggin gene and insertion of a β-galactosidase reporter gene (noggin(−/−);lacZ) (a gift from R Harland, Berkeley, USA) or the wild-type noggin(+/+) were crossed into the DBA/1 background for more than eight generations. mBSA-induced arthritis (colony induced arthritis [CIA]), a model of cartilage destruction (methylated BSA [mBSA]-induced mono-arthritis) and a model of ankylosing enthesitis and spondyloarthritis (spontaneous arthritis in male DBA/1 mice).

Results Noggin haploinsufficiency did not affect the incidence or clinical severity of CIA in DBA/1 mice. No differences in histological severity were seen. The histological severity of mBSA-induced monoarthritis in noggin(−/−);lacZ mice was similar to that of wild-type mice. However, cartilage destruction as determined by digital image analysis of proteoglycan content was significantly reduced in noggin(−/−);lacZ mice suggesting a protective role for BMP signaling. Disease incidence and severity of spontaneous arthritis was similar in noggin(−/−);lacZ and wild-type DBA/1 mice. However, histological analysis of this arthritis showed a slower disease progression in the haploinsufficient mice. Progression of ankylosing enthesitis, in particular chondrocyte hypertrophy and new bone formation, was delayed as compared with wild-type mice. The involvement of noggin in these processes was confirmed by immunohistochemistry for noggin in wild-type mice and LacZ staining in noggin(−/−);lacZ mice.

Conclusions Noggin haploinsufficiency has a protective effect on proteoglycan loss in a mouse model of cartilage destruction. Noggin haploinsufficiency also slows the progression of ankylosing enthesitis in a mouse model of spondyloarthritis. The role of noggin in ankylosing enthesitis is similar to what is seen during endochondral bone formation in development. These data provide further evidence that embryonic molecular signaling pathways, and BMP signaling in particular, are involved in the balance between tissue destruction, homeostasis and repair.


Acknowledgements MD and RL contributed equally to this work. RJUL is the recipient of a post-doctoral fellowship from the Fund for Scientific Research Flanders. This work was supported by research grant 0.390.03 from the Fund for Scientific Research Flanders and a Bristol-Myers-Squibb EULAR Young Investigator Award to RJUL.

P119 Toll-like receptor expression in synovial fibroblasts and normal skin fibroblasts and induction of matrix metalloproteinase expression by various Toll-like receptor ligands
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Toll-like receptors (TLRs) are pattern recognition receptors of the innate immune system. TLR2 has been demonstrated to be expressed in synovial tissue of patients with rheumatoid arthritis (RA) as well as in cultured synovial fibroblasts of patients with RA and osteoarthritis. However, it is not known whether other members of the TLR family are expressed in synovial fibroblasts. We have therefore examined the expression of TLR1–TLR9 in these cells and performed stimulated expression experiments using specific TLR ligands. TLR and matrix metalloproteinase (MMP) mRNA expression was analysed by real-time PCR using 18S-cDNA as an internal control. A difference of five or more cycles between cDNA of the samples and non-RT control was considered to be the detection limit. While all fibroblasts expressed TLR1–TLR6, the expression of TLR2 and TLR3 was significantly higher in synovial fibroblasts from patients with RA as compared with normal skin fibroblasts. TLR7, TLR8 and TLR9 mRNA did not reach the detection level. To assess the function of these TLRs, cultured synovial and skin fibroblasts were stimulated with the TLR ligands bacterial lipopolysaccharide, poly (I:C), lipopolysaccharide and flagellin. All ligands stimulated the expression of MMP1, MMP3, MMP9 and MMP13 to a certain extent. Whereas the TLR2 ligand bacterial lipopolysaccharide preferentially induced the expression of MMP1 and MMP3, the TLR3 ligand poly (I:C) was a more efficient inducer of MMP13 and MMP3 and also induced MMP1 to a lesser extent. Normal skin fibroblasts expressed significantly lower levels of MMP3 and MMP13 mRNA as compared with synovial fibroblasts of patients with RA. Our data extend previous reports on the expression of TLRs on synovial fibroblasts to include TLR1–TLR9 and document that these TLRs are functional. Further experiments, focused on the TLR ligand and MMP expression is differentially induced. This supports the notion that activation of TLR signalling pathways might contribute to joint inflammation and destruction in RA.

P120 Exploring mechanisms of inflammatory hyperalgesia in murine collagen-induced arthritis
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Rheumatoid arthritis (RA) is an autoimmune inflammatory disorder, characterised by joint swelling and diffuse chronic pain. RA patients display both hyperalgesia (an exaggerated painful response to a noxious stimulus) and allodynia (a painful response to a non-noxious stimulus). Collagen-induced arthritis (CIA) in the mouse is a well-established model of RA that may be useful in the study of inflammatory hyperalgesia.

The aim of this study was to establish CIA as a model for studying inflammatory hyperalgesia by examining the nociceptive changes that occur in the nociceptive system during the course of arthritis.

Arthritis was induced by injection of 2 mg/ml bovine type II collagen in complete Freund’s adjuvant into the base of the tail of male DBA/1 mice (n = 30). Behavioural analysis was performed for 28 days following arthritis onset. Mechanical and thermal hyperalgesia was assessed using the Plantar Von-Frey microsensor system and the Hargreaves Plantar test, respectively. Animals were sacrificed at intervals after arthritis onset, and the lumbar spinal cord was collected and immunostained for astrocytes using antibodies to glial fibrillary acidic protein.
The development of mechanical hyperalgesia in mice with collagen-induced arthritis.

Prior to onset of inflammation (post immunisation), little hyperalgesia occurred. Following arthritis onset there was a rapid decrease in both mechanical (Fig. 1) and thermal thresholds, reaching a maximum at 7–10 days after onset. Thermal threshold return to naïve levels 24 days following arthritis onset, while mechanical hyperalgesia remained throughout the study. Increased gial fibrillary acidic protein expression was detected in the spinal cord from the day of arthritis onset, indicating that astrocytic activation occurs in CIA. This is in agreement with a well-established inflammatory model used for the study of pain, complete Freund’s adjuvant-induced monoarthritis.

Our results indicate that CIA can be used in the study of pain, and that changes occur in the nociceptive system during inflammation. As CIA is a well-established and validated model of RA, it may be of benefit to test analgesics aimed at inflammatory hyperalgesia.

Acknowledgement This work is supported by GlaxoSmithKline.

P121

Association of FCGR3A and FCGR3B haplotypes with rheumatoid arthritis and primary Sjögren's syndrome

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Background Rheumatoid arthritis (RA) is an autoimmune disease that is thought to arise from a complex interaction between multiple genetic factors and environmental triggers. We have previously demonstrated an association between a Fc gamma receptor (FcγR) haplotype and RA in a cross-sectional cohort of RA patients. We have sought to confirm this association in an inception cohort of RA patients and matched controls. We also extended our study to investigate a second autoantibody associated rheumatic disease, primary Sjögren’s syndrome (SjS).

Methods The FCGR3A-158F/V and FCGR3B-NA1/NA2 functional polymorphisms were examined for association in an inception cohort of RA patients (n = 448), and a well-characterised SjS cohort (n = 83) from the United Kingdom. Pairwise disequilibrium coefficients (D') were calculated in 267 Blood Service healthy controls. The EHPplus program was used to estimate haplotype frequencies for patients and controls and to determine whether significant linkage disequilibrium was present. A likelihood ratio test is performed to test for differences between the haplotype frequencies in cases and controls. A permutation procedure implemented in this program enabled 1000 permutations to be performed on all haplotype associations to assess significance.

Results There was significant linkage disequilibrium between FCGR3A and FCGR3B (D' = -0.445, P = 0.001). There was no significant difference in the FCGR3A or FCGR3B allele or genotype frequencies in the RA or SjS patients compared with controls. However, there was a significant difference in the FCGR3A-FCGR3B haplotype distributions with increased homozygosity for the FCGR3A-FCGR3B 158V-NA2 haplotype in both our inception RA cohort (odds ratio = 2.15, 95% confidence interval = 1.1–4.2 P = 0.027) and SjS (odds ratio = 2.83, 95% confidence interval = 1.0–8.2, P = 0.047) compared with controls.

The reference group for these analyses comprised individuals who did not possess a copy of the FCGR3A-FCGR3B 158V-NA2 haplotype.

Conclusions We have confirmed our original findings of association between the FCGR3A-FCGR3B 158V-NA2 haplotype and RA in a new inception cohort of RA patients. This suggests that there may be an RA-susceptibility gene at this locus. The significant increased frequency of an identical haplotype in SjS suggests the FcγR locus may contribute to the pathogenesis of diverse autoantibody-mediated rheumatic diseases.

Acknowledgements SM and JR are joint first authors. This work was funded by the Arthritis Research Campaign.

P122

Non-traditional risk and protective factors for cardiovascular disease in systemic lupus erythematosus

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Background There is an important inflammatory and autoimmune component to atherosclerosis and cardiovascular disease (CVD). It is therefore interesting that the risk of CVD is so exceedingly high in patients with systemic lupus erythematosus (SLE).

Objective To investigate the role of non-traditional risk and protective factors for CVD related to inflammation and immune activation in SLE-associated CVD.

Methods Twenty-six women (52 ± 8.2 years) with SLE and a history of CVD (SLE cases) were compared with 26 age-matched women with SLE and no clinical manifestations of CVD (SLE controls) and 26 age-matched healthy women (population controls). As a surrogate measure of atherosclerosis, common carotid intima-media thickness and plaque occurrence were detected by B-mode ultrasound. Circulating levels of oxidized low-density lipoprotein (LDL) were measured by a mAb-4E6-based competition ELISA. Several novel non-traditional risk factors identified by us and others were determined in serum: heat shock protein (HSP)-related factors (Hsp60, Hsp70 and anti-human Hsp60, anti-human Hsp70 and anti-mycobacterial Hsp65 antibody levels), platelet activating factor-acetylhydrolase activity (PAF-AH) and secretory phospholipase A2 G2A (sPLA2). Anti-bodies against endothelial cells (aEC) were measured by in-house ELISA.

Results The circulating levels of oxidized LDL and activity levels of PAF-AH, but not HSP-related measurements, aEC antibodies or sPLA2, were significantly raised in SLE cases. Oxidized LDL levels and PAF-AH discriminated between SLE controls and SLE cases (P = 0.0282 or P = 0.008, respectively). PAF-AH was significantly associated with LDL and cholesterol among SLE/CVD (r = 0.50, P = 0.009 and r = 0.54, P = 0.004), but not in the other groups tested.

Conclusion The difference in oxidized LDL levels between SLE cases and SLE controls may indicate that increased LDL modification by oxidation is one of the underlying factors implicated in SLE-related CVD. The association between PAF-AH and LDL adds support to the notion that PAF-AH, which binds to LDL, might contribute to atherosclerosis in SLE patients. We cannot exclude that PAF-AH is simply a secondary marker of other as yet unknown processes. The role of HSP-related measurements in CVD in general is complex, since aHSP65 appears to be atherogenic while HSP70 may be protective. In the present cross-sectional study, the HSP-related measurements and those of aEC and sPLA2 were not associated with SLE.

P123

Immunomodulatory effect of unpulsed-immature dendritic cells in collagen-induced arthritis

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Objective Dendritic cells (DC) play an important role for initiation and regulation of immune response. Recent experimental evidence points out the fact that immature dendritic cells (IDC) can mediate tolerance, presumably by the induction of regulatory T cells. Therefore, we explored the effects of IDC injection on the development of collagen-induced arthritis in mice and compared them with tumour necrosis factor-matured DC, which we were previously shown efficient in collagen-induced arthritis.

Methods Murine bone marrow-derived DC cultured in the presence of GM-CSF and IL-4 for 6 days and were incubated or not for 24 hours with bovine type II collagen (bCII). The immature phenotype of DC was controlled by flow
cytometry, IL-12p40 secretion and MLR assays. The iDC were repetitively injected 7, 5 and 3 days before arthritis induction with bCII. Mice were boosted on day 21 and the disease course was monitored until day 50. Paw swellings were measured over time, and radiological and histological analyses of paws were performed at euthanasia. The antigen-specific T-cell proliferative response of spleen cells, the Th1/Th2 cytokine production, and the serum levels of IgG1, IgG2, anti-bCII antibodies were measured.

Results The repetitive injection of tumour necrosis factor alpha-modulated DC loaded with bCII protects the mice from severe arthritis. This protective effect is antigen dependent of the DC loading with bCII. The immunosuppressive effect is associated with a decrease of the anti-bCII antibodies from the IgG2a isotype, together with the inhibition of interferon gamma synthesis and the decrease proliferation of bCII-specific cells.

Our data show that repetitive injection of immature unloaded DC protects the animals significantly as 70% of the mice did not develop clinical signs of the disease. We quantitated the various regulatory populations in the vaccinated mice, and observed in the liver and spleen an increase of the T-cell population expressing the CD49b molecule (DX5 cells). The relevance of this population in induced protection is under investigation.

Conclusion The use of iDC to modulate the autoimmune response is a rational approach for cell therapy in diseases such as rheumatoid arthritis.


In the synovial membrane, early mRNA elevations of IL-1β and IL-6 (6 hours; 450-fold and 200-fold, respectively) positively correlated with the joint swelling. A siflod tumour necrosis factor alpha increase was not significant. Not only IL-2 and interferon gamma (INF-γ) (104-fold and 200-fold, respectively), but also IL-5 and IL-10 increased acutely (6 hours–day 1; threefold and 35-fold, respectively). In general, the protein levels for IL-1β, IL-6, tumour necrosis factor alpha, INF-γ, IL-4, and IL-10 (increase between fourfold and 15-fold) matched the course of mRNA expression.

In the inguinal lymph node there were early mRNA elevations of IL-6 (6 hours; 2.5-fold; positively correlated with the joint swelling) and IL-2 (6 hours; fourfold), as well as later rises of IL-4 and IL-5 (day 3; 2.5-fold and fourfold, respectively). At the protein level no significant elevations were observed in comparison with day 0, except for IL-1β (day 6) and IL-10 (day 1).

In the spleen, there were significant mRNA elevations at 6 hours of IL-1β (1.5-fold), IL-6 (fourfold; positively correlated with the joint swelling), INF-γ (threefold), and IL-2 (sevenfold to 10-fold), IL-6 and IL-10 (twofold and threefold, respectively) increased by day 3. Increases at the protein level were significant compared with day 0 only in the case of IL-2 (day 6).

