of or mir-140 expression level correlates with the disease progression of knee OA (Zhang et al.; Chao et al.). Under certain circumstances, miRNAs can be released into the body fluids and easily be detected in the blood samples. Therefore, miRNAs are hot candidates as biomarkers for early diagnosis or structural progression of OA.

Objectives: The aim of this study was to evaluate circulating miRNAs in patients with hand osteoarthritis (HOA) and healthy individuals. Simultaneously, we studied specific miRNAs in order to differentiate between erosive and non-erosive subsets of the disease.

Methods: Eight patients with HOA (erosive: n=4, 3 females, mean age=63.7±7 yrs; non-erosive: n=4, 3 females, mean age=62.4±6 yrs) and 4 healthy controls (3 females, mean age=63.5±7 yrs) were included in this study. Firstly, Advanced TaqMan low-density assay (TLDA) was performed for the purpose of miRNA high-throughput screening. Differently expressed miRNAs were further verified by real-time qPCR on the validation cohort in 31 patients with hand OA (19 females, mean age=68.2±7 yrs, erosive: n=9, non-erosive: n=10, healthy controls: n=12).

Results: TLDA profiling displayed 346 circulating miRNAs in plasma of patients with HOA and healthy controls. We demonstrated 40 differently expressed circulating miRNAs in patients with HOA compared with healthy controls. Using a real-time qPCR, we verified increased expression levels of 10 circulating miRNAs in patients with HOA compared with healthy controls, e.g. miR-191-5p (3.4 fold), miR-151a-3p (3.4 fold) or miR-222-3p (2.4 fold). We did not find any specific miRNA, which could distinct erosive from a non-erosive subset of the disease.

Conclusion: Extensive profiling of circulating miRNAs revealed several miRNAs that can be associated with HOA and can help to better understand OA pathogenesis.

REFERENCES:

Disclosure of Interests: Supported by AZV NV18-01-00542, MCR No. 023728.

DOI: 10.1136/annrheumdis-2021-eular.2327

AB0039
AGRIN REPAIRS BONE AND CARTILAGE IN VIVO

S. Eldridge1, A. Barawi1, H. Wang2, A. Roelofs3, M. Kaneva1, Z. Guan4, H. Lydon5, B. Thomas4, A. S. Thorup1, B. F. Fernandez5, S. Daxstrahan1, A. Ali1, K. Shannuganathan1, C. Pittalis1, J. Whiteford2, F. Henson3, A. Mccaskie3, C. De Ban1, F. Dell’acchio1.
1The William Harvey Research Institute, Experimental Medicine and Rheumatology, London, United Kingdom; 2University of Aberdeen, Aberdeen Centre for Arthritis and Musculoskeletal Health, AB25 2ZD, United Kingdom; 3University of Cambridge, Department of Veterinary Medicine, Cambridge, United Kingdom; 4The William Harvey Research Institute, Centre for Microvascular Research, London, United Kingdom; 5University of Cambridge, Department of Surgery, Cambridge, United Kingdom

Background: Cartilage defects in the joints are reported in 61% of all arthroscopies1,2. The size of the cartilage repair market is estimated to be $2.195 million in 2018.

We observed a similar phenotype of OA-FLS and MSC with regard to their multipotency, surface markers, and metabolic-related markers using flow cytometry, immunofluorescence staining, cell morphology, and protein expression patterns were analyzed using qPCR and mass spectrometry.

Results: We observed a similar phenotype of OA-FLS and MSC with regard to the minimal characteristics that define a MSC phenotype. In-depth comparison of

AB0040
PYRUVATE DEHYDROGENASE KINASES AS A POTENTIAL TARGET IN THE TREATMENT OF OSTEARTHRITIS TO UNLEASH THE METABOLIC FLOW?

A. Dameraj1,2, M. Kirchner3, M. Pfeifenberger1,2, A. Lang2,3, F. Buttgeriet1,2, T. Gaber1,2,3.
1Charité – Universitätsmedizin Berlin, Corporate Member of Freie Universität Berlin, Humboldt-Universität zu Berlin, and Berlin Institute of Health, Department of Rheumatology and Clinical Immunology, Berlin, Germany; 2German Rheumatism Research Centre (DRFZ) Berlin, a Leibniz Institute, Berlin, Germany, Rheumatism Research, Berlin, Germany; 3Berlin Institute of Health (BIH) and Max Delbrück-Centrum für Molekulare Medizin (MDC), Proteomics Core Facility, Berlin, Germany

Background: While osteoarthritis (OA) is the most common joint disease world-wide, rheumatoid arthritis (RA) represents the most frequent type of autoimmune arthritis. In both diseases, fibroblast-like synoviocytes (FLS), which maintain the structural and dynamic integrity of the joint, have been identified as key drivers of cartilage degradation. FLS can be divided into two major populations. The destructive phenotype which is restricted to the THY1-FLS of the synovial lining promotes bone erosion, while THY1+ FLS of the sublining layer drives synovitis. FLS phenotype is shaped by glucose metabolism, which promotes disease progression in patients with synovitis. However, profound knowledge about the contribution of FLS to pathogenic mechanisms in cartilage degradation is limited.

Objectives: Here, we present the phenotypic features of FLS obtained from patients with OA (OA-FLS) compared to bone marrow-derived mesenchymal stromal cells (MSC) on transcripthonic, proteomic and metabolic levels with the aim to identify novel targets for the development of disease-modifying osteoarthritis drugs and (ii) to distinguish both cell types.

Methods: To this end, we comprehensively compared human bone marrow-derived MSC with OA-FLS isolated from human knee joint sections. MSC and OA-FLS were characterized in detail according to their multipotency, surface markers pattern, cell viability, proliferation rate, morphology and expression of fibroblast- and metabolic-related markers using flow cytometry, immunofluorescence staining, cell morphology, and protein expression patterns were analyzed using qPCR and mass spectrometry.

Results: We observed a similar phenotype of OA-FLS and MSC with regard to the minimal characteristics that define a MSC phenotype. In-depth comparison of