and RADFs (GFR MG: 4.4 fold, MG: 4.8 fold) to GFR MG was observed compared to MG.

Discussion According to present knowledge and in comparison to results obtained from RASFs, SScDFs do not show the ability to migrate from their application site to internal organs. Adhesive properties do not differ from healthy controls. Nevertheless, SScDFs are mediators of organ fibrosis, but it seems that there is no contribution of SScDFs to the spreading of the disease.

A10.2 ANTI-AT1R AND ANTI-ETAR AUTOANTIBODIES IN PATHOGENESIS OF SYSTEMIS SCLEROSIS

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Background and Objectives SSc is a prototypic multiorgan disease characterised by vascular damage, autoimmunity and fibrosis with still unkown aetiology. Recently identified functional autoantibodies simultaneously targeting the angiotensin-II type-1 receptor (AT1R-Abs) and the endothelin-1 receptor type A (ETAR-Abs) were linked to vascular and fibrotic complications in SSc. Presence of both autoantibodies moreover predicted mortality due to cardiopulmonary complications implicating their contribution in SSc pathogenesis. Here, autoantibody mediated effects on endothelial cell activation and their blockade by receptor inhibitors were studied.

Materials and Methods Human microdermal endothelial cells-1 (HMEC-1) and human dermal fibroblasts were treated with IgG from SSc patients containing anti-AT1R and anti-ETAR Abs (SSc-IgG) or with IgG from healthy donors (NC-IgG) as negative control. In parallel, SSc-IgG treated cells were incubated with AT1R-and ETAR- antagonists alone and in combination. Activation of endothelial cells was assessed by qRT-PCR and sandwich ELISA and of fibroblasts with immunocytochemistry.

Results Human endothelial cells showed increased expression and production of the pro-inflammatory chemokine interleukin-8 (IL-8) upon treatment with SSc-IgG positive for anti-AT1R and anti-ETAR Abs compared to control treatment with NC-IgG as analysed on mRNA and on protein levels. Furthermore, endothelial cells showed increased expression of the adhesion molecules vascular cell adhesion molecule-1 (VCAM-1) and intercellular adhesion molecule-1 (ICAM-1) with SSc-IgG versus NC-IgG treatment on mRNA levels. Expression of IL-8 and VCAM-1 was significantly decreased by receptor inhibition. Human dermal fibroblasts showed increased collagen 1 production upon treatment with SSc-IgG versus NC-IgG that was also reduced by receptor inhibition.

Conclusions Our data sugests a direct involvement of anti-AT1R and anti-ETAR Abs in endothelial cell and fibroblasts activation that is mediated by AT1R and ETAR activation. Increased expression of IL-8 and of VCAM-1 and ICAM-1 indicate a direct endothelial cell activation and inflammation. Increased collagen 1 production indicates fibroblast activation and pro-fibrotic events. Therefore, anti-AT1R and anti-ETAR Abs induce pro-inflammatory and pro-fibrotic events and could be directly involved in the pathogenesis of SSc. In vivo experiments are underway to analyse anti-AT1R and anti-ETAR Abs mediated pathogenic events in SSc.

A10.3 ARTHRITIS IN PATIENTS WITH IDIOPATHIC INFLAMMATORY MYOPATHIES

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Background and Objectives Arthritis in idiopathic inflammatory myopathies (IIM) is frequently observed in clinical practise, but, to our knowledge, there is lack of systemic reports of prevalence and/or characteristics of arthritis in myositis patients. The aim of this study is to determine prevalence of arthritis in IIM patients; it's relation to the course of the muscle disease; characteristics of arthritis with respect to seriousness, distribution and extent as well as it's relation to autoantibody profiles and others disease's characteristics.

Materials and Methods In this cross-sectional study, clinical aspects of disease, history of arthritis and autoantibody profiles were obtained from 106 consecutive patients with definite diagnosis of IIM. In all of them the 68-joint index was investigated. In 55 IIM patients and in 60 control patients with rheumatoid arthritis (RA) German Ultrasound Score 7 (US-7) was performed.