By day 6 (transition to the chronic phase) the mRNA for cytokines declined to or and IL-2 (sevenfold to 10-fold). IL-5 and IL-10 (twofold and threefold, respectively) peaked, GM-CSF was elevated in mice with arthritis. The cytokine profile at day 3 increased with the protein level in all cases and at the IL-2 (day 6).

The repetitive injection of immature unloaded DC protects the mice from severe arthritis. This protective effect is antigen dependent of the DC loading with bCII. The immunosuppressive effect is associated with a decrease of the anti-bCII antibodies from the IgG2a isotype, together with the inhibition of interferon gamma synthesis and the decrease proliferation of bCII-specific cells.

Our data show that repetitive injection of immature unloaded DC protects the animals significantly as 70% of the mice did not develop clinical signs of the disease. We quantitated the various regulatory populations in the vaccinated mice, and observed in the liver and spleen an increase of the T-cell population expressing the CD49b molecule (DX5 cells). The relevance of this population in induced protection is under investigation.

Conclusion The use of iDC to modulate the autoimmune response is a rational approach for cell therapy in diseases such as rheumatoid arthritis.

P125 Long-term immune reconstitution after autologous stem-cell transplantation for severe autoimmune diseases T Alexander1, G Massenkeil2, E Grommatic-Ihe2, GB Burmester3, A Radbruch4, R Arnold5, F Hiepe†, A Thié6 1Department of Rheumatology and Clinical Immunology, University Hospital Charité, Berlin, Germany; 2Division of Rheumatology, Department of Internal Medicine III, Medical University of Wuerzburg, Germany; 3Charité University Hospital, Berlin, Germany Arthritis Res Ther 2005, 7(Suppl 1):P125 (DOI 10.1186/ar1648)

Objectives We performed a detailed analysis of the newly developing immune system in patients treated with autologous stem-cell transplantation (ASCT) for severe autoimmune diseases with special respect to the origin and the kinetics of reconstituting B- and T-cell subsets in correlation to the clinical response.

Methods Peripheral blood lymphocytes were analyzed using multiparameter flow cytometry, including monitoring of the TCR-Vbeta repertoire on CD4+ Th cells. Thymic activity was determined assessing absolute counts of peripheral blood CD4+ T cells and TCRVbeta spectratyping.

Patients and results Thirteen patients with a median follow-up of 54 months have so far been included in the trial: polychondritis (n = 1), systemic lupus erythematosus (SLE) (n = 6), systemic sclerosis (SSc) (n = 3), panniculitis (n = 1) and multiple sclerosis (n = 2). Clinical remission has been achieved in all patients with polychondritis (n = 1), SLE (n = 6) and multiple sclerosis (n = 2) whereas we observed progression of disease in all patients with SSc (n = 3) and panniculitis (n = 1). One SLE patient relapsed after being free of any clinical and serological symptoms for 17 months.

T-lymphocyte compartments reconstituted functionally in all patients, indicated by the reappearance and persistence of CD45RA⁺/CD31⁺ thymic naive Th cells in high numbers with high levels of T-cell receptor excision circles and restored diversity of the T-cell receptor repertoire. In terms of Th-cell memory no autoreactive Th cells could be detected in responding patients. Reconstituted B cells were primarily of naïve phenotype (9g0CD27⁺) in the first 12–18 months after ASCT. As a cellular marker for disease activity, frequencies of CD19⁺CD27⁺/CD++CD20- plasma blasts, elevated in SLE patients prior to ASCT, normalized after treatment in all cases of the non-renal form of SLE and were not affected by treatment. However, no major differences in the pattern of lymphocyte reconstitution could be detected as compared with responding patients.

Conclusion The newly developing immune system after immunotherapeutic therapy could be characterized as ‘juvenile’in all patients. However, in some patients the naïve immune system appeared to not be sufficient to regain self-tolerance. We conclude that both the resetting of central and peripheral tolerance and the effective eradication of autoreactive lymphocytes seem to be a prerequisite for stable induction of remission.

P126 The effect of B-cell depletion with an anti-CD20 antibody on the immunoglobulin heavy-chain repertoire in a patient with rheumatoid arthritis A-S Rouzière1, C Kneitz2, TDörner2, H-P Tony1 1Department of Medicine II, Rheumatology and Clinical Immunology, University of Wuerzburg, Germany; 2Charité Hospital Buch, Berlin, Germany Arthritis Res Ther 2005, 7(Suppl 1):P126 (DOI 10.1186/ar1647)

Purpose B-cell depleting therapy has been described to have beneficial effects to patients suffering from rheumatoid arthritis (RA). Nevertheless, the role of B cells in pathogenesis is not clear. In particular, it is not known whether B-cell depletion causes changes in the B-cell repertoire after peripheral regeneration. Therefore we analysed the distribution of the immunoglobulin heavy-chain (Ig VH) genes usage of a RA patient before, 7 months and 17 months after anti-CD20 therapy with rituximab.

Methods A patient with active RA has been treated with four weekly doses of 375 mg/m² rituximab. During the treatment phase, prednisolone was escalated up to 12.5 mg daily for 4 weeks. After that, the patient remained on a stable dose of 5 mg prednisolone per day without further anti-proliferate treatment. Ig VH genes were amplified from genomic DNA of peripheral B cells by nested PCR using family-specific oligonucleotides. PCR products were subcloned and the sequences of more than 500 clones were analysed.

Results Following antibody treatment, the patient experienced a good clinical response lasting over 1 year. Before therapy, the overall VH gene usage of the RA patient was largely similar to the distributions expected from published data for normal individuals, except for certain genes (4-34, 1-69, 3-07), which have already been reported with a biased distribution in autoimmune disorders. In addition, several clonally related sequences were found in the VH5 family. B-cell regeneration occurred 7 months after anti-CD20 anti-body therapy. Significant changes in the distribution of different genes could be observed: 4-34 and 1-69 decreased to a proportion that would be expected in healthy individuals. Clonally related sequences were not found anymore. A greater overall variety of the VH gene segments used was observed, in particular in the larger families like VH6 and VH4. Interestingly, somatic hypermutation was significantly enhanced at the time point of B-cell regeneration.

Seventeen months after therapy, the general distribution of the VH genes was comparable with that observed before treatment, except for some genes (4-34 remained at the level found after therapy). No clonally related sequences were found. Somatic hypermutation was significantly reduced to the frequency determined before therapy.

Conclusion B-cell depletion by anti-CD20 monoclonal antibody leads to a significant modulation of the expressed immunoglobulin-VH gene repertoire after B-cell regeneration, which is accompanied with a clinical benefit in a single patient.


Introduction Chronic arthritis usually leads to loss of periarticular bone. Inflammatory bone loss results from an imbalance between bone formation and bone resorption. Recent research has focused on the role of osteoclast formation and
bone resorption in arthritis. However, bone resorption cannot be seen isolated since it is closely linked to bone formation and changes in bone formation may also affect inflammatory bone loss.

Methods To assess bone resorption and bone formation simultaneously, we developed a histological technique that allowed visualization of osteoblast function by in situ hybridization for osteocalcin and osteocalcein function by histochemistry for tar- trate-resistant acid phosphatase simultaneously on the same sample. Paw sections from human tar- rite-necrosis factor transgenic mice, which develop erosive arthritis, were analyzed at three different sites: subchondral bone erosions, adjacent Haver- sian bone channels and endosteal regions distant from bone erosions.

Results In subchondral bone erosions, resorption sites were far more common than formation sites. Thus, both the areas covered by osteoblasts as well as numerous osteoclasts showed a fivefold increase in bone resorption compared to osteoblasts and osteoblast numbers, respectively. In contrast, adja- cent Haversian channels showed a completely different bone turnover, with func- tional osteoblasts significantly more frequent than osteoclasts. Bone turnover in Haversian channels was even higher (50% bone surface covered by osteoblasts or osteoblasts) than in subchondral bone erosions (30%). At endosteal sites distant from bone erosions, bone turnover was far lower (8%) and again bone for- mation exceeded bone resorption.

Conclusion These data indicate that bone resorption dominates at skeletal sites close to synovial inflammatory tissue, whereas more distant sites such as the Haver- sian channels attempt to counterregulate this process by increased bone formation.

P128

Antibodies to ferritin in rheumatoid arthritis are associated with disease severity

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Background and objectives A number of autoantibodies have been described in individuals with rheumatoid arthritis (RA) leading to interest in their use as diagnos- tic or prognostic markers in RA as well as their pathogenic relevance. By immuno-screening of a phage-display expression cloning system with RA patient sera we isolated a CDNA clone encoding the ferritin H chain polypeptide. The objectives of this study were to establish the frequency and clinical associations of anti-ferritin antibodies in RA.

Methods We employed an ELISA for the measurement of anti-ferritin antibodies in RA sera. Briefly, 96-well plates were coated overnight with purified ferritin from equine spleen. Sera diluted in 100 were reacted with the plates for 16 hours at 4°C. After three washes, a goat anti-human IgG/horseradish peroxidase conjugate was used to detect bound IgG. The signal for each serum sample was normal- ised using a reference serum included on each plate. Anti-ferritin antibodies were measured in 291 subjects with RA, 73 healthy blood donors and 91 sub- jects with osteoarthritis. Antibody-positive and antibody-negative individuals were compared with respect to severity of disease as measured by modified Larsen’s score, demographic variables, rheumatoid factor status and carriage of HLA DRB1 shared epitope alleles. Correlations were examined between antibody levels and severity of joint damage assessed by the Modified Larsen’s score.

Results Using a cut-off index of three standard deviations above the mean of the control group, 49/291 (16.8%) RA patients were positive versus 2/73 (2.7%) healthy donors and 2/91 subjects with osteoarthritis (P < 0.01). In six positive and six negative sera these findings were confirmed by western blotting. Anti-fer- ritin antibodies were more common in males with RA (25.3% males versus 13.7% females, P < 0.02) and levels were positively associated with severity of joint disease (r = 0.33, P < 0.02).

Conclusions Anti-ferritin antibodies are present in a subset of individuals with RA and are associated with severe joint damage. Ferritin is an abundant protein in serum and synovial fluid, and therefore ferritin/anti-ferritin immune complexes could form in these individuals and contribute to joint damage. An alternative pos- sibility is that anti-ferritin antibodies could modulate the iron-binding properties of ferritin and so lead to the release of toxic-free iron in the joint. We are currently examining the frequency of anti-ferritin reactivity in patients with early RA at two timepoints in order to establish whether or not these antibodies are present in early disease or are simply a result of longstanding disease, as well as their fre- quency in other autoimmune diseases. These data will be presented.

P129

Polymorphism within the telomeric MHC and expression of rheumatoid arthritis candidate genes

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Background and objectives Several recent studies have indicated a second susceptibility locus for rheumatoid arthritis (RA) in the telomeric MHC close to the tumour necrosis factor locus, a region containing a number of genes of unknown function including HLA-B associated transcripts 1 and 2 (BAT1 and BAT2) and lymphotixin alpha (LTA). Several single-nucleotide polymorphisms have been described in this region, however, the functional significance is not known. In this study we sought to examine the association of individual single-nucleotide polymorphisms with expression of each mRNA transcript in response to an inflammatory stimulus.

Methods Peripheral blood mononuclear cells were collected from healthy blood donors and adherent cells were allowed to differentiate into macrophages by culture in the presence of 5% serum for 7 days. Cells were then stimulated with 100 ng/ml lipopolysaccharide and harvested at 4-hour and 18-hour timepoints. Total RNA was prepared using standard methods and reverse transcription per- formed with ImpromII™ (Promega, Madison, WI, USA). The resulting cDNA was used as a template for real-time PCR using gene-specific primers for each gene. Each PCR product was detected with the double-stranded DNA-binding dye SYBR Green® (Applied Biosystems, Foster City, CA, USA) and the ABI 7900HT sequence detection system (Applied Biosystems). Quantification was per- formed using standard curves generated from plasmid DNA containing each cloned PCR product and 18S was used as a loading control. Levels of mRNA transscripts were expressed in relative units (RU). Genotyping was performed for the BAT1 –991 (1751763), BAT2 (1688188), LTA (1720807) and TNF –308 (1718089) polymorphisms using TaqMan allelic discrimination assays. Expres- sion levels of each mRNA transcript were compared between individuals of geno- type 1.1, 1.2 and 2.2 using Kruskal–Wallis tests.

Results Expression of BAT1 mRNA transcripts was significantly less in BAT1 –991 2.2 individuals (n = 6) compared with both 1.1 (n = 6) and 1.2 (n = 5) (median levels 0.22 RU compared with 0.76 RU and 1.1 RU, respectively) (P = 0.02). Expression of BAT2 transcriptions was increased in 1.1 individuals compared with both 1.2 (n = 8) and 2.2 (n = 4) genotypes (median levels 0.43 RU compared with 0.77 RU and 0.82 RU, respectively) (P = not significant). For LTA expression, indi- viduals of genotype 2.2 (n = 4) produced the highest levels, those of genotype 1.1 (n = 6) the lowest, with those of 1.2 genotype (n = 6) intermediate (median levels 6.1 RU compared with 0.81 RU and 2.1 RU, respectively) (P = 0.02). Expression of all three transcripts had to fall low to the levels by the 18-hour timepoint and no differ- ences were apparent between individuals of different genotype.

Conclusions Polymorphism in the BAT1 –991, BAT2 and LTA genes are associ- ated with levels of each mRNA transcript produced in response to an inflammatory stimulus. This suggests the possibility that they may be able to influence suscepti- bility to RA, and that the protein products they encode may play a role in inflamma- tory signalling. We are currently extending this genotype–phenotype analysis to the other members of this gene cluster particularly 1C7, LST1 and AIF1.
also prevented oxidative stress in PB T cells exposed to SF monocytes, which suggested a central role for CD28. PB T cells were therefore stimulated with TNF-α, interferon gamma, IL-1β, or transforming growth factor beta, in the presence or absence of anti-CD28. Here we found that stimulation with and without anti-CD28 by itself was sufficient to induce Rap1 inhibition and induce a moderate increase in ROS production. Co-incubation of PB T cells with TNF-α strongly enhanced the intracellular ROS production.

