<0.05, q = 0.02), supporting the idea that they should be involved in the pathophysiology of the disease.
Conclusion: These preliminary data confirm that the innate immune cells could play an important role in AxSpA. MAIT cells are at the forefront of the expression of IL-17A before γδ T, CD4+T and CD8+T. Neutrophils do not appear to participate in the production of IL-17A, but the high expression of AS linked genes in these cells suggests their involvement in AxSpA.

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FRI0362 HIGH-DIMENSIONAL MULTIPARAMETRIC CHARACTERIZATION OF THE REGULATORY T CELLS LANDSCAPE IN SPONDYLOARTHRITIS

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Background: The Spondyloarthritides (SpA) are immune-mediated conditions characterised by spinal and joint inflammation. The pathogenic role of Th17 lymphocytes has been shown by multiple studies but few reports exist on the phenotype of regulatory T cells (Tregs) and their role in the course of the disease. Studying Tregs is particularly challenging because of their heterogeneous phenotype and potential plasticity at the site of inflammation. Given the complexity of the Treg landscape, a multi-dimensional approach, including both protein and gene analysis, offers novel mechanistic insights that can be leveraged to develop new treatments.
Objectives: 1) To describe the Treg phenotype in SpA patients compared to controls. 2) To identify differential expression of markers, such as trafficking molecules or co-inhibitory molecules, within Tregs at the inflammatory site. 3) To define the gene expression landscape in Tregs in the peripheral blood and synovial fluid in patients with active SpA.
Methods: A total of 61 patients with SpA (38 with Ankylosing Spondylitis (AS), 23 with Psoriatic Arthritis (PsA)) and 16 age-matched healthy controls were recruited. Peripheral blood (PB) and paired synovial fluid (SF) mononuclear cells (n=8) were also analyzed. Isolated mononuclear cells were stained with 3 multicolor flow cytometry panels, including a total of 35 surface and intracellular protein markers. Manual gating was done in parallel with unsupervised data analysis using FlowSOM and SPADE. Cells from blood and synovial fluid from three treatment-naive PsA patients were isolated and their RNA sequenced at a single cell level with the 10x Genomics platform.
Results: Whereas no major difference in the Treg frequency was observed comparing the PB of SpA patients and healthy controls, in the SF we observed a higher Treg frequency, with a striking prevalence of the memory (CD45RA-) compartment (mean: 11.7 vs 4.7%; p=0.01) and a higher expression of Foxp3 (p=0.04). Trafficking markers demonstrated considerable heterogeneity, as visualized on SPADE analysis, mirroring the classification of T helper cells, but little difference in terms of relative frequency compared to healthy controls. Within the Treg compartment we identified populations of Helios-negative Th17-like cells able to secrete higher levels of IL-17A (mean: 2.8 vs 1.2%; p=0.02) while expressing normal levels of Foxp3; and putative regulatory CD8+ T cells expressing classical Treg features (Foxp3, CTLA4).
The analysis of the single cell transcriptomic data confirmed a high degree of heterogeneity, both in the SF and the PB, with consistent findings across patients. Unsupervised clustering identified different subsets that share a core of regulatory transcripts, onto which additional programs are added, including a very distinct Th17-like module. Of note, various Treg subsets express preferentially different co-inhibitory genes, suggesting a functional specialization.
Conclusion: High-dimensional immunoprofiling in SpA patients shows normal frequency of Tregs in the PB, but increased Tregs with activated phenotype in the inflammatory site. The presence within the Treg population of Th17-like and CD8+ populations are intriguing preliminary findings that require further evaluation. Preliminary transcriptomic analysis confirms the presence of specialized subsets within the Treg compartment.
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FRI0363 AUTOANTIBODIES TO THREE NOVEL PEPTIDES IN EARLY AXIAL SPONDYLOARTHRITIS IN TWO INDEPENDENT COHORTS

