Set Enrichment Analysis (GSEA) enrichment analysis, screening of differentially expressed genes (DEGs), Gene Ontology (GO) function annotation, Kyoto Encyclopedia of Genes and Genomes (KEGG) pathway analysis of DEGs were conducted. Protein-Protein Interaction (PPI) network of DEGs was constructed, and cluster association analysis was performed by MOCDGE plug-in in cytoscape software. Human autophagy-related genes were downloaded from Human Autophagy Database (HADb). Finally, we took the intersection of human autophagy-related genes and those involved in the top 5 clusters by cluster association analysis.

**Results:** 1467 DEGs were identified by DESeq2 package in R. Among them, 394 genes were significantly up-regulated while 1083 genes were significantly down-regulated. GO and KEGG enrichment analysis of DEGs revealed several terms related to cell cycle. GSEA analysis of all sequencing data revealed a number of terms related to cell cycle and lysosomes. The PPI network of 1467 DEGs was constructed by using STRING database, and 45 clusters were obtained by using MOCDGE plug-in of cytoscape software for cluster association analysis. The intersection of genes involved in the top 5 clusters and 219 autophagy-related genes downloaded from HADb were conducted to obtain 3 autophagy-related genes of AS, which were BIRC5, TP53 and CTSB.

**Conclusion:** Through RNA seq and bioinformatics analysis, we identified 3 potential autophagy-related genes of AS. BIRC5, TP53 and CTSB may inhibit the occurrence and development of AS by regulating autophagy.

**Acknowledgements:** NIL.

**Disclosure of Interests:** None Declared.

**REFERENCES:**


**Methods:** A cohort of 20 patients with axSpA was selected based on the radiographic progression for the purpose of this preliminary study. Baseline and two-year radiographs of the cervical and lumbar spine were independently assessed by two blinded readers using modified Stoke Ankylosing Spondylitis Spine Score (mSASSS). No radiographic progression and significant radiographic progression were characterized as a change in mSASSS ≤0 and >2, respectively, from baseline to year two. Disease activity was determined using C-reactive protein (CRP), Ankylosing Spondylitis Disease Activity Score (ASDAS) and Bath Ankylosing Spondylitis Activity Disease Activity Index (BASDAI). The proteome of the plasma samples was profiled using liquid chromatography with tandem mass spectrometry detection, and the difference in protein concentration was evaluated using linear mixed-effects modelling.

**Results:** Our cohort included ten patients without radiographic spinal progression (mean±SD age 34.9±9.0 years, 40% female) and ten patients (mean±SD age 40.8±9.0 years, 40% female) who developed the progression after two years (mean±SD change in mSASSS 9.8±5.1). Additionally, of all included patients, 14 were classified as radiographic axSpA (mean±SD age 36.9±8.6 years, 28.6% female) and six as non-radiographic axSpA (mean±SD age 40.2±9.2 years, 66.7% female). The high-throughput profiling of plasma proteome detected 489 quantifiable proteins and our statistical analysis revealed 30 proteins with different concentrations between patients without and with radiographic progression (p<0.05 for all). Out of these proteins, haptoglobin (1.76-fold, p<0.001) and serum amyloid P-component (SAP) (1.57-fold, p<0.001) were upregulated, while gelsolin (1.23-fold, p = 0.001) was downregulated in patients with mSASSS progression compared to those without radiographic progression (Figure 1A). In addition, all these proteins significantly correlated with mSASSS, CRP or ASDAS (Figure 1B). However, after adjustment for CRP, only SAP and gelsolin, which were previously associated with axSpA[1,2], were independently associated with structural progression.

**Conclusion:** We identified two plasma proteins with the potential to independently predict the radiographic progression of axSpA. Further studies in a larger cohort of patients are needed to validate these data.

**REFERENCES:**


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**Disclosure of Interests:** None Declared.

**POST439**

**SCREENING FOR PLASMA BIOMARKERS PREDICTING RADIOGRAPHIC PROGRESSION IN PATIENTS WITH AXIAL SPONDYLOARTHRITIS: A PRELIMINARY STUDY**

**Keywords:** -omics, Spondyloarthritis, Biomarkers

**Methods:**

**Background:** Axial spondyloarthritis (axSpA) is an immune-mediated rheumatic disease that has a significant impact on a patient’s quality of life. Therefore, early diagnosis and recognition of patients with potentially rapid structural progression of the disease are of great importance.

**Objectives:** This study aimed to investigate proteomic data in patients’ plasma to discover candidate biomarkers differentiating axSpA patients with radiographic progression after two years.

**Results:** We identified two plasma proteins with the potential to independently predict the radiographic progression of axSpA. Further studies in a larger cohort of patients are needed to validate these data.

**REFERENCES:**


**Conclusion:** We identified two plasma proteins with the potential to independently predict the radiographic progression of axSpA. Further studies in a larger cohort of patients are needed to validate these data.

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**Disclosure of Interests:** None Declared.

**POST440**

**INCREASED FREQUENCY OF ACTIVATED MAIT CELLS EXPRESSING THE GUT HOMING RECEPTORCCR9 IN PATIENTS WITH RADIOGRAPHIC AXIAL SPONDYLOARTHRITIS**

**Keywords:** Spondyloarthritis, Gastrointestinal tract, Innate immunity

**Methods:** We identified two plasma proteins with the potential to independently predict the radiographic progression of axSpA. Further studies in a larger cohort of patients are needed to validate these data.

**REFERENCES:**


**Conclusion:** We identified two plasma proteins with the potential to independently predict the radiographic progression of axSpA. Further studies in a larger cohort of patients are needed to validate these data.

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**Disclosure of Interests:** None Declared.