Conclusion In vitro exposure of PB T cells from rheumatoid arthritis patients to synovial monocytes leads to a strong increase in intracellular ROS production. This is mediated by simultaneous Ras activation and inhibition of Rap1. Where Ras can be activated by a variety of stimuli, Rap1 inhibition is induced by SF monocytes through CD28 costimulatory signaling.

P132 Molecular response to cartilage injury F Dell’Accio, C De Bari, C Pitzalis Department of Rheumatology, King’s College London, UK Arthritis Res Ther 2005, 7(Suppl 1):P132 (DOI 10.1186/ar1652) Background Post-traumatic osteoarthritis (OA) represents 13% of all OA of the knee, 9% in the hip, and 73% of all OA of the ankle [1]. The molecular mechanisms that underlie the development of chronic joint surface degeneration following a localised, acute joint injury are not known. The aim of this study is to utilise the cartilage explant model system to identify molecular mechanisms of cartilage damage and repair induced by acute mechanical injury.

Methods Explants of articular cartilage from preserved areas of the femoral condyles or the patellar groove of patients undergoing total knee prosthesis were cultured in vitro under different conditions. After 4 days in culture the samples were subjected or not to mechanical injury by performing full thickness cuts at a distance of 1 mm. At different time-points the explants were partly snap-frozen for further histochecmical/immunohistochemical evaluation and partly used for RNA extraction and RT-PCR analysis. The original cartilage was graded using the Mankin score.

Results Gene regulation was detected as early as 4 hours and lasting for at least 6 days after mechanical injury. BAX mRNA, possibly associated with apoptosis of chondrocytes, MMP-9 and TIMP-1 mRNA were upregulated in the injured explants. BMP-2 mRNA was also upregulated by mechanical injury. We could not detect changes upon damage of cell proliferation as measured by PCNA mRNA levels at the analysed time points.

Conclusions The explant model system represents a controlled experimental set-up to study the molecular mechanisms of cartilage degeneration in post-traumatic OA and to identify potential molecular targets for its prevention.

Reference

P133 Stat1 and phosphorylated Stat1 are increased in lymphocytes and monocytes of patients with systemic lupus erythematosus M Aringer, T Karontis, CW Steiner, E Feierl, G Steiner, JS Smolen Department of Rheumatology, Internal Medicine III, Medical University of Vienna, Austria Arthritis Res Ther 2005, 7(Suppl 1):P133 (DOI 10.1186/ar1654) Background Both interferon alpha (IFN-α) and interferon gamma (IFN-γ) are thought to be involved in systemic lupus erythematosus (SLE) immunopathogenesis. In their signal transduction, both cytokines lead to the tyrosine-phosphorylation and consequent nuclear translocation of the transcription factor Signal Transducer and activator of transcription 1 (Stat1).

Objective To evaluate Stat1 protein and Stat1 phosphorylation in SLE patients or vivo and after stimulation with IFN-α as well as IFN-γ.

Methods Peripheral blood mononuclear cells of 25 patients fulfilling ACR criteria for SLE and of 12 healthy individuals were prepared over Ficoll Paque gradients. Cells were either stained directly after preparation or after 15 min of incubation in medium with or without the addition of 100 U/ml IFN-α (Strathmann Biotech) or IFN-γ (R&D Systems). Intracellular staining was performed using either a monoclonal anti-Stat1 antibody and a FITC-labelled rabbit anti mouse antibody (Dako) with the Fix+Perm kit (An der Grub) or a directly PE-labelled monoclonal anti-phospho-Stat1 (pStat1) antibody (BD Biosciences Pharmingen) after fixation with 2% paraformaldehyde and permeabilization with 90% methanol. After staining, the cells were analyzed on a Becton Dickinson FACScan® flowcytometer. Gates were set for monocytes and for lymphocytes, and the logarithmic mean fluorescence intensity (mfi) was determined.

Results The amount of Stat1 protein, as measured by the mfi, was increased in lymphocytes of SLE patients as compared with healthy lymphocytes (21.4 ± 14.9 [mean ± standard deviation] versus 7.04 ± 2.54, P < 0.0001, t-test), and in monocytes from SLE patients as compared with healthy monocytes (25.1 ± 13.2 versus 10.4 ± 2.54, P < 0.0001).

Lymphocytic and monocytic Stat1 mfi correlated both for SLE patients (Pearson r = 0.57, P < 0.005) and for healthy individuals (r = 0.75, P < 0.005). The amount of phosphorylated Stat1, as measured by pStat1 mfi, was significantly increased in SLE as compared with healthy lymphocytes (4.03 ± 2.64 versus 3.24 ± 1.21, P = not significant). Nevertheless, the pStat1 mean fluorescence intensities of lymphocytes and monocytes were highly correlated with Stat1 mfi (0.33 ± 0.40 versus 1.36 ± 0.22, P < 0.02), but not significantly increased in SLE monocytes as compared with healthy monocytes (4.03 ± 2.64 versus 3.24 ± 1.21, P = not significant).

As compared with incubation in medium alone, incubation with either IFN-α or IFN-γ increased the amount of pStat1 in SLE lymphocytes (from 1.57 ± 0.29 in medium alone to 1.82 ± 0.36 [P < 0.01, paired t-test] with IFN-α and to 1.85 ± 0.40 [P < 0.002] with IFN-γ). In contrast, IFN-γ, but not IFN-α, increased the pStat1 mfi in healthy lymphocytes (from 1.41 ± 0.15 in medium alone to 1.83 ± 0.48 [P < 0.002] with IFN-γ, but to 1.40 ± 0.18 [P = not significant] with IFN-α). Likewise, SLE monocytes increased their pStat1 contents upon incubation with either IFN-α or IFN-γ (from 3.74 ± 1.8 to 4.86 ± 1.50 [P < 0.05] and 7.28 ± 4.14 [P < 0.001] for IFN-α and IFN-γ, respectively), while healthy monocytes responded to IFN-α (pStat1 mfi from 3.52 ± 1.11 to 5.23 ± 2.25, P < 0.01), but not IFN-γ (pStat1 mfi 3.96 ± 5.36, P > 0.001 versus medium).

Conclusions Peripheral lymphocytes and monocytes of patients with SLE contain more Stat1 protein than those from healthy individuals and show increased Stat1 phosphorylation. While healthy peripheral blood mononuclear cells phosphorylate Stat1 when stimulated with IFN-γ only, SLE lymphocytes and monocytes are primed in a way that enables them to also react to IFN-γ.

P134 Kinetic and influence of angiogenesis in the course of collagen-induced arthritis G Clavel, C Valvasor, D Lemeiter, M-C Boissier, N Bessis UPR5 EA-3408 and Rheumatology Department, University Paris 13 and CHU Avicenne (APHP), Paris, France Arthritis Res Ther 2005, 7(Suppl 1):P134 (DOI 10.1186/ar1655) Background Angiogenesis is involved in rheumatoid arthritis since it allows leukocytes and inflammatory mediators infiltration in the synovium. In turn, inflammation also keeps angiogenesis going as inflammatory mediators stimulate endothelial cell proliferation.

Objectives We aimed to evaluate the reciprocal relationship between synovium inflammation and angiogenesis in mice with collagen-induced arthritis (CIA), a model for rheumatoid arthritis.

Methods CIA was induced by immunization of DBA/1 mice with collagen II in adjuvant. Endothelial cells were detected using a GSL-1 lectin-specific immuno-histochemical staining on knee slides. Angiogenesis, clinical scores and histological signs of arthritis were evaluated each week from the induction of CIA to the
end of the experiment. Angiogenesis was quantified by counting both the isolated endothelial cells and vessels stained on each slide. To evaluate the effect of an angiogenesis increase on CIA, vascular endothelial growth factor (VEGF) gene transfer was performed with adenovirus adenovirus vector VEGF (AAV-VEGF) injection in the muscles of mice with CIA (1010 AAV-VEGF particles intramuscularly 3 weeks before CIA induction). The AAV vectors used in this study contained either mVEGF164 (AAV-VEGF) or lacZ (AAV-lacZ) cDNA, whose expression were driven by the cytomegalovirus promoter.

**Results**

As expected, clinical and histological scores of arthritis, evaluated each week from day 0 to day 55 after induction of CIA, were correlated (P < 0.0001, r = 0.74, Spearman correlation test). More importantly, angiogenesis increased as a function of the disease course. A correlation was observed between joint vascularization and clinical scores of arthritis (P < 0.0001, r = 0.61). A correlation was also shown between vascularization and histological scores (P = 0.0006, r = 0.51). The overexpression of VEGF induced by gene transfer was followed by an aggravation of arthritis as compared with the AAV-lacZ control group (P < 0.0001, analysis of variance test). Histological and quantification of angiogenesis are in progress in this experiment.

**Conclusion**

Angiogenesis and inflammation evolved in the same way during the course of CIA. Stimulation of angiogenesis in mice with CIA led to a worse clinical inflammation. These results suggest an early involvement of angiogenesis in joint inflammation development, and emphasize the critical role of angiogenesis in chronic inflammatory arthritis.

**Acknowledgement**

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P135

**Free radicals regulate glucocorticoid-induced apoptosis in T lymphocytes**

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**Background**

Glucocorticoid-induced apoptosis is a phenomenon of considerable biological and clinical significance. In particular, lymphoid cells are susceptible to glucocorticoid-induced apoptosis. In patients with rheumatoid arthritis, one of the critical hallmarks of synovial T cells is that they suffer from severe oxidative stress. During the past decade, reduction-oxidation (redox) reactions that generate reactive oxygen species (ROS) have been identified as important chemical mediators in the regulation of signal transduction processes. In particular, free radicals appear to have a central role in the balance between cell growth, survival and apoptosis.

**Objective**

To investigate the role of free radicals in corticoid-induced apoptosis.

**Materials and methods**

T lymphocytes were isolated from peripheral blood (PB) and synovial fluid through a negative isolation procedure (Dynal). The cells were treated with different concentrations of methylprednisolone, in combination with different inhibitors and substrates of oxidases. Apoptosis was assessed by annexin V/FITC staining, and oxidation of the dye DCF was used to measure ROS production. Control, active Ras (RasV12) and inhibitory Rap1 constructs (RapGAP) were introduced in PB T lymphocytes by nucleofection techniques.

**Results**

A time-dependent and concentration-dependent apoptosis is induced in T lymphocytes after treatment with methylprednisolone. But where concentrations over 200 µM methylprednisolone were required to induce apoptosis in T cells isolated from PB from healthy donors and patients, apoptosis in T cells isolated from the synovial fluid could be readily detected at concentrations of 5–10 µM. To test whether the disturbed redox balance plays a central role in sensitising T cells for glucocorticoid-induced apoptosis, PB T cells were first incubated for 12 hours with subapoptotic concentrations of H2O2 (6–50 µM), and for 48 hours with BSO (which results in intracellular gluthathione depletion) and NAC (which increases intracellular gluthathione). Here, both pretreatment of the T cells with H2O2 and BSO sensitised the T cells for apoptosis, whereas NAC protected T cells from glucocorticoid-induced apoptosis. Moreover, other T cells that are known to suffer from oxidative stress also showed increased apoptosis following treatment with methylprednisolone: both HIV-infected CD4 lymphocytes that were isolated from patients diagnosed with AIDS (n = 3) and T cells that were nucleofected with RasV12 and Rap1GAP also showed apoptosis at 5–10 µM methylprednisolone. Coimmunot with the apoptosis, a 1.5-fold to 2.5-fold increase in intracellular ROS production was measured in the pre-apoptotic cells. This increase of intracellular ROS seems to be a critical process in the apoptotic process as incubation in oxygen-deprived conditions inhibited the apoptosis. Also, addition of rotenone inhibited both ROS increase and apoptosis after methylprednisolone treatment, suggestive of a mitochondrial source of the free radicals.

**Conclusions**

Cells suffering from oxidative stress are sensitised to glucocorticoid-induced apoptosis.

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P136

**T-cell receptor-independent induction of interferon gamma expression in human memory Th cells**

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**Background**

In murine Th1 cells, interferon gamma (IFN-γ) expression can be induced by two alternative pathways: a T-cell receptor (TCR)-dependent pathway and an IL-12/IL-18-dependent pathway. IL-12/IL-18-induced IFN-γ production might perpetuate inflammatory loops in autoimmunity leading to chronicity of inflammation. To evaluate a possible role for IL-12/IL-18 induced IFN-γ secretion in human autoimmune diseases we analyzed here the requirements for TCR-independent IFN-γ expression in human resting memory Th cells mimicking the inflammatory milieu found at the site of inflammation in rheumatoid arthritis (RA).

**Methods**

Highly purified CD45RO° memory/effector Th cells from healthy blood donors were cultured in the absence of antigen-presenting cells, but in the presence of different cytokine/chemokine combinations known to be overexpressed in the joints of RA patients. After different timepoints cells were analyzed on the single-cell level for the expression of IFN-γ and other cytokines. In addition, surface molecules such as activation markers and cytokine receptors were analyzed by FACS. To evaluate intracellular activation pathways, p38 MAP-kinase inhibitors or cyclosporinA were added in some experiments.

**Results**

IFN-γ production could be induced, starting at 18 hours, peaking at 36 hours, in a subset of 2–10% of human memory/effector Th cells with acocktail of inflammatory cytokines including IL-1β/IL-6/IL-7/IL-8/IL-12/IL-15/IL-18/MIP1α and tumour necrosis factor alpha. In contrast to mice, IL-12, IL-18 and an IL-2-receptor common γ-chain signalling cytokine (IL-2 or IL-7 or IL-15) were determined to be the minimum effective combination. Cytokine-stimulated IFN-γ Th cells did not co-produce IL-2/IL-4/IL-5/IL-10 or tumour necrosis factor alpha. TCR-dependent activation in cytokine-stimulated IFN-γ Th cells was excluded as cyclosporinA did not block IFN-γ production. However, cytokine-induced IFN-γ production was dependent on the p38 MAP-kinase pathway. In contrast to TCR-triggered IFN-γ Th cells, cytokine-stimulated IFN-γ Th cells did not upregulate 4-1BB (CD137).

**Conclusions**

In this study, we have characterized human cytokine-induced IFN-γ Th cells. Our results should help to clarify the role of inflammatory cytokine networks for the perpetuation of human Th-cell-driven autoimmune disorders such as RA.