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Background: Diagnosis of axial spondyloarthritis (axSpA) is challenging since clinical manifestations, such as inflammatory back pain, peripheral arthritis, enthesitis and inflammatory bowel disease, often overlap with other disorders. Current laboratory markers for axSpA, Human Leukocyte Antigen (HLA)-B27 and C-reactive protein (CRP) are not sufficiently specific for diagnosis. Despite being considered a "seronegative" disease, emerging evidence supports the involvement of antibodies in axSpA. In order to identify novel autoantibodies in axSpA patients, we recently screened an axSpA cDNA phage display library for reactivity with immunoglobulin G (IgG) antibodies in plasma of early axSpA patients. This resulted in autoantibodies to 9 novel University of Hasselt (UH) axSpA peptide targets, corresponding to fragments of known proteins and novel lineair peptides.
Objectives: The aim of this study was to determine the diagnostic potential of autoantibodies to the 9 novel UH axSpA peptides in axSpA patients and controls from 2 independent cohorts.
Methods: Using enzyme-linked immunosorbent assays (ELISA), presence of antibodies to the 9 UH axSpA peptides expressed on phage particles was determined in 76 early axSpA patients, 75 chronic low back pain patients (LBP), 60 early rheumatoid arthritis patients (RA) and 94 healthy controls (HC) from the UH cohort. Antibody reactivity was further validated in 174 patients from the **Leuven** Spondyloarthritis (Biologics) Cohort ((**Bio)SPAR**), including 79 early axSpA patients.
Results: Antibody reactivity against at least one of 9 novel UH axSpA peptides was found in 54% (41/76) of early axSpA patients, 26% (24/94) of HC (*p=0.0002*), 39% (29/75) of LBP (*p=0.0731*) and 38% (23/60) of RA patients (*p=0.0845*) from the UH cohort, as compared to 43% (74/174) of the axSpA patients from the (Bio)SPAR cohort. By combining the three UH axSpA peptides with highest positive likelihood ratios (LR+) into a panel, antibodies against these 3 peptides were detected in 14.2% (22/155) of early axSpA patients from the combined UH and (Bio)SPAR cohorts and in only 5% (4/75) of persons with LBP (*p=0.*0484), resulting in a specificity of 95%.. The LR+ for confirming axSpA using antibodies to these 3 UH axSpA peptides was 2.7, which is the same as for the currently used laboratory marker CRP. Assuming a 5% pretest probability of axSpA in persons with LBP, a combination of the presence of inflammatory back pain (LR+ 3.1) and a positive test result for the laboratory markers HLA-B27 (LR+ 9.0) and CRP (LR+ 2.5) provides a disease (posttest) probability of 79%. When we added a positive test result for the presence of antibodies to the 3 UH axSpA peptides (LR+ 2.7), posttest probability could be increased to 91%.
Conclusion: Antibodies to 3 UH axSpA peptides were significantly more present in early axSpA patients compared to LBP and could provide a novel tool for objective diagnosis of a subset of axSpA patients.
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FRI0364 T REGULATORY CELLS AS BIOMARKER OF DISEASE ACTIVITY AND RESPONSE IN PSORIATIC ARTHRITIS PATIENTS: RESULTS FROM APREMILAST-TREATED COHORT

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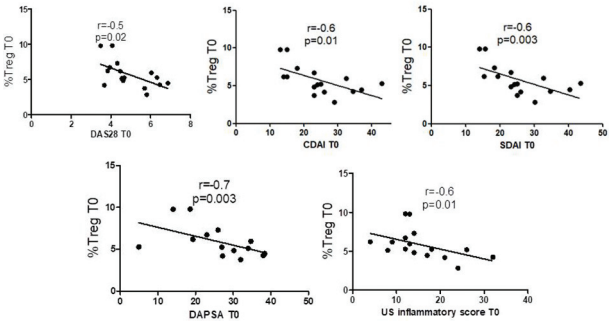
Background: The PDE4-inhibitor apremilast has been recently introduced in the treatment of Psoriatic Arthritis (PsA). It acts by down-regulating intracellular inflammatory mediators synthesis by elevating cAMP levels. Tregs, a subset of FOXP3+ CD4 T cells, play a key role in preventing immune responses and could exert their suppressive function via cAMP (1). Reduced frequencies of circulating Tregs have been observed in inflammatory disorders, nonetheless very few data are available on PsA patients.

Objectives: We evaluated peripheral Tregs in a cohort of PsA patients treated by apremilast.

Methods: Seventeen PsA patients (M/F 3/14; median age 56.0 years, IQR 20.0; median disease duration 15.0 years, IQR 11.0) with polyarticular subset treated by apremilast, were evaluated at baseline (T0) and after 6 (T1) and 12 weeks (T1). Clinimetric evaluation included DAS28, DAPSA, CDAI, and SDAI. Moreover, US assessment was performed at wrists, metacarpophalangeal (MCP), and proximal interphalangeal (PIP) joints: synovial effusion/hypertrophy and power Doppler were scored by a semi-quantitative scale (0-3), obtaining a total score (0-198). Treg frequency was assessed in peripheral blood mononuclear cells by flow cytometry, as the percentage of CD127low FOXP3+ in live CD4+ T cells (%Treg).