Results Arthritis at any time of course of myositis occurred in 65 patients (61.3%); 42 had arthritis at the beginning of myositis (in 22 patients before and in 16 together with onset of muscle weakness). 52 patients presented arthritis at clinical examination (25 poly-, 17 oligo-, and 10 with monoarthritis). Most frequently affected joints were wrists (21.7%) and shoulders, metacarpophalangeal, and proximal interphalangeal joints (20.8%). From 29 anti-Jo-1 positive patients 28 had arthritis and significant association between arthritis and anti-Jo-1 positivity was found ($p < 0.0001$). 39 out of 55 (70.9%) patients had Gray-Scale (GS) synovitis on ultrasound; in 34 of them also Power-Doppler (PD) positivity was found. Only 4 patients had ultrasonographic tenosynovitis and 3 had bony erosions. From 60 RA patients 57 (95%) had GS synovitis, which was PD-active in 54. Tenosynovitis was found in 25 patients. 25 RA patients had one or more joint erosions. Mean US-7 score as well as scores of individual joints or modality subscores were significantly lower in IIM than in RA, but, when compared only those patients with positive findings, the differences were found in total US-7 score, and GS-synovitis and PD-tenosynovitis subscores, but not in PD-synovitis, GS-tenosynovitis as well as in scores of individual joints.

Conclusions Our data suggest that arthritis is common feature of myositis. It is often present at the beginning of muscular manifestation of disease, or it even precedes the onset of muscle weakness. Most common presentation is symmetrical, non erosive polyarthritis affecting particularly wrists, shoulders, metacarpophalangeal and proximal interphalangeal joints of the hands. We confirmed strong association of arthritis with anti-Jo-1 antibody. Ultrasound investigation of joint involvement in IIM shows less frequent involvement than in RA, but comparable activity of synovitis measured by PD in affected joints. IIMs have less erosions and tenosynovitis than RA.

A10.4 AUTOMATED AND STANDARDISED ANALYSIS FOR HIGH DIMENSIONAL CYTOMETRIC DATA PROVIDES NEW OPTIONS FOR COMPLEX CELL-ASSOCIATED BIOMARKER SCREENING

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Background and Objectives Flow cytometry (FCM) is widely used in clinical research and offers rapid and quantitative characterisation at single cell level. Traditional analysis is a semiautomated, time-consuming process of gating and successive 2-D projections, influenced by investigator-specific settings. With an increasing number of parameters for multiplexing, the manual analysis step is most limiting and impedes high throughput analysis in FCM.

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Therefore, we developed a new algorithm for automated and standardised analysis of multiplex FCM data.

Materials and Methods Automation included asinh-transformation of data, cell grouping, population detection and population feature extraction. For grouping of cells, an unbiased unsupervised model based t-mixture approach with Expectation Maximisation (EM)-iteration was applied. Populations were detected and identified by meta-clustering of several experiments according to position and extension of cell-clusters in multi-dimensional space and by including a General Procrustes Analysis (GPA) step. For validation, peripheral leukocytes from healthy donors and patients with rheumatoid arthritis (RA) were prepared by hypoosmotic erythrocyte lysis and stained with different sets of lineage-specific antibodies, including CD3, CD4, CD8, CD56, CD19, CD14 and CD15. In parallel, different leukocyte samples were depleted of one of these populations by magnetic beads. Qualitative and quantitative characteristics of major populations were compared with conventional manual analysis.

Results Whole blood leukocytes stained simultaneously with up to 7 markers were correctly distinguished in all major populations including granulocytes (CD15+), T-cells and their subpopulations (CD3+, CD4+, CD8+), monocytes (CD14+), B-cells (CD19+), and NK-cells (CD56+). The result was comparable to the "gold standard" of manual evaluation by an expert. The new technology is able to detect subclusters and to characterise so far neglected smaller populations based on the new parameters generated. Automated clustering did not require fluorescence compensation of data. Cell-grouping is applicable even for large FCM datasets of at least 10 parameters and more than 1 million events. Comparing the cell-clusters between RA and healthy controls, differences were detectable in several cell (sub-)populations, stable enough to perform correct classification into controls and disease.