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P137

**Active immunization (vaccination) against peptides of IL-1β induces self anti-IL-1β antibodies and protects against collagen-induced arthritis**

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**Objectives**

IL-1β is a critical cytokine in inflammation and is involved in the pathogenesis of rheumatoid arthritis. Blocking IL-1β is efficient in the treatment of inflammation. Our goal is to inhibit inflammatory arthritis with a new approach consisting of targeting specific IL-1β peptides in the receptor binding site, and to prove this concept in an experimental model of arthritis.

**Materials**

Epitopes of IL-1β to be blocked were defined in silico by molecular modelling. Synthesized peptides (Fmoc strategy) were linked to KLH. Anti-IL-1β antibodies generated by vaccination of mice against each peptide coupled to KLH were tested by ELISA and neutralisation assay, determining their ability to inhibit IL-2 production by EL4/NOB1 cells. Collagen-induced arthritis (CIA) was induced in DBA/1 mice with type II collagen in complete Freund adjuvant. Mice were vaccinated blindly for clinical arthritis, and joint histology was performed at sacrifice (60 days post-immunization with type II collagen). Mice were immunized by peptide conjugated to KLH 11 weeks prior to induction of CIA. Control groups received KLH alone or saline.

**Results**

Six peptides were obtained and were able to generate anti-IL-1β antibodies in mice (positive ELISA and neutralization assay). Three of them, chosen on the basis of the ability to generate the highest antibody response, were selected for CIA. One of them (IL-1β6) yielded a significantly improved resolution of CIA (P = 0.0003 as compared with KLH control, analysis of variance); the maximal arthritic score mean was also reduced in the treated group (9.4 ± 1.9 and 14.2 ± 1.7, P < 0.05). Histological analysis showed a clear-cut significant reduction in inflammation (P < 0.001) and destruction (P < 0.01) scores in the triggered IFN-γ γ Th cells treated with IL-1β6.

**Conclusions**

Active immunization with targeted peptides of IL-1β was able to generate neutralizing anti-IL-1β auto-antibodies. Vaccination of mice with one of them, IL-1β6, was efficient in CIA.
P138
Autoactive T cells to histone H1 and core histones in patients with systemic lupus erythematosus
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Background Autoantibodies directed against nucleosomal antigens such as dsDNA and histones are hallmarks of systemic lupus erythematosus (SLE). Histone H1 constitutes the major antigen in LE cell formation and antibodies to H1 have been shown to be more specific for SLE than other anti-histone antibodies [1,2]. In order to address the role of histone H1-specific T cells in SLE we investigated the ex vivo cellular reactivity to histone antigen in SLE patients and controls, and characterised H1-specific T-cell clones.
Methods Peripheral blood mononuclear cells of 39 SLE patients and 20 healthy controls (HC) were exposed to purified histones (H1, H2A, H2B, H3, H4), and proliferation as well as cytokine production was measured. In addition, H1-specific T-cell clones were drawn by limiting-dilution cloning of T-cell lines. T-cell phenotyping was done by FACS analysis and the cytokines IL-4, interferon gamma (INF-γ) and tumour necrosis factor alpha (TNF-α) were measured in the supernatants by ELISA.
Results After stimulation with histone H1, SLE patients showed a significantly elevated proliferative response as measured by stimulation indices (SI) when compared with HC (SI mean ± SD, 2.2 ± 1.4 versus 1.5 ± 0.4, P < 0.03) and a positive response (i.e. SI > 2) in 16 patients compared with only two responders among HC (Fig. 1). The proliferative response to H2A was also elevated in SLE patients (SI, 2.9 ± 2.5 versus 1.7 ± 0.8 in HC, P < 0.03), whereas the response to H2B, H3 and H4 did not differ between patients and HC. Cellular responses to H1 correlated with the presence of anti-histone antibodies but not with clinical features or SLE disease activity. H1-specific T-cell clones obtained from one SLE patient and two HC showed a Th1-like phenotype producing large amounts of INF-γ and TNF-α but no IL-4.
Conclusion The increased Th1 auto-reactivity to histones H1 and H2A in SLE patients suggests that these T cells play an important role in the pathogenesis of SLE not only by driving autoantibody responses but also by virtue of production of the proinflammatory cytokines INF-γ and TNF-α.

References

Figure 1
Elevated proliferative responses to histone H1 in patients with systemic lupus erythematosus (SLE). Proliferation of peripheral blood mononuclear cells from 39 SLE patients and 20 healthy controls (HC) was analysed by measuring [3H]Tdr incorporation, and a stimulation index (SI) > 2 was considered a positive response.

P139
CCL21 relationship with lymphoid neogenesis and lymphatic vascular system in chronically inflamed synovium
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Background CCL21 expression in secondary lymphoid organs is instrumental in mediating L-selectin+ CCR7+ naive T-cell and B-cell recruitment from the blood-stream via PNAd+ high endothelial venules (HEV). CCL21 is also constitutively produced by lymphatic vessels functioning as a recruiting factor for CCR7+ mature dendritic cells from peripheral tissues to regional lymphoid organs. The same factor participates to the inflammatory cascade being associated with lymphoid neogenetic events and being upregulated in peripheral lymphatic vessels, increasing the magnitude of T-cell response by favouring dendritic cell recruitment to draining lymph nodes.

Objectives In this study we analysed CCL21 protein and mRNA expression in rheumatoid synovium and its relationship with the organizational features of the inflammatory infiltrate and the vascular system (blood and lymphatic vessels).

Methods Thirty-one rheumatoid synovial samples characterized by a variable degree of inflammation and aggregational tendency were analysed by immunohistochemistry and in situ hybridization for CCL21. Molecular features of synovial vessels were analysed by immunohistochemistry for pan-vascular (CD31), HEV (PNAd) and lymphatic (LYVE-1) markers.

Results Two distinct patterns were recognized: vascular and non-vascular. Non-vascular CCL21-producing cells were specifically localized within lymphoid aggregates, frequently surrounding PNAd+ HEV. This pattern was demonstrated to be similar to human secondary lymphoid organs where, different from the mouse, no CCL21 mRNA was detected directly in HEV. In contrast, CCL21+ vessels did not show a specific association with lymphoid organization, lacking PNAd expression and being recognized inside but also outside pervascular aggregates. Serial section analysis demonstrated the colocalization of CCL21+ vessels with LYVE-1.

Conclusion This study emphasizes a differential regulation of CCL21 in the context of synovial lymphoid organization. The anatomical relationship of CCL21-producing cells with synovial PNAd+ HEV suggests its involvement in cellular homing although, contrary to the mouse, CCL21 is actually produced pervascularly. Furthermore, CCL21 colocalization with LYVE-1 suggests multiple functions of CCL21 in mediating CCR7+ leucocyte homing, intrasynovial cluserization and promoting exit via lymphatics to draining lymph nodes. These results define CCL21 potential roles in the pathogenic cascade of rheumatoid synovitis.
FcγR-mediated uptake and processing of antigen–immunoglobulin complexes by professional antigen-presenting cells

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Rheumatoid arthritis is characterized by the presence of autoantibodies. Various animal models for arthritis have shown a critical role for antibodies in the induction and progression of the disease, with complement and Fc receptors as the key effector mechanisms activated by antigen–antibody immune complexes (IC) in the effector phase of the disease. Although they are required for the perpetuation of the disease, the possible mechanisms by which Fc receptors could contribute to the chronic inflammation in arthritis are still unclear. It is known, however, that crosslinking FcγR on effector cells induces a variety of cellular responses, ranging from phagocytosis to secretion of inflammatory mediators and antibody-dependent cell cytotoxicity. Furthermore, FcγRs on dendritic cells (DC) are involved in the enhanced MHC class II-restricted presentation of antigen from IC to CD4+ T cells. Considering that also other antigen-presenting cells (APC) (like B cells and macrophages) express FcγR, this could be a possible mechanism of exacerbating/maintaining inflammation in arthritis. Therefore, we sought to explore the role of FcγR and complement in the MHC class II-restricted antigen presentation in vivo and to identify the APC involved in this process.

To gain more insight into the ability of various types of APC to take up and present IC to T cells in vivo, we infused ovalbumin (OVA)-IC into naïve mice. Direct ex vivo isolation of the different APC subsets showed that only CD11c+ cells, but not macrophages and B cells, are able to (cross-)present efficiently antigen from IC to T cells, although both macrophages and DC are able to capture IC efficiently. Furthermore, depletion of CD11c+ cells, using transgenic mice, abrogated the enhanced presentation of antigen in IC, confirming that DC are the predominant APC involved in the IC-mediated presentation of IC.

To study the contribution of different FcγRs (FcγRI, FcγRII, and FcγRIII) in IC-facilitated antigen presentation, we injected OVA-IC in wild-type mice and FcγR-knockout mice that have received 3 days earlier CFSE-labeled OVA-specific T cells. Our results indicate that activation of OVA-specific T cells in vivo is 10 times more efficient upon uptake of antibody-complexed OVA than soluble OVA. This effect was absent in mice lacking FcγRI, FcγRII, and FcγRIII, but not in complement factor 3-/- mice, indicating that the enhanced efficiency was FcγR mediated. Together, these results indicate that the enhanced presentation of antigen in IC and the subsequent activation of T cells in vivo is mediated primarily by DC, not by macrophages or B cells. Therefore, we consider it more likely that the IC-dependent contribution of macrophages to rheumatoid arthritis is associated with the release of proinflammatory cytokines and molecules upon activation induced by FcγR crosslinking, rather than to the enhanced activation of autoreactive CD4+ T cells. The ability to orchestrate and steer the T-cell responses is the responsibility of DC, further emphasizing the crucial role of DC in controlling (ongoing) T-cell responses.

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Treatment of collagen-induced arthritis with cholera toxin-treated dendritic cells

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Dendritic cells (DC) are professional antigen-presenting cells with the unique ability to stimulate naïve T cells and to trigger strong immune responses. Dendritic cells (DC) are professional antigen-presenting cells with the unique ability to stimulate naïve T cells and to trigger strong immune responses. In certain conditions, depending on their differentiation/activation status. In particular, treatment of DC with cAMP-elevating agents promotes impaired dendritic cell maturation and inhibition of T-cell responses, therefore providing a potential therapy for autoimmune disorders.

Our objective was to study the effect of cholera toxin (CTx)-treated DC in the development of mouse collagen-induced arthritis (CIA), a well-established animal model of rheumatoid arthritis. CTx was chosen because it maintains sustained high cAMP levels by irreversibly binding to adenylate cyclase. Arthritis was induced by intradermal injection of 200 μg bovine type II collagen (bCII) in complete Freund’s adjuvant in the base of the tail of male DBA/1 mice. Bone marrow-derived DC, loaded with bCII (50 μg) and treated with CTx (1 μg/ml), were injected at the time of immunization. Arthritis incidence and severity were assessed for 21 days following arthritis onset. For in vitro analysis of the effect of DC in T-cell activation, lymph nodes from bCII-immunized mice were collected before arthritis onset and stimulated with CTx-treated DC. Proliferation and interferon gamma production were determined by thymidine incorporation and capture ELISA, respectively. In vivo, CTx-treated DC resulted in a decreased arthritis incidence (Fig. 1) and reduced severity, compared with non-DC treated animals. This effect required the combination of CTx and antigen specificity, as DC treated with CTx in the absence of bCII, as well as non-treated DC in the presence of bCII, did not show a significant reduction in the incidence of arthritis. Furthermore, treatment with DC alone results in an acceleration of disease progression. In vitro analysis of T-cell responses revealed that CTx-treated DC were able to inhibit both proliferation and interferon gamma production from lymph nodes of immunized mice. Interestingly, this inhibition was not antigen specific, as it was also observed in the absence of bCII, suggesting that additional mechanisms are involved in the reduced arthritis incidence observed in vivo. In summary, our data indicate that manipulation of dendritic cell activity with cAMP-elevating agents provides a therapeutic tool for the treatment of antigen-specific autoimmune disorders.

P143

Decreased binding of annexin V to endothelial cells: a novel mechanism of atherothrombosis in patients with systemic lupus erythematosus

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Background Patients with systemic lupus erythematosus (SLE) are at high risk of cardiovascular disease, due to atherothrombosis in particular. The mechanisms are not clear; however, recently annexin V, an anticoagulant protein, and antiphospholipid antibodies have been implicated.

Methods Twenty-six women (52 ± 8.2 years) with SLE and a history of cardiovascular disease (SLE cases) were compared with two age-matched control groups: 26 women with SLE but no cardiovascular disease (SLE controls) and 26 healthy women (population controls). Common carotid intima-media thickness was determined by immunohistochemistry. Annexin V levels in circulation and anti-annexin IgG and IgM antibodies were measured by a commercially available high-sensitivity ELISA. Pooled sera with high capacity to inhibit annexin V binding were preabsorbed against different concentrations of antigens such as cardiac and against unconjugated antigen tetanus toxoid. Annexin V-binding assay with flow cytometry was performed.

Results Binding of annexin V was significantly lower when plasma from SLE cases was used as compared with controls (SLE cases versus population controls P = 0.002, SLE cases versus SLE controls P = 0.02). There was a striking positive correlation between annexin V binding and intima-media thickness (R = 0.73, P < 0.001) among SLE cases. The annexin V levels were increased in SLE cases compared with both SLE controls and PC (P = 0.03 and P = 0.004), but no differences were detected in anti-annexin V IgG or IgM levels. Depletion of annexin V was associated with lower serum levels of annexin V.

Available online http://arthritis-research.com/supplements/7/S1
IgG from sera with high capacity to inhibit binding of annexin V induced a 2.7-fold increase in binding and precubation of sera with cardiolipin and phospholipid-choline resulted in increase of median fluorescence intensity of annexin V binding to human umbilical vein endothelial cells. Immunohistochemical analysis revealed the presence of annexin V in all plaques tested.

Conclusions Decreased annexin V binding to endothelium caused by immunoglobulin may represent a novel mechanism of atherothrombosis. Increasing annexin V binding may thus represent a novel therapeutic possibility.