Figure 1: Correlation between %Treg and disease activity indices (DAS28, CDAI, SDAI, DAPSA, US inflammatory score.



Results: At baseline we identified a median%Tregs of 4.6 (IQR 1.1), inversely correlating with DAS28 (r=-0.5, p=0.02), DAPSA (r=-0.7, p=0.003), CDAI (r=-0.6, p=0.01), SDAI (r=-0.6, p=0.003 and US inflammatory score (r=-0.6, p=0.01) (Figure 1). Treatment with apremilast was able to induce a significant improvement in all activity indices at T1 (DAS28, P=0.009; DAPSA, P=0.01; CDAI, P=0.005; SDAI, P=0.006; US score, P<0.0001) and T2 (DAS28, P<0.0001; DAPSA, P=0.007; CDAI, P=0.008; SDAI, P=0.006; US score, P=0.0005). Furthermore, responding patients according with EULAR criteria at T2 showed significantly higher%Treg at baseline in comparison with non-responder patients (median 4.8, IQR 1.2 versus median 2.9, IQR 1.1; P=0.02).

Conclusion: The results of our study demonstrate that%Treg is a marker of disease activity in PsA patients. Moreover, the baseline value of Tregs could predict the response to apremilast after 12 weeks of treatment.

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FRI0365 PDE4 TARGETING SELECTIVELY INHIBITS INFLAMMATORY-DRIVEN OSTEOCLASTOGENESIS

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Background: Patients suffering from Psoriatic arthritis (PsA) commonly develop bone erosions and inflammatory-induced bone loss. This process is mediated by osteoclasts derived from monocytic precursors, and modulated by inflammatory cytokines (i.e. TNF, IL-1, IL-6, IL-17, IL-10 and GM-CSF) from immune and stromal cells. In immune cells (including $CD14^+$ osteoclast pre-cursors), PDE4, an enzyme responsible for hydrolysing cyclic AMP to inactive AMP, drives inflammatory effects [1]. Importantly, Apremilast (APR; a selective PDE4 inhibitor) has known efficacy in PsA [2], and decreases pro-inflammatory mediators whilst increasing anti-inflammatory mediators (IL-10) [3]. Although published data indirectly suggest a positive impact of APR on bone in PsA, data is lacking with regard to the impact on bone resorption.

Objectives: To evaluate the impact of a selective inhibition of PDE4 by APR on osteoclastogenesis from human $CD14^+$ precursors.

Methods: Osteoclasts were differentiated from primary human $CD14^+$ blood monocytes (healthy controls) with RANKL and MCSF, in the presence or absence of APR. To specifically study the impact of APR on osteoclastogenesis in an inflammatory context, osteoclastogenesis was also undertaken in the presence of: ***(i)*** TNF, ***(ii)*** Supernatants from activated Peripheral Blood Mononuclear Cells (PBMC) or activated CD3 cells, treated with or without APR, ***(iii)*** Co-culture with activated PBMC or activated CD3 cells, treated with or without APR. $TRAP^+$ multinucleated cells (mature osteoclasts) were enumerated via microscopy.

Results: In a non-inflammatory context, PDE4 inhibition by APR did not affect the differentiation of $CD14^+$ precursors into mature osteoclasts. However, TNF-enhanced osteoclastogenesis was significantly decreased by APR (-30.0% +/- 14.9; p=0.0279).The treatment of either activated PBMCs or purified $CD3^+$ T cells with APR substantially reduced cellular activation. In PBMCs this decrease in cellular activation resulted in a decrease in conditioned media-driven osteoclastogenesis (-49.7% +/- 13.2; p=0.0385). In comparison, APR treatment of purified $CD3^+$ T cells did not reduce their osteoclastogenic potential.

Conclusion: The results of this study reveal that PDE4 targeting potently inhibits inflammatory-driven osteoclastogenesis. Moreover, these data also suggest that $CD3^+$ T cells are not the main target of PDE4 inhibition in this context. In summation, our study supports the hypothesis that APR can modulate bone integrity in inflammatory condition such as PsA.

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