Conclusions Our approach reveals first promising results for the analysis of large datasets as generated by multiplex FCM analysis in an automated and time-saving way. Defined clustering algorithms avoid operator-induced bias. In addition, our unsupervised procedure is able to detect unexpected sub-clusters and to characterise so far neglected smaller populations, which may help not only to distinguish normal from disease but also to develop markers for disease activity and therapeutic stratification.

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A10.5 COMPARATIVE EFFECTIVENESS OF BIOLOGICAL THERAPIES IN RHEUMATOID ARTHRITIS IS INFLUENCED BY RESPONSE MEASURES AND DISEASE ACTIVITY STATE

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Background and Objectives Several biological therapies have become available in the last years in the management of rheumatoid arthritis (RA). Two of the most common drug classes include anti-tumour necrosis factor (TNF) and anti-interleukin-6 (IL-6) agents, which target central cytokines in the disease pathway. We have previously shown that the proportion of patients achieving remission was higher in the tocilizumab group, an anti-IL-6 agent, compared to anti-TNF therapies, but the magnitude of the effect was associated with the disease activity measure used, namely DAS28, CDAI or SDAI. The aim of this study is to assess whether this difference remains significant in other RA disease activity states.

Materials and Methods We included biologic-naïve RA patients registered in the Rheumatic Diseases Portuguese Register, Reuma.pt, who have started therapy with anti-TNF (adalimumab, infliximab, golimumab) and anti-IL-6 (tocilizumab) monoclonal antibodies after 1st January 2008. Our primary outcome was the proportion of patients in each disease activity state (remission, low, moderate, high) at 6 months, applying DAS28, CDAI and SDAI. Univariate and multivariate logistic regressions were performed to compare the groups.

Results 220 RA patients were enrolled, 180 treated with anti-TNF monoclonal antibodies and 40 treated with tocilizumab. Both groups had similar baseline characteristics but tocilizumab-treated patients had significantly higher SJC, DAS28, SDAI and CDAI as well as shorter disease duration. At 6 months, a significantly higher proportion of patients in the tocilizumab group had reached the DAS28 (n = 21, OR 0.16, p < 0.0001, 95%CI 0.06–0.38) and SDAI (n = 9, OR 0.29, p = 0.03, 95%CI 0.09–0.91) remission thresholds, but no significant difference was seen for CDAI (n = 8, OR 0.41, p = 0.12), in the adjusted logistic multivariate model. Moreover, the proportion of patients with moderate (n = 85, OR 3.49, p = 0.006, 95%CI 1.44–8.43) and high disease activity (n = 30, OR 6.13, p = 0.028, 95%CI 1.32–30.89) was higher in the anti-TNF group only according to DAS28. No differences were seen in the low disease activity class.

Conclusions Globally, tocilizumab-treated patients had better disease activity outcomes, but the magnitude of the effect was dependent on the disease activity measure used, confirming our previous results and underlining the pronounced reduction of inflammatory markers such as ESR and CRP, translated by lower DAS28 and SDAI, respectively. Furthermore, this effect was also related to the disease activity state considered. This may be explained by the fact that these different indexes distinctly weigh the different components and/or do not classify the same patients in the same disease activity state.

A10.6 DISSECTING DISEASE-SPECIFIC DIFFERENCES IN RA AND OA BY TRANSCRIPTOME ANALYSES OF SYNOVIAL TISSUE, BLOOD AND BONE MARROW MONOCYTES

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Background and Objectives Rheumatoid arthritis (RA) is a chronic inflammatory disease associated with joint destruction. Joint inflammation is characterised by infiltration and activation of various immune cells. To avoid difficulties in sampling synovial tissue and to avoid fluctuation in cellular composition of leukocytes, which accompanies inflammation both in synovial tissue and blood, this study was focused on transcriptome analyses of synovial tissues, blood and bone marrow monocytes. The main aim was to analyse potential of blood monocytes in dissecting inflammation in RA and in reflecting inflammation that is evident in synovial tissue. Osteoarthritis (OA), which represents a non-inflammatory disease was used as control in this study.

Materials and Methods Synovial tissues from 10 RA and 10 OA patients were used for gene-expression profiling by Affymetrix HG-U133A arrays. Blood and bone marrow monocytes, obtained from

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