P144 TLR-9, but not TLR-2, TLR-3 and TLR-4, is upregulated on peripheral blood mononuclear cells of patients with active systemic lupus erythematosus

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Background Innate immune responses may augment adaptive immune responses via the adjuvant effect of endogenous apoptotic cell death derived nucleic acids that activate Toll-like receptors (TLRs). In animal models of lupus, activation of TLR-9 accelerates renal disease. We studied the expression of TLR-2, TLR-3, TLR-4 and TLR-9 in the peripheral blood mononuclear cells from patients with systemic lupus erythematosus (SLE).

Materials and methods Peripheral blood mononuclear cells from 18 SLE patients, four patients with other rheumatic disorders and three normal controls were studied for the expression of TLRs by FACS analysis. TLR-2, TLR-3, TLR-4 and TLR-9 expressions was studied in total lymphocytes, CD19+ and CD14+ cells. Disease activity was assessed by the SLEDAI. Patients were divided into those with active/severe disease and those with inactive/mild disease.

Results Eight out of 18 patients had active disease with mean SLEDAI score 12.3 (± 9.9) while 10 had inactive disease with mean SLEDAI score 2.8 (± 0.9). Lymphocyte expression of TLR-9 (mean value and standard deviation) was higher among patients with active/severe disease in comparison with patients with inactive lupus (64 ± 18%, n = 8 versus 19 ± 12%, P < 0.003) (Table 1).

Table 1

<table>
<thead>
<tr>
<th>Active disease</th>
<th>Inactive disease</th>
<th>Other rheumatic diseases</th>
<th>Healthy controls</th>
</tr>
</thead>
<tbody>
<tr>
<td>(n = 8)</td>
<td>(n = 10)</td>
<td>(n = 4)</td>
<td>(n = 3)</td>
</tr>
<tr>
<td>TLR-9 in lymphocytes</td>
<td>64 ± 18</td>
<td>19 ± 14</td>
<td>22 ± 21</td>
</tr>
<tr>
<td>TLR-9 in CD19+ cells</td>
<td>42 ± 25</td>
<td>25 ± 24</td>
<td>17 ± 14</td>
</tr>
<tr>
<td>TLR-9 in CD14+ cells</td>
<td>31 ± 18</td>
<td>16 ± 13</td>
<td>6 ± 5</td>
</tr>
</tbody>
</table>

There were no differences between patients and healthy controls regarding the expression of TLR-2, TLR-3 and TLR-4. The expression of TLR-9 on various B-cell subpopulations of patients with SLE is currently under investigation.

Conclusions TLR-9, but not TLR-2, TLR-3 and TLR-4, is upregulated in peripheral lymphocytes from SLE patients with active/severe disease compared with patients with inactive/mild disease. There is also a trend for increased expression of TLR-9 at least on CD19+ and CD14+ cells. Experiments in progress examine the response of these cells to TLR stimulation.

P145 Bystander-activated CD4+ memory lymphocytes: a role in the pathology of rheumatoid arthritis?

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Background Previous studies in this laboratory have highlighted the importance of the proinflammatory cytokine tumour necrosis factor alpha (TNF-α) in the pathogenesis of rheumatoid arthritis (RA) and suggested a role for bystander-activated lymphocytes in its chronic production in the RA joint. Normal peripheral blood (PB) lymphocytes cultured in the presence of a ‘cocktail’ of inflammatory cytokines (IL-2/IL-6/IL-10) generated effector cells (Teff) capable of inducing both immunoglobulin production by B cells [1] and TNF-α production by monocytes in a contact-dependent manner. This was in contrast to lymphocytes activated antigen dependently, via the T-cell receptor (TcR), which induced production of both TNF-α and the anti-inflammatory cytokine IL-10 [2,3]. Lymphocytes isolated from the RA synovial membrane exhibited contact-dependent cytokine induction properties similar to Teff, not TcR cells [4].

Objective We have examined the population dynamics and phenotypic changes induced in PB lymphocytes during culture with IL-2/IL-6/IL-10 to determine how such cells resemble those found in the RA joint. As the predominant infiltrating lymphocyte population found to accumulate in the RA synovial membrane is the CD4+ T cell we have also explored the possibility of generating monocyte TNF-α-inducing effector cells from purified CD3+CD4+ populations.

Results Lymphocytes cultured with IL-2/IL-6/IL-10 for 8 days demonstrated a threefold expansion of the natural killer cell population, while the proportion of T cells remained static. However, both these natural killer and T-lymphocyte populations were independently able to induce contact-dependent TNF-α production in monocytes. Interestingly, effector cells generated by culture of the purified CD3+CD4+ fraction with IL-2/IL-6/IL-10 for 8 days were able to induce at least threefold more TNF-α production compared with such effectors generated from the corresponding unfractionated lymphocyte population. We subsequently characterised the different naïve and memory cell populations found within the CD4+ fraction of our bystander-activated lymphocyte cultures (as defined by Lanazavchia and colleagues [5]). Despite an overall net loss in the percentage and number of total CD4+ T cells, both naïve (CD45RA+CCR7+) and memory populations (effector:CD45RO+CCR7−; central CD45RO+CCR7+) were still present after 8 days of culture. However, a preferential retention of effector memory over central memory lymphocytes has been observed in most donors.

Further phenotypic studies have shown that bystander-activated lymphocytes also express high levels of components of the adhesion molecules VLA-1, VLA-4, VLA-5 and LFA-1 (β1, β2 and β3), but lower levels of L-selectin (CD62L). Such properties are associated with the ability of effector lymphocytes to migrate from lymph nodes and into tissues.

Conclusions Our results suggest that exposure of PB lymphocytes to a cocktail of proinflammatory cytokines induces the outgrowth of an activated effector memory lymphocyte population with the capacity to migrate to inflammatory sites. Studies currently underway will examine the effector function of different CD4+ subsets in terms of their ability to induce monocyte TNF-α production. This work will more closely define pivotal cell types responsible for cognate-dependent cytokine production in diseased joints as well as advancing our understanding of the effects and consequences of prolonged cytokine exposure in chronic inflammation.

References


Acknowledgement This work was funded by the Arthritis Research Campaign, UK.

P146 In vivo induction of foxp3 in collagen-induced arthritis treatment with modified dendritic cells

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We studied the prevention of a mice model of rheumatoid arthritis, the collagen-induced arthritis (CIA) model, with DNA-matured dendritic cell injection and then studied the induction of Treg through this innate immunity stimulation. CIA was induced as described in DBA/1 mice with bovine type II collagen intradermal injections. Immediate DNA-matured dendritic cells were injected at D14 intraperitoneally. The clinical course of arthritis was followed and B-cell and T-cell responses were assayed. The induction of CD4+CD25+ was tested by flow cytometry and the induction of Foxp3 markers was quantified by quantitative RT-PCR. Treatment of CIA with intermediate DNA-matured dendritic cells could prevent arthritis as well as lipopolysaccharide-matured dendritic cells. Neither B-cell and T-cell responses were not modified nor was a TH2 response observed.
The induction of Treg (CD4+CD25+) cells was observed in blood, and lymph nodes. The induction of FoxP3 could be quantified and increased with DNA-matured dendritic cells in peripheral nodes. In conclusion we could observe a prevention of CIA with the injection of DNA-matured dendritic cells that did not modify the specific response against bovine type II collagen. Because of the absence of T-cell and B-cell response modification as well as TH2 modification, we do believe that the induction of CD4+CD25+ cells that expressed FoxP3 are involved in the prevention of CIA we observed.

P147
Investigation of the relationship between the HLADRB1 genotype and the presence of autoantibody to cyclic-citrullinated peptide in patients with rheumatoid arthritis
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Background The aetiology of rheumatoid arthritis (RA) has been suggested to be an interaction between genetic and environmental factors. Genetic susceptibility to this disease in most of the population is associated with MHC II molecules that contain an amino acid motif known as the shared epitope (SE). These MHC molecules may bind arthritogenic peptides for presentation to autoreactive T cells. The nature of the arthritogenic peptide is not known, but recent studies have identified post-translationally modified proteins containing citrulline as targets of anti-cyclic-citrullinated peptide (anti-CCP) autoantibodies. It has been shown that in HLA-DRB1*04:01 transgenic mice the conversion of arginine to citrulline at the peptide side chain position interacting with the SE significantly increases peptide--MHC affinity, and leads to the activation of CD4+ T cells in the transgenic mice.

Objective The aim of this work was to investigate the relationship between the HLADRB1 genotype and the presence of anti-CCP IgG antibodies in sera of patients with RA.

Methods HLA-DRB1 genotyping was performed using PCR sequence-specific primers from the DR low resolution kit and DRB1*01, DRB1*04 subtyping kits as well. IgG anti-CCP antibody levels were measured by the ImmunoscanRA ELISA kit. Rheumatoid factor was determined by the nephelometric method (Behring).

Results SE is present in 75 (57.2%) and absent in 56 (42.7%) patients. The prevalence of anti-CCP autoantibodies is significantly higher in the group of SE-positive patients (n = 44, 76%) than in the group of non-SE carriers (n = 28) (P = 0.03, chi-squared test). The average autoantibody level measured in anti-CCP-positive patients carrying SE is 742.7 U/ml while in the absence of SE alleles it is 437.5 U/ml, which does not differ statistically.

Conclusion Association of the SE and citrullinated antigens may be one of the triggers initiating the production of anti-CCP antibodies.

Acknowledgement This work was supported by the grant OTKA T037876.

P148
Endothelial function and activation in women with systemic lupus erythematosus
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Background Cardiovascular disease (CVD) is common in systemic lupus erythematosus (SLE) patients although it is not clear whether an increased risk of CVD is a general feature of SLE, or whether this applies only to a subgroup of patients.

Objective To measure early signs of atherosclerosis/vascular dysfunction in women with SLE with or without CVD and in controls, to investigate whether these correlate to circulating markers of endothelial activation.

Methods Twenty-six women with SLE and a history of CVD (defined as a history of objectively verified angina pectoris, myocardial infarction, cerebral infarction or intermittent claudication; age 52 ± 8.2 years) were compared with age-matched SLE women without CVD (SLE controls) and population-based age-matched controls (population controls). Flow-mediated dilatation (FMD) of the brachial artery after reactive hyperemia and after sublingual nitroglycerine administration was performed on women who were not already on nitro-related medication. Levels of thrombomodulin, tumour necrosis factor (TNF) alpha, sTNF receptors, homocysteine and fibrinogen have been associated with endothelial activation/inflammation and were measured in the circulation by use of the ELISA technique.

Results SLE controls and controls did not differ with respect to FMD after reactive hyperemia or after nitroglycerine administration. Only two SLE cases could be investigated for endothelial function because of nitro-related medication. However, sTNFR1, sTNFR2, and homocysteine differed between SLE cases, SLE controls and population controls (P < 0.05 for all), whereas thrombomodulin (P = 0.001) and fibrinogen (P = 0.02) only discriminated between SLE controls and population controls.

Conclusion Women with SLE who did not have manifest CVD did not differ from age-matched controls with respect to FMD, a measure of endothelial dysfunction. Higher levels of circulating markers of endothelial activation/inflammation were present in SLE cases, SLE controls and population controls, but these did not correlate to measures of endothelia dysfunction, which may not be a general feature of SLE.

P149
Citrullinated peptide-specific CD19+ B cells are present in syновial tissue and peripheral blood of patients with rheumatoid arthritis
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Background Rheumatoid arthritis (RA) is characterized by chronic inflammation of the synovial joints leading to irreversible joint destruction. To prevent and/or slow down progressive joint destruction, the diagnosis of RA at early stage in the disease is important. The autoantibodies against citrullinated proteins (aCCP) provide such ability, representing a marker for early RA. However, a remarkable variety in the reactivity against different citrulline-containing peptides has been described, which indicates that not only citrulline but also its flanking amino acid sequences play a role in antigenicity and that autoantibodies recognizing such targets are polyclonal. Furthermore, B cells isolated from synovial fluid of aCCP-positive RA patients were shown to produce aCCP antibodies spontaneously, whereas peripheral blood B cells require a stimulus to produce these antibodies. The predominance of IgG production in synovial fluid and synovial tissue was observed in comparison with serum. These findings altogether provide the evidence for the local antigen-driven maturation of B cells into aCCP-producing plasma cells within inflamed RA synovium due to the presence of citrullinated synovial proteins.

Objective The aim of the study was to analyze the occurrence of the aCCP-specific B cells in peripheral blood and synovial tissue of patients with RA.

Methods PB and ST were collected from nine patients with RA. Biotylated citrulline-containing peptides derived from human natural proteins were used in order to test the hypothesis of polyclonal production of aCCP autoantibodies.

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the patients, the synovial tissue contains cellular infiltrates that have formed organized structures resembling structures normally observed in lymph nodes, comprising follicular dendritic cells (FDCs), with distinct T-cell and B-cell areas, typical of ectopic lymphoid structures. In the remainder of the patients the tissues do not contain FDCs and show either a diffuse lymphoctic infiltrate or an aggregated T-cell and B-cell infiltrate [1].

The aim of our study is to identify the genes that are expressed in tissues with these ectopic lymphoid structures by cDNA microarray analysis to gain more insight into this specific disease process. We previously showed that the gene expression signatures of synovial tissues from RA patients showed considerable variability, resulting in the identification of distinct molecular forms of RA [2,3]. To evaluate whether the genes involved in the formation of ectopic lymphoid structures could be detected by microarray analysis of whole synovial tissues, we performed an analysis focused on a selection of genes that are known to be involved in normal lymph node development from murine knockout studies.

Indeed, four out of 13 tissues showed an elevated expression of lymph-node-associated genes, indicating that microarray analysis of whole synovial tissue allows the detection of these genes. The expression of the FDC-specific marker CD21L and immune histochemical staining of synovial tissue sections confirmed the presence of ectopic lymphoid structures in these tissues. Detailed histochromatic analysis further allowed us to subclassify the tissues without lymphoid structures into tissues containing T-cell and B-cell aggregates and tissues with a diffuse type of infiltrate.

Comparison of large-scale gene expression profiles between tissues with the three different types of cellular infiltrates revealed differential expression of genes involved in several processes such as apoptosis, antigen presentation, angiogenesis, chemotaxis and extracellular matrix formation. The results indicate that tissues with ectopic lymphoid structures comprise a distinct type of gene expression that includes a spectrum of genes encoding for adhesion molecules, chemokines, cytokines and their receptors that is required to maintain their highly organized structure.

