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COMPARATIVE METABOLOMIC AND LIPIDOMIC ANALYSIS OF SERUM SAMPLES FROM PATIENTS WITH SERONEGATIVE RHEUMATOID ARTHRITIS AND PSORIATIC ARTHRITIS

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Introduction Rheumatoid arthritis (RA) is a chronic autoimmune disease causing polyarthritis and joint destruction and affecting 1% of the population. Psoriatic arthritis (PsA) is a chronic inflammatory arthropathy which affects 20%–30% of patients with psoriasis. The diagnosis of RA is based on the clinical symptoms and the serological titer of rheumatoid factor (RF) and the anti-citrullinated peptide antibodies (anti-CCP). Although most RA patients are seropositive, in about 15%–20% of the cases the level of RF and anti-CCP remains within the normal range.

Objectives Since the symptoms between RA and PsA can be very similar, the differential diagnosis between seronegative RA (negRA) and PsA is often difficult. Early differential diagnosis is important for the choice of the best treatment strategy. By assessing the serum metabolomic and lipidomic profiles of PsA and negRA patients, we aimed at identifying potential biomarkers to distinguish these pathologies.

Methods Serum from 31 negRA and 77 PsA patients were collected for metabolic profiling using ¹H NMR spectroscopy.

For all samples, regular ¹H acquisition with presaturation and Carr–Purcell–Meiboom–Gill (CPMG) spectra were acquired using a 600 MHz Bruker NMR spectrometer. Spectra were processed with TopSpin using 0.3 Hz of line broadening and manual phasing. For metabolomics and lipidomics integration, spectra were subjected to bucketing by AMIX from 0.75–8.5 ppm (excluding the solvent region) with the spectral area normalised to the sum of all points. For statistical analysis Metaboanalyst software was used, where after interquantile range filtering and auto-scaling, partial least squares discriminant analysis (PLS-DA) was performed. Chemomx software was applied for the identification of metabolites.

Results In the untargeted metabolomic analysis using the CPMG pulse sequence, PLS-DA was able to separate the negRA from PSA patients. Based on our PLS-DA results Methionine, Glutamine, 4-Hydroxyphenyllactate and O-Acetylcarnitine were identified in spectral regions separating the two groups. Regular ¹H spectra were used for the untargeted lipidomic analysis. Due to the broad characteristic of the lipid signals seven groups of lipids (L1–L7) were assessed and designated by moieties. PLS-DA was performed, and the results suggest that the lipid profiles from those groups could differentiate between negRA and PsA.

Conclusions Our findings show that there are differences between the lipidomic and metabolomic profiling of negRA and PSA patients, and targeted analysis based on our present data is planned in order to identify more distinguishing metabolites and lipids.

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Disclosure of Interest None declared.