order to evaluate the diagnostic accuracy of miR-146a in PB and SF for distinguishing RA patients from healthy controls (HCs). Concentrations of IL-17A in matched serum and SF samples were determined by Human IL-17A ELISA kit (Gene probe, Diaclone). The results were compared to HCs as well as within the RA group.

Results miR-146a was overexpressed in 70.83% of RA SF ($p=0.007$) when compared to HCs SF. The ROC curve analysis showed diagnostic accuracy for miR-146a in SF with $AUC=0.769$ (95 CI: $0.600\div0.938$) with 75.0% sensitivity and 72.3% specificity ($p=0.006$). SF levels of miR-146a were overexpressed in 52.17% of the RA patients compared to its systemic levels. Levels of IL-17A were higher in RA SF compared to serum (8.645 pg/ml versus 0.315 pg/ml, $p=0.012$).

Conclusions The difference between the systemic and local levels of miR-146a and IL-17A in RA patients indicates that the local inflammatory process leads to their deregulation with a possible role of both molecules in the disease pathogenesis. The higher local levels of miR-146a and IL-17A suggest the possible relationship between miR-146a expression and the production of IL-17 from IL-17 expressing cells.

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P101 SYSTEMIC AND LOCAL IL-17A AND MIR-155 LEVELS IN RHEUMATOID ARTHRITIS PATIENTS

¹R Shumaliyeva*, ²D Kachakova, ³T Velikova, ¹S Monov, ²R Kaneva, ¹Z Kolarov. ¹Department of Internal Medicine, Clinic of rheumatology; ²Molecular Medicine Center, Department of Medical Chemistry and Biochemistry, Medical University – Sofia; ³Clinical Immunology, University Hospital Lozenetz, Sofia, Bulgaria

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Career situation of first and presenting author Assistant.

Introduction Interleukin 17 (IL-17) is a proinflammatory cytokine, which overproduction promotes the autoimmune reaction in rheumatoid arthritis (RA). Posttranscriptional regulation of IL-17 by specific microRNAs (miRNAs) is of great interest in the recent years. Studies have shown that miR-155 enhances Treg and Th17 cells differentiation and IL-17A production by directly targeting the suppressor of cytokine signaling (SOCS) 1.^{1,2}

Objectives To examine a possible deregulation of the expression levels of miR-155 and levels of IL-17A in peripheral blood (PB) and synovial fluid (SF) of RA patients.

Methods Expression levels of miR-155 were determined in matched PB and SF samples of RA patients by relative quantitation method $2^{-\Delta\Delta C_t}$. As reference control for normalization RNU6B gene was used. Receiver operating characteristic (ROC) curve analysis using RQ values was constructed in

order to evaluate the diagnostic accuracy of miR-155 in PB and SF for distinguishing RA patients from healthy controls (HCs). Concentrations of IL-17A in matched serum and SF samples were determined by Human IL-17A ELISA kit (Gene probe, Diaclone). The results were compared to HCs as well as within the RA group.

Results miR-155 was overexpressed in 79.17% of RA SF ($p=1.63 \times 10^{-4}$) when compared to HCs SF. The ROC curve analysis showed diagnostic accuracy for miR-155 in SF with $AUC=0.858$ (95 CI: $0.757\div0.959$) with 81.3% sensitivity and 81.8% specificity ($p=2.3 \times 10^{-4}$). SF levels of miR-155 were overexpressed in 76.09% of the RA patients compared to its systemic levels. Levels of IL-17A were higher in RA SF compared to serum (8.645 pg/ml versus 0.315 pg/ml, $p=0.012$).

Conclusions The difference between the systemic and local levels of miR-155 and IL-17A in RA patients shows that the inflammatory process leads to their deregulation with a possible role of both molecules in the disease pathogenesis. The higher local levels of miR-155 and IL-17A confirm the data about the possible role of miR-155 in regulating the production of IL-17.

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P102 HIGH DIMENSIONAL PROFILING OF REGULATORY T CELLS IN SPONDYLOARTHRITIS REVEALS CELLULAR HETEROGENEITY

D Simone*, MH Al Mossawi, I Brough, L Chen, F Penkava, A Ridley, H Shi, L Tucker, N Yager, P Bowness. Nuffield Department of Orthopaedics, Rheumatology and Musculoskeletal Sciences, University of Oxford, Oxford, UK

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Career situation of first and presenting author Student for a master or a PhD

Introduction The Spondyloarthritides (SpA) are immune-mediated conditions characterised by spinal and joint inflammation. Numerous studies implicate Th17 lymphocytes in pathogenicity but few reports exist on the role played by regulatory T cells (Tregs) in the disease.

Objectives

- To describe Treg frequency and phenotype in SpA patients compared to controls.
- To identify differential expression of trafficking molecules and activation markers within Tregs at the inflammatory site.

Methods A total of 61 patients with SpA (38 with AS, 23 with PsA) and 16 age-matched healthy controls were recruited. Peripheral blood (PB) and paired synovial fluid (SF) mononuclear cells ($n=8$) were stained for with 3 multicolor flow cytometry panels, including a total of 35 surface and