Results


P151

Immunophenotype and functional characteristics of rheumatoid arthritis derived myeloid dendritic cells and plasmacytid dendritic cells

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Background Dendritic cells (DC) comprise a heterogeneous network of professional antigen presenting cells, directly linking innate and adaptive immunity. While implicated in the pathogenesis of different chronic inflammatory arthritides, the analysis of DC subsets has been hampered by a lack of specific DC markers and reliable quantitation. Previously, we have described the significant reduction of circulating peripheral blood (PB) plasmacytoid DC (pDC) in both RA and psoriatic arthritis patients. Furthermore, we have shown that both of these DC subsets are present in synovial fluid (SF) from RA and psoriatic arthritis patients, although mDC significantly exceed pDC.

Objectives This present study characterises the immunophenotype and functional characteristics of RA-derived mDC and pDC in order to assess their potential pathogenic role in arthritis.

Methods pDC and mDC were sequentially purified by magnetic cell sorting with normal healthy controls (mDC, n = 3) and SF (n = 3) and compared with data from peripheral blood of 18 RA donors, 14 OA donors and 14 healthy donors.

Results In SF of RA patients, higher numbers (17%) of CD3+RANKL+ monoclelar cells (synovial fluid mononuclear cells) were found than in peripheral blood mononuclear cell (PBMC) preparations (5%, P = 0.07). In contrast, relatively more RANKL+CD14+ monocytes (79%) exist in peripheral blood than in SF (20%) in the same individuals. When PBMCs in different groups were analysed, significantly higher numbers of CD3+ (8%) and CD4+ (8.8%) PBMCs bearing RANKL on the surface were found in the RA group than in the OA group (3.5% and 4.7%, P = 0.03 and 0.02). In addition, RA patients had significantly higher proportions of CD14+RANKL+ PBMC (45.6%) than controls (30.2%, P = 0.013) or OA patients (29.7%, P = 0.046). On the other hand, RANKL expression on CD14+ PBMC appeared diminished in RA patients (17.3%) when compared with controls (39.5%, P = 0.013).

Conclusions Our findings suggest that the induction of bone erosions may depend rather on surface-bound RANKL than on its soluble form. This hypothesis is supported by our previous findings (see rationale) as well as by differences in RANKL expression on SF and peripheral blood CD3+ cells and the increased numbers of RANKL+ lymphocytes in the peripheral blood CD3+ and CD4+ compartments in RA patients. The lower ratio of CD14+RANKL+ monocytes in peripheral blood of RA patients could reflect selective recruitment of RANK+ cells into the sites with elevated RANKL expression. In such a process, a soluble form of RANKL would probably play an important role [3].

References


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P153
Expression of programmed death (PD)-1 and PD-1 ligands (PD-L1, PD-L2) in peripheral blood mononuclear cells of patients with systemic lupus erythematosus
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Background Programmed death (PD)-1 is a newly described member of the immunoglobulin super-family that is expressed on activated T lymphocytes and B lymphocytes. Engagement of PD-1 with its specific ligands, PD-L1 (B7-H1) and PD-L2 (B7-DC), inhibits lymphocyte proliferation and cytokine expression, and may play a role in peripheral tolerance and negative regulation of T-cell and B-cell responses in vivo. We sought to investigate the expression profiles of PD-1 and PD-1 ligands in peripheral blood cells of patients with systemic lupus erythematosus (SLE).
Materials and methods Blood was drawn from patients with SLE (n = 16), rheumatoid arthritis (n = 16), other inflammatory disease (n = 4), and healthy controls (n = 9). Peripheral blood mononuclear cells were separated on a ficoll-density gradient, and flow cytometry analysis was performed using monoclonal antibodies against CD3, CD19, CD14, CD25, CD69, PD-1, CD-L1, and PD-L2.
Results See Table 1.

Table 1

<table>
<thead>
<tr>
<th>Disease group</th>
<th>Healthy controls</th>
<th>Systemic lupus erythematosus</th>
<th>Rheumatoid arthritis</th>
<th>Inflammatory disease</th>
</tr>
</thead>
<tbody>
<tr>
<td>Mean SEM</td>
<td>Mean SEM</td>
<td>Mean SEM</td>
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<td>Mean SEM</td>
</tr>
<tr>
<td>PD-1 (%)</td>
<td>CD3*</td>
<td>0.6</td>
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<td>0.4</td>
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<tr>
<td>PD-L1 (%)</td>
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<td>1.2</td>
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<td></td>
<td>CD19*</td>
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<tr>
<td>PD-L2 (%)</td>
<td>CD3*</td>
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<td>0.2</td>
<td>0.5</td>
</tr>
<tr>
<td></td>
<td>CD14*</td>
<td>2.0</td>
<td>0.5</td>
<td>1.4</td>
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</tbody>
</table>

SEM, standard error of the mean. No statistically significant differences were observed.

Conclusions In this preliminary report, SLE patients showed a trend for lower expression of PD-1 and higher expression of PD-L1 in unstimulated peripheral blood mononuclear cells compared with other disease controls. These results corroborate findings linking SLE with polymorphism of the PD-1 gene resulting in putative altered expression of the PD-L2 [1]. Lower expression of PD-1 in SLE lymphocytes could be related to ineffective suppression of autoreactive lymphocytes and thus to disease evolution. Currently, we investigate expression of PD-1 and its ligands on subpopulations of lymphocytes (CD45RO*, CD27*), as well as the kinetics of expression upon stimulation.

Reference

P154
Cultured salivary gland epithelial cells from patients with primary Sjögren’s syndrome and disease controls are sensitive to signaling via Toll-like receptors 2 and 3: upregulation of intercellular adhesion molecule-1 expression
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Background In previous studies, our laboratory has shown that the salivary gland epithelial cells (SGEC) of patients with primary Sjögren’s syndrome (SS) display an intrinsically activated phenotype, as characterised by high expression of adhesion, costimulatory and antigen-presenting molecules. Stimulation of Toll-like receptors (TLRs) expressed by epithelia by native or synthetic ligands of TLR2, TLR3 and TLR4 may be critically involved in the regulation of immune responses through the induction of various immunomodulatory molecules, such as the intercellular adhesion molecule-1 (ICAM-1/CD54).
Materials and methods Cultured, non-neoplastic SGEC lines derived from minor salivary gland biopsies of patients with SS (SS-SGEC, n = 4) and controls (n = 4) were studied. The expression of TLR2, TLR3 and TLR4 mRNA was examined by PCR. SS-SGEC were stimulated with L. monocytogenes lipopolysaccharide (100 µg/ml, TLR2-ligand), the synthetic analogue of dsRNA poly-inosinic:cytidylic acid (poly(C) (5 µg/ml, TLR3-ligand) and E. coli lipopolysaccharide (100 ng/ml, TLR4-ligand), for 24 and 48 hours. In certain experiments, cells were also primed with interferon alpha (500 IU/ml) for 24 hours, prior to the stimulation with poly(C). The induction of ICAM-1 expression was analysed by flow cytometry on resting and stimulated cells.
Results SGEC lines were found to express TLR2, TLR3, and TLR4 mRNA. In agreement with their intrinsic activation status and previously published reports, SS-SGEC lines displayed high constitutive ICAM-1 expression, compared with control-SGEC lines. Triggering of TLR3 with poly(C) had resulted in significantly increased ICAM-1 expression (SS-SGEC: sixfold, controls: twofold) after 24-hour stimulation. Despite expression of TLR4 mRNA (by PCR), as well as of surface CD14 protein (by flow cytometry), lipopolysaccharide stimulation failed to upregulate ICAM-1 expression.
Conclusions Our results indicate the SGEC lines are able to respond to synthetic microbial analogues that stimulate TLR2 and TLR3 by upregulating the expression of the adhesion molecule ICAM-1/CD54.

P155
Prevalence of non-rheumatoid arthritis-associated autoantibodies in sera of anti-cyclic citrulline antibody-positive patients
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Background Serological markers, especially autoantibodies with high disease specificity, have their emphasized role in support of the diagnosis of autoimmune diseases. Detection of anti-cyclic citrulline (anti-CCP) antibodies has gained increasing interest in clinical practice as they have shown to have strikingly high (80–89%) specificity for rheumatoid arthritis (RA).
Objective The aim of this study is to summarize our experience in testing anti-CCP and other autoantibodies on a large number of sera from patients with suspected and definite connective tissue disease.
Methods A total of 2061 sera derived from 1750 patients were requested for detection of anti-CCP and rheumatoid factor (RF) autoantibodies. Conventional autoantibodies were also tested according to the requests of clinicians in cases of 1560 samples. Anti-CCP antibodies were detected with the ImmunoscanRA Elisa kit, and RF by nephelometry (Behring). Antinuclear antibodies, anti-DNA, anti-chromatin, anti- cardiacin were measured using ELISA kits (Inova). Anti-CCP antibodies exceeding the level of 25 U/ml were considered positive. Samples expressing antinuclear antibodies at dilution of 1:200 or higher were evaluated.
Results Anti-CCP and RF were present in sera of 331 patients, while 59 patients were positive only for anti-CCP antibodies.
Autoantibory profile detected in anti-CCP-positive and RF-positive patients (n = 331) – antinuclear antibody positive samples, n = 54 (16.3%): including polymyositis, sclerodema associated antibodies, n = 7 (2%); systemic lupus erythematosus associated antibodies (anti-DNA, anti- chromatin, anti-histone, anti-Sm), n = 12 (3.6%); MCTD associated antibodies, n = 8 (1.5%); Sjogren syndrome associated autoantibodies, n = 10 (3%); anti-centromere antibodies, n = 4 (1.3%); and primary biliary cirrhosis associated antibodies, antimichondrial antibody, n = 4 (1.3%). In four cases the presence of anti-neutrophil cytoplasmatic antibodies was also seen. In the group of patients with only anti-CCP positivity (n = 59) – two (3%) samples were positive for anti-centromer, one of them for Sc/70 as well, one was positive for PM/Sc/+ like antibodies, one for anti-DNA, one for anti-Ro/SSa antibody, and one sample showed strong antinuclear antibody positivity.
Conclusion These results show a more complex picture of the occurrence of anti-CCP antibodies as they may associate with different stages of connective tissue diseases. We also aimed to initiate further clinical studies to define the role of this family of autoantibodies in the diagnosis of RA-associated secondary diseases, and also in overlap syndromes.
Acknowledgement This work was supported by Hungarian grant OTKA T037876.
Identification of hnRNPA2-B1 (RA33) as a major B-cell and T-cell autoantigen in pristane-induced arthritis

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Background Pristane-induced arthritis (PIA) in rats is considered an excellent model for rheumatoid arthritis (RA) since it fulfills the criteria for RA including a chronic relapsing disease course and is not dependent on immunization with exogenous antigen. Although the advent pristane is not immunogenic, the disease is MHC associated and dependent on the activation of (autoimmune) T cells. However, so far it has not been possible to link the immune response to joint antigens or other endogenous components. hnRNPA2-B1, the RA33 autoantigen (A2/RA33), is a multi-functional RNA binding protein involved in splicing and other aspects of post-transcriptional regulation of gene expression. Autoantibodies as well as autoreactive T cells against A2/RA33 have been found in patients with RA but the pathogenetic role of these autoimmune responses is unresolved [1].

Methods Autoantibodies against A2/RA33 were determined by immunoblotting, and MHC association of the anti-A2/RA33 immune response was specified by the presence of autoantibodies, delayed-type hypersensitivity reactions and T cell cytoxicity in relation to A2/RA33 in rats of different rat strains. Interferon gamma and tumour necrosis factor secretion by T cells isolated from draining lymph nodes 10 days after pristane injection and restimulation with A2/RA33 in vitro was determined. Expression of A2/RA33 in joints and organs was analysed by immunohistochemistry and western blotting. Nasal vaccinations were performed with A2/RA33 7 days prior to pristane injection.

Results Although anti-A2/RA33 autoantibodies were detected in all four rat strains investigated, the immune response appeared to be particularly linked to the F and U rat strains. A2/RA33 was found in 80% of DA1,F sera, and T cells of all DA1,F rats tested produced intermediate to high levels of interferon gamma and tumour necrosis factor in response to A2/RA33. The reaction seemed stronger in rats suffering from acute PIA. The A2/RA33 autoantigen is targeted by autoantibodies and Th1 cells showing a Th1 phenotype. Furthermore, nasal vaccination with A2/RA33 significantly delayed the onset and decreased severity of arthritis in DA1,F rats. Finally, immunohistochemical and western blot analysis revealed pronounced overexpression of A2/RA33 in joints of rats suffering from acute PIA, but not in healthy joints or in joints from animals with chronic PIA.

Conclusion The A2/RA33 autoantigen is targeted by autoantibodies and Th1 cells in rats with PIA shortly after pristane injection. The presence of autoimmune Th1 cells in conjunction with synovial overexpression of A2/RA33 strongly suggests involvement of this autoantigen in the pathogenesis of PIA. This is further bolstered by the observed alleviation and delay of onset of PIA following nasal vaccination with A2/RA33. The reaction seemed stronger in rats suffering from acute PIA. This work was supported by a grant from the Austrian Academy of Sciences and by Marie Curie Host Fellowship number HPMT-CT-2000-00126 of the European Commission Research Directorate.

Acknowledgements

References

P157 Influence of methotrexate, leflunomide and tumour necrosis factor alpha inhibitors on immune competence in rheumatoid arthritis patients: a long-run monitoring of Epstein-Barr virus load

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Background The risk to develop lymphoma is doubled in patients with rheumatoid arthritis (RA) in the absence of immunosuppressive therapy. This risk is slightly increased by the use of methotrexate or tumour necrosis factor alpha inhibitors (infliximab and etanercept) [1]. Epstein-Barr virus (EBV) is detected in about one-third of lymphomas developing in RA patients. The reason why some patients develop lymphoma is unknown. We have previously shown that RA patients have an almost 10-fold increase of EBV load in their peripheral blood mononuclear cells (PBMCs), compared with normal controls [2]. RA patients’ peripheral blood EBV load is similar to that of healthy transplant recipients (10 copies per 500 ng DNA). In immunosuppressed transplant recipients, elevation of PBMC EBV load above 5,000 copies/500 ng DNA predicted the emergence of lymphoma.

Objectives We evaluated RA patients to evaluate the effects of disease-modifying anti-rheumatic drugs (DMARDs) (methotrexate and leflunomide) and tumour necrosis factor alpha inhibitors (infliximab and etanercept) on PBMC EBV load and to protect lymphoma development.

Methods One hundred and nineteen patients fulfilling the 1987 ACR criteria for RA were followed for periods of 6 months–4 years. Twenty patients received methotrexate or leflunomide, eight received only infliximab, 61 received methotrexate and infliximab, and 30 received etanercept. A 214 bp fragment from the consensus Long Internal Repeat (LIR) of the EBV genome was amplified by quantitative PCR to evaluate EBV DNA load. Effect of treatment duration on EBV load was analyzed by the method of generalised estimation equations.

Results EBV load decreased between the beginning and the end of the study in patients receiving DMARDs (mean: 20.24 and 3.27) or etanercept (mean: 4.44 and 0.67). This decrease was significant for DMARDs (P = 0.0038). However, EBV load evolution was not significantly related to treatment duration in patients under infliximab (mean: 6.36 and 7.82) or infliximab plus methotrexate (mean: 13.49 and 11.92). Of interest, in one patient receiving infliximab plus methotrexate, EBV load reached 540 copies/500 ng over a short period of time.

Conclusion Methotrexate and etanercept decrease EBV load over time. Infliximab alone or without methotrexate does not influence significantly EBV load. Monitoring EBV load might help detecting the few patients who are likely to develop lymphoma.

Acknowledgements Supported by PHRC 2003, SFR and ARP.

P158 A revised assay for the measurement of T-cell receptor excision circles as a quantitative measure of thymic function in systemic lupus erythematosus

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In 1998 Douek and colleagues described a novel approach to measuring thymic output using T-cell receptor excision circles (TREC) measured in CD4+ and CD8+ T-cells. TREC's are byproducts of T-cell receptor gene re-arrangements, whereby sections of excised DNA re-form as stable episomes that do not replicate with cells arising from the thymus are thus ‘sluited’ upon T-cell division and can be used as a surrogate marker of thymic output. However, the interpretation of TREC number in lymphocyte subsets is confounded by the influences of T-cell proliferation, intracellular TREC degradation and T-cell death, and it has been criticised as a measurement of thymic function. Here, we describe a method for quantifying TREC’s in whole blood. This revised assay provides a representation of ‘total peripheral TREC’s’. The effects of T-cell proliferation and cell death on the determined absolute TREC level are minimised, providing us with an improved estimation of thymic function over time. In a series of validation experiments our assay has been shown to have excellent intra-assay and inter-assay reproducibility and to generate results consistent with previously published work in healthy controls. We are now using this assay to determine thymic function in the autoimmune disease systemic lupus erythematosus to test our hypothesis that a defect in thymic function contributes to lupus pathogenesis.

To measure the absolute TREC number per unit volume of blood (as a representation of ‘total peripheral TREC’s’), the amount of DNA extracted from a volume of whole blood must be representative of ‘total’ DNA in that volume of blood. We have compared four methods of DNA extraction from whole blood for consistency of yield and purity. Figure 1a shows the mean DNA yield from parallel extractions (n = 10) performed after (a) 1 hour, (b) 6 hours and (c) 24 hours from collection for a single sample. The overall mean yield was 32.23 µg/ml ± 2.3 standard deviations (SD). Two further, separate, samples were similarly prepared in parallel to confirm consistency – (d) 26.8 µg ± 1.97 SD and (e) 26.9 µg ± 2.23 SD (n = 10). To measure TREC’s in samples we have used a quantitative real-time PCR (TAQMAN)® assay to amplify a known proportion of the extracted DNA. The total TREC number per sample is determined absolutely from a standard curve (derived from a plasmid containing TREC sequence) and final values are presented as TREC’s per million of whole blood. Figure 1a (top axis) shows that the TREC number is reproducibly calculated by parallel extractions (n = 10). The intra-assay coefficient of variation is 1.4% (range 0.8–2.5%) while the inter-assay co-efficient of variation is 2.4% (range 0.6–4.4%). The coefficient of variation is negatively correlated with TREC number (r²)}
Germany; necrosis factor therapy in rheumatoid arthritis

Acknowledgement of thymic function in systemic lupus erythematosus. and reproducibly estimating total peripheral TRECs we aim to minimise the tion of the TREC number within lymphocyte subsets is confounded. By reliably abundant auto-antigen provides a constant T-cell-activating stimulus, interpreta-

hypothesis that a defect in thymic function contributes to lupus pathogenesis. TREC number in the autoimmune disease systemic lupus erythematosus to test our keeping with the known reduction in thymic volume over time. TRECs are not

Figure 1

(a) Lower axis: serial DNA extractions (see text). Bars represent mean of 10 ± standard deviation. Upper axis: T-cell receptor excision circles (TRECs) per millitre of blood from the same samples (mean ± deviation). (b) TRECs per millitre of whole blood declines with age over a range of ~2 logs from birth.

= 0.83 and 0.66, respectively. Using this assay we have also shown that TRECs are reliably detectable in healthy controls (Fig. 1b) and show an age-related decline in keeping with the known reduction in thymic volume over time. TRECs are not detectable in RAJ1 (human B-cell lymphoma line) or SW48 (human colonic carci-
noma cell line) (data not shown). We are now using this assay to determine the TREC number in the autoimmune disease systemic lupus erythematosus to test our hypothesis that a defect in thymic function contributes to lupus pathogenesis. While measurement of TRECs in T cells and their subsets provides a representa-
ton of thymic function in the steady state, in the context of autoimmunity, where abundant auto-antigen provides a constant T-cell-activating stimulus, interpreta-
tion of the TREC number within lymphocyte subsets is confounded. By reliably and reproducibly estimating total peripheral TRECs we aim to minimise the impact of T-cell turnover on TREC number in order to gain a better understanding of thymic function in systemic lupus erythematosus.

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P159

Microarray analysis for molecular characterization of disease activity and measuring outcomes of anti-tumour necrosis factor therapy in rheumatoid arthritis

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Introduction In the pathogenesis of rheumatoid arthritis (RA), macrophages (Mø) play a pivotal role in synovitis, especially at the cartilage–pannus junction. Both Mø and peripheral blood monocytes (MO) are activated and release proinflamma-
tory cytokines (IL-1β), tumour necrosis factor (TNFα). Neutralization of IL-1β and TNFα leads to clinical improvement in RA.

Objective To characterize MO expression profiles of patients with active RA before and after treatment with adalimumab, a fully human, anti-TNF monoclonal antibody, using microarray analysis. To identify differences in expression of signature genes between patients with uncontrolled, active RA and those in remission induced by anti-TNF therapy.

Methods Genome-wide microarray analyses (HG-U133A/B) were performed to identify signature genes and RA-MO pathways and to establish a customized cDNA array suitable for monitoring anti-TNF therapy. Untouched MO were nega-
tively selected by magnetic cell sorting from 40 ml peripheral blood samples. Total RNA was extracted for cRNA synthesis, and was hybridized with whole genome oligonucleotide and customized cDNA microarrays. The customized cDNA array consisted of 313 cDNAs derived from gene subtraction analysis and from compar-

ative genome-wide U133A analysis. The array includes RA-relevant signature genes, and genes triggered or repressed during anti-TNF treatment. To identify significant gene expressions, bioinformatical MAS 5.0, self-organizing map cluster-

ing and predictive analysis for microarrays (PAM) analyses were performed.

Results Genome-wide analysis of MO mRNA expression in patients with active RA before and after receiving anti-TNF-α (n = 7) revealed significant differences in upregulated and downregulated genes. Self-organizing map analysis revealed six different gene expression clusters. MAS 5.0 and PAM analyses identified 103 differentially expressed genes and permitted the separation of RA patients into two subgroups of ‘responders’ and ‘non-responders’, correlating with clinical data (DAS28 and ACR response criteria). Results were confirmed by a cus-
tomized array using most of the PAM-selected genes. Twenty-four genes were further evaluated by real-time PCR using MO from normal donors and from patients with RA before and during therapy. Signature genes identified were characterized as: disease-relevant genes differentially transcribed in activated RA-MO compared with normal donor MO; genes reversed to ‘normal levels’ by anti-TNF treatment; or pharmacodynamic marker genes probably indicative of anti-TNF action. Selected genes, which may be indicative for the response to therapy, are currently being further evaluated in extended collections of samples.

Conclusions Signatures are important to define MO activation to characterize disease activity and to support therapeutic stratification. The current gene selec-
tion could contribute to the investigation of the role of MO in a wide range of rheumatic diseases and therapeutic intervention, improving rheumatologists’ understanding of regulated MO pathways.

P160

Amelioration of joint inflammation by a PAR-2-specific monoclonal antibody

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Background Protease-activated receptor-2 (PAR-2) is a G-protein-coupled receptor recognized to mediate inflammatory responses. Using a PAR-2 ‘knock-

out’ mouse, we previously demonstrated this receptor to play a crucial role in chronic joint inflammation [1]. Inhibition of PAR-2 activation therefore potentially represents a novel therapeutic target in treatment of arthritis, but selective antag-
onists are not yet available.

Objective To test the hypothesis that acute joint inflammation could be inhibited by targeting the ‘tethered ligand’ sequence of PAR-2 using a specific monoclonal antibody (SAM-11).

Methods The presence of synovial PAR-2 was confirmed in wild-type (PAR-2+/+), C57BL/6J mice by western blotting using SAM-11 (Santa Cruz, USA). The anti-
inflammatory potential of this antibody, which inhibits PAR-2 activation by prevent-

ing release of its activating ligand, was investigated by intra-articular administration of SAM-11 to mice prior to induction of acute joint inflammation (under halothane/O2/N2O anaesthesia) by injection of 20 µl 2% carrageenan and 4% kaolin (C/K) into the knee joint. Joint swelling was assessed by comparing caliper-

measured knee joint diameter pre and 24 hours post-injection. The swelling response was compared in untreated, and in two parallel groups of inflamed mice that had received intra-articular injection of SAM-11 at 5 ng or 10 ng, 5 min prior to C/K administration. Selectivity of SAM-11 for PAR-2 was confirmed by immuno-
histochemical analysis (in combination with the Animal Research Kit Dako, USA) of the wild-type mouse brain, which expresses PAR-1, PAR-2, PAR-3 and PAR-4.

Results Western blotting demonstrated the presence of PAR-2 in normal murine synovium and substantial upregulation in acutely inflamed joints. Immunohisto-

chemical analysis of the murine brain with SAM-11 revealed staining in PAR-2+/+ mice but not in PAR-2–/– mice. Further evaluation by real-time PCR using MO from normal donors and from patients with RA before and during therapy. Signature genes identified were characterized as: disease-relevant genes differentially transcribed in activated RA-MO compared with normal donor MO; genes reversed to ‘normal levels’ by anti-TNF treatment; or pharmacodynamic marker genes probably indicative of anti-TNF action. Selected genes, which may be indicative for the response to therapy, are currently being further evaluated in extended collections of samples.

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P160

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Results Western blotting demonstrated the presence of PAR-2 in normal murine synovium and substantial upregulation in acutely inflamed joints. Immunohisto-

chemical analysis of the murine brain with SAM-11 revealed staining in PAR-2+/+ mice but not in PAR-2–/– mice, confirming PAR-2 specificity of this monoclonal antibody. C/K resulted in substantial knee joint swelling, which was significantly and dose-dependently (P < 0.00001; one-way analysis of variance; n = 4 per group) inhibited by SAM-11 pretreatment (Fig. 1). These findings are consistent with a proinflammatory role for PAR-2 in arthritis, and demonstrate that antibody inhibition of PAR-2 activation ameliorates acute joint inflammation.

Reference


Figure 1

Twenty-four hours after intra-articular injection of kaolin, knee joint swelling is dose-dependently reduced by SAM-11 pre-treatment. ** P < 0.00001, * P < 0.01 (n = 4 per group). NS, no significantly.
Real-time quantitative PCR used as a biomarker for synovial gene expression after oral prednisolone therapy in patients with rheumatoid arthritis

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The objective of this study was to evaluate the use of real-time quantitative PCR (Q-PCR) using a cellular standard to detect changes in gene expression in synovial tissue samples that could potentially serve as such biomarkers correlating with clinical disease activity. Therefore, the effects of treatment with corticosteroids, a known effective therapy, were analyzed in patients with active rheumatoid arthritis. Patients were randomized to receive either oral prednisolone (n = 10, 60 mg daily for the first and 40 mg daily for the second week) or placebo (n = 11). All patients underwent an arthroscopic synovial biopsy procedure directly before and after 14 days of treatment. Real-time Q-PCR was used to quantify gene expression of tumour necrosis factor alpha, IL-1β, IL-8 and MMP-1 in the synovial tissue samples. The values were expressed as relative units compared with a cellular-based standard. Statistical analysis was performed using an analysis of covariance model. The mean DSAS2 was 2.0 units lower (95% confidence interval, 1.0–3.0) after prednisolone therapy compared with placebo. The mean DSAS2 (± standard deviation) decreased from 6.27 ± 0.95 to 4.11 ± 1.43 after prednisolone therapy, but not in the placebo group. For gene expression of IL-8 and MMP-1, the estimated effect of prednisolone compared with placebo was large, and confidence intervals excluded the likelihood of no effect. A clear trend towards reduction was seen in IL-1β and tumour necrosis factor alpha mRNA expression in the prednisolone group, but confidence intervals included the value for no effect. The results of this study show that mRNA expression of IL-8 and MMP-1 quantified by Q-PCR may serve as biomarkers in small proof of principle trials designed to screen for potential efficacy in rheumatoid arthritis patients.

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Expression profiling in synovitis: ranking of candidates, diagnostic performance and individualized interpretation

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Objective To provide a systematic overview on expression profiles, to determine a ranking score and to give insight in to the heterogeneity of individual patients within the group of arthritis patients.

Methods Synovial tissue specimens of 10 rheumatoid arthritis (RA), 10 osteoarthritis and 10 normal donors were subjected to GeneChip HG-U133A expression profiling according to the standard protocol, starting with 5 µg total RNA and using 15 µg cRNA for hybridization. Signals were generated with the GeneChip Operating System and scaled to equal intensities of the whole array. Further analysis included t test and analysis of variance (ANOVA) statistics as well as functional profile component analysis. Classification was performed according to the Prediction Analysis for Microarrays algorithm. Systematic multiple testing with statistics and classification tools was programmed in perl using subgroups of patients and subgroups of genes.

Results To characterize the homogeneity of each group, ANOVA and t test statistics were applied using ‘leave one out’ and ‘leave two out’ for candidate selection. Subsequently, these one or two donors were tested for the predictive value of the selected candidates. This revealed that one RA donor, if not participating in the selection process, grouped to osteoarthritis. Analysis for functional profile components showed less infiltration and less inflammation in this donor. However, if this RA donor contributed to the candidate selection, all RA patients were correctly classified. Furthermore, donors of other groups were also classified error-free. This demonstrates that RA with reduced molecular markers of inflammation can still be separated from osteoarthritis and that incorporation of such RA patients in the selection process of candidate genes is mandatory for correct classification.

To characterize the importance of each gene for classification, ranking of candidate genes according to the significance level by t test was performed. Multiple subgroups were systematically tested and the ranking of genes was compared. Using an averaged rank list, gene sets were stepwise expanded and systematically tested for classification potential. In addition, the contribution of each gene to the correct classification was assigned to each donor. All together, this information can be visualized on a gene and donor specific way including annotation of significance, classification and proportionate contribution to classification.

Conclusion Systematic multiple testing of gene expression profiles provides a powerful tool to identify the quality of array data. Therefore, the ranking of gene candidates provides insight into patient specific contribution to classification and thus an individualized interpretation of gene expression data.

A role for CD8+ cells in cell-contact-mediated inflammation

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Background While the aetiology of rheumatoid arthritis (RA) is unknown, emerging data suggest that T cell/macrophage cell–cell interactions are critical in disease perpetuation. Cytokine/mitogen-activated CD4+ T cells or CD4+ T cells directly from RA synovium are known to induce tumour necrosis factor alpha (TNF-α) production by monocytes via a cell-contact-mediated mechanism. However, little is known about the ability of CD8+ cells to drive such effects. Objective To investigate the potential role of CD8+ cells in cell-contact-mediated stimulation of monocytes, via induction of cytokines. To examine whether CD8+ cells isolated from RA SF, like their CD4+ counterparts, have an inherent ability to drive monocyte activation.

Methods CD8+ or CD4+ cells from healthy volunteer or RA peripheral blood were isolated by immunomagnetic bead depletion and activated by phorbolmyristate acetate, IL-15 or a cytokine cocktail (IL-6, IL-15 and TNF-α) for 3/6 days, respectively. SF T cells were purified by immunomagnetic bead separation. T cells were paraformaldehyde-fixed prior to co-culture with autologous immunomagnetically purified CD14-positive cells. CD8+/CD4+ cells isolated from RA SF were fixed without prior stimulation. Secretd cytokine production by monocytes was measured by ELISA/Luminex after 48 hours. The purity of isolated CD8+/CD4+ populations was assessed by FAC5 analysis and was routinely > 95%.

Results Mitogen-activated peripheral blood CD8+ cells induced TNF-α production by monocytes in a cell-contact-dependent manner. Peripheral blood CD8+ cells previously activated by IL-15 alone or a cocktail of cytokines similarly stimulated monocyte TNF-α production. Moreover, CD8+ cells isolated directly from RA SF induced monocyte secretion in the absence of exogenous TNF-α. Levels of monocyte cytokine production stimulated by CD8+ cells were comparable with levels induced by CD4+ cells in all circumstances investigated.

Conclusion The ability of CD8+ cells to stimulate monocyte inflammatory cytokine production via a contact-dependent mechanism provides a novel means by which T-cell subsets activated within the local cytokine milieu in RA may contribute to the ongoing disease process. Further understanding of the contribution made by this population to monocyte/macrophage activation is therefore crucial.

Complement and Fcγ receptor cross-talk in the Arthus reaction: the inflammatory cascade confirmed and refined

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Complement and Fcγ receptor (FcR) effector pathways are central targets of immune inflammation; however, the exact mechanisms for their cooperation with effectors of tissue injury, and their nature remain elusive. Here we describe a novel regulatory cross-talk between complement and FcγR on macrophages as the dominant event in the Arthus reaction, the classical animal model of immune complex disease. Specifically, initial contact between immune complexes and macrophages results in cellular regulation: plasma complement-dependent CSAs production; selective G-dependent C5aR expression and C5aR-mediated AR alterations towards FcγR. Subsequently, the previously shown main inducer of tumour necrosis factor alpha and CXC/CR2 ligand production. Distinct inhibitors of this refined inflammatory cascade are each effective in disease prevention, thus indicating cellular components of the C5aR–FcγR axis as potential new therapeutic targets in the treatment of inflammation and autoimmune diseases.

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Pharmacokinetic study of oral prednisolone compared with intravenous methylprednisolone in patients with vasculitis of rheumatic disease

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Introduction Corticosteroids are the drugs of choice for many rheumatic diseases, including vasculitis. There is controversy concerning the route of administration. If the target to the vasculitis and the blood vessels of the gastrointestinal tract are affected, there may be impaired absorption of oral corticosteroids.

Purpose To determine whether patients with active vasculitis, as evidenced by elevated neopterin, von Willebrand factor antigen (vWFAg), and abnormal nailfold capillaroscopy (NFC), have equivalent bioavailability of oral prednisolone (OP) compared with intravenous methylprednisolone (IVMP).

Methods Six patients with rheumatic disease involving vasculitis (juvenile dermatomyositis, scleroderma, or overlap syndrome), four females, two males (mean age 17.8 years [range 11–27]; one Hispanic, one Asian, one African American, three Caucasian) were admitted to an IRB-approved Clinical Research Center protocol. After fasting overnight, they received 50 mg/m² OP on day 1, and
50 mg/m² IVMP on day 2. Baseline blood samples were drawn 1 min prior to each corticosteroid dose (neopterin and vWFAg on day 1; prednisolone level on day 2), at 5, 15, 30, 45, 60, and 90 min and then hourly from the second through the eighth hour. After extraction, samples were analyzed by reverse-phase HPLC for the levels of prednisolone (day 1 samples) and methylprednisolone (day 2 samples). The area under the serum OP or IVMP concentration versus time curve (AUC) was determined using the trapezoidal method. NFC images were evaluated by freeze-frame video microscopy as previously described.

Results See Table 1. There was a positive correlation coefficient for ∆AUC (IVMP–OP) with vWFAg, neopterin, and NFC avascularity score of 0.74, 0.68, and 0.68, respectively; there was a negative correlation coefficient for ∆AUC (IVMP–OP) with NFC vWF, low capillary/mm of 0.64. Linear regression analysis of ∆AUC (IVMP–OP) and vWFAg approached statistical significance (P = 0.08) and given that only six patients were evaluated this may be clinically significant.

Table 1

<table>
<thead>
<tr>
<th>Patient</th>
<th>Diagnosis</th>
<th>Neopterin (nmol/l)</th>
<th>vWFAg capillary score</th>
<th>NFC avascularity score</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>JDM</td>
<td>+651897</td>
<td></td>
<td>0.8</td>
</tr>
<tr>
<td>2</td>
<td>JDM</td>
<td>–21012</td>
<td>3.5</td>
<td>10.49</td>
</tr>
<tr>
<td>3</td>
<td>JDM</td>
<td>+392990</td>
<td>3756</td>
<td>4.18</td>
</tr>
<tr>
<td>4</td>
<td>JDM</td>
<td>–268419</td>
<td>89/B</td>
<td>14.50</td>
</tr>
<tr>
<td>5</td>
<td>Overlap</td>
<td>+924390</td>
<td>14.6</td>
<td>6.28</td>
</tr>
<tr>
<td>6</td>
<td>Scleroderma</td>
<td>–708797</td>
<td>179/A</td>
<td>5.16</td>
</tr>
</tbody>
</table>

Conclusion Patients with elevated vWFAg, neopterin, and/or evidence of abnormal nailfold by capillaroscopy may have decreased absorption of OP. We speculate that this observation can provide the rationale for the greater efficacy of IVMP in the therapy of patients with active vasculitis of rheumatic disease. More patients will be evaluated to further establish the use of IVMP over OP in active vasculitis.

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P166 Characteristics and outcomes in sero-positive late-onset rheumatoid arthritis patients who start a new disease modifying anti-rheumatic drug

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Background Controversy exists in delineating the characteristics and therapeutic implications involved in late-onset rheumatoid arthritis (LORA) and younger-onset rheumatoid arthritis (YORA). Many studies have suggested that the disease process of the LORA patient is distinctively different, and thus requires different treatment. Our preliminary work using a rigidly defined, rheumatoid factor (RF)-positive rheumatoid arthritis prospective cohort of 263 patients suggests that LORA and YORA patients are similar after correcting for age-related factors, for example erythrocyte sedimentation rate and C-reactive protein. In the same cohort of patients, Wu and colleagues recently demonstrated that the presence of both shared epitope-containing DRB1*04 alleles and novel RANKL polymorphisms was associated with an 18–20 year earlier onset of rheumatoid arthritis in YORA patients and did not predict increased severity of disease.

Objective Aim 1 To demonstrate that RF-positive YORA and LORA patients with the same disease duration have similar baseline disease-related characteristics, after adjusting for age-related processes. Aim 2 To compare outcomes of RF-positive LORA and YORA patients with the same disease duration, after accounting for age-related processes.

Hypothesis 2A Responses to disease-modifying anti-rheumatic drug treatments will be similar between LORA and YORA patients with equivalent disease duration. Hypothesis 2B LORA and YORA patients with equivalent disease duration will have comparable side effects to disease-modifying anti-rheumatic drugs.

Methods This study will use the Consortium of Rheumatology Researchers of North America and the Rheumatoid Arthritis Disease-Modifying Anti-Rheumatic Drug Intervention and Utilization Study 142 databases, consisting of 15,000 rheumatoid arthritis patients. Patients with known RF positivity will be included in the cohort, with LORA > 60 and YORA < 60 years of age. We will control for duration by stratification. We will use two methods to demonstrate similarity between YORA and LORA subjects: equivalence testing and confidence intervals. Alternate statistical analyses include generalization matched by the propensity score method and regression analyses.

Significance LORA patients have been treated inconsistently and with much apprehension, due to uncertainty about the diagnosis of LORA and concern about prescribing toxic medications to the elderly. With strictly defined cohorts showing similar characteristics/outcomes, treatment of the LORA and YORA patients by physicians should be similar.

P167 Toll-like receptor 4 polymorphisms and ankylosing spondylitis

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Introduction Ankylosing spondylitis (AS) is a chronic systemic rheumatic disorder, which is characterised by sacroiliitis, enthesopathy, and a variety of extra-articular manifestations. Despite having the strongest association ever described with the HLA-B27 antigen, HLA B27, the pathogenesis of AS remains poorly understood. Immunoregulatory genes and Gram-negative gut bacteria are thought to be important in disease expression. It is now known that mammalian immune response to Gram-negative bacteria is mediated by Toll-like receptor 4 (TLR4), a pattern recognition receptor. Two co-regulating missense mutations have recently been described in TLR4 that lead to a diminished host response to Gram-negative bacteria. We hypothesise that TLR4 mutations occur with an increased frequency in AS B27-positive individuals who develop AS than in healthy HLA B27-positive controls, and allow increased survival and the systemic distribution of Gram-negative gut bacteria to the joints. This study aims to compare the frequency of two common TLR4 mutations (Asp299Gly and Thr399Ile) between AS patients and HLA B27 healthy controls.

Methods The TLR4 genotypes of over 100 patients and 100 HLA B27 healthy controls were determined using allele-specific PCR and restriction fragment length polymorphism analysis. The allele frequencies were compared using a chi-squared test of association.

Results There was no significant difference between the frequency of the Asp299Gly allele or the Thr399Ile allele in AS and healthy HLA B27 controls.

Conclusion Two common TLR4 polymorphisms, which cause a functional deficiency in host immune response to Gram-negative bacteria, are not significant in AS.

S9 Follow up study of B-lymphocyte depletion in the treatment of patients with systemic lupus erythematosus

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Background Systemic lupus erythematosus (SLE) is an autoimmune rheumatic disease in which B-lymphocytes play an pivotal role. We have induced B cell depletion utilising a combination of rituximab, cyclophosphamide, and steroids given intravenously. This regime depletes B-lymphocytes in the peripheral blood.

Objective To report a long-term follow up study of 24 patients who had failed conventional immunosuppression.

Methods 24 patients (22 female, 2 male, mean age 30 years, range 17–49) were treated. The mean disease duration was 7.9 years (range 1–18 years). Twelve of the patients were Caucasian, 8 Afro-Caribbean and 4 of Asian origin. The majority of these patients were treated with two infusions of 1 g rituximab, two infusions of 750 mg cyclophosphamide and two infusions of methylprednisolone 100 mg. Patients were allowed to continue on prednisolone and hydroxychloroquine.

Responses to disease-modifying anti-rheumatic drug treatments will be similar between LORA and YORA patients with equivalent disease duration. Hypothesis 2B LORA and YORA patients with equivalent disease duration will have comparable side effects to disease-modifying anti-rheumatic drugs.

Results The global BILAG score reduced from a median of 13.9 at baseline (SEM = 1.18) to 5 (SD = 1) at three months and 5.0 (SEM = 0.6) at six months. 23/24 patients achieved depletion in the peripheral blood (CD19+ <0.005%) and there was improvement in BILAG score in each of the eight systems or organs. The period of B lymphocyte depletion ranged from three to eleven months except in 1 patient who remained depleted for > 4 years. Whereas the mean total serum immunoglobulins levels remained within the normal range, analysis of the serum C3 levels (in 21 patients) showed a statistically significant improvement (P < 0.0005) at six months as did anti-dsDNA binding (P < 0.02). 1 patient scored the most active (BILAG global score 45) of depletes five months after the infusion having shown a considerable improvement at three months. 1 patient had a severe infusion reaction. No other serious adverse events were observed. 7 patients have now been retreated, 1 on two further occasions. 1 patient failed to deplete on retreatment due to a documented specific HACA response.

Conclusion B-lymphocyte depletion therapy utilising rituximab has shown to be an effective treatment for active refractory lupus. Our data further indicate that both clinical and serological improvement is seen in the majority of these patients. The efficacy and apparent safety of this treatment in established cases of lupus indicate the possible use of this treatment in patients earlier in the course of their disease.