tissue disease (MCTD), undifferentiated connective tissue disease (UCTD) and healthy controls (HC) will be analysed to identify clinically relevant clusters.
Methods: A European multi centre, non-randomised, cross-sectional clinical study was conducted in 18 sites and 9 countries. Collection of OMIC data including genetic, epigenomic, transcriptomic (from peripheral blood and from isolated cells), flow cytometry, metabolomics and proteomic in plasma and urine, exosome analysis and classical serology (antibodies and autoantibodies) was organised. Novel and innovative methodologies including fine flow cytometry were conducted. Quality procedures were established to ensure standardisation of samples collection, processing, transportation and storage. Techniques were validated to ensure reproducibility of analyses. Unsupervised bioinformatics and biostatistics approaches will be applied.
Results: Recruitment started in December 2014 and ended in October 2017. A total of 2656 participants were recruited: 377 RA, 470 SLE, 402 SSc, 385 SjS, 99 MTCD, 106 PAPs, 166 UCTD patients and 651 HCs. Median age was between 46 and 59 years and was consistent with each disease onset peak. 97% of the population was Caucasian. Most of the patients were treated with standard of care therapies and less than 10% were on biologics. OMICs and bioinformatics analyses are on-going.
Conclusions: We have established one of the largest collaborative multi-OMICs studies from patients with SADs. The most important challenge is now the integration of all these novel data to support hypothesis-free, machine learning-led analytical protocols. It is expected that the integration of data from affected patients, in comparison with well-matched controls, will provide new biomarker-led descriptions of clusters of potentially etiologically distinct disease entities.
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AB1373 URINARY PROTEIN PROFILE COMPARISON BETWEEN SLE PATIENTS WITH AND WITHOUT RENAL INVOLVEMENT

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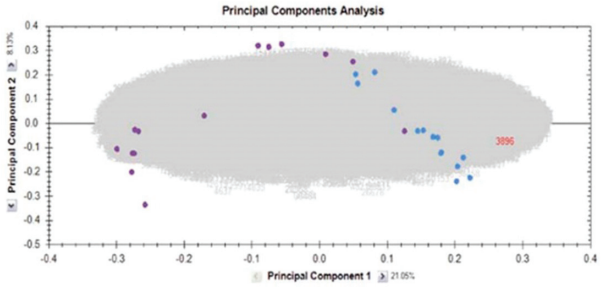
Background: Lupus nephropathy (NL) is an important cause of morbidity and mortality in patients with Systemic Lupus Erythematosus (SLE). The objective of the renal biopsy is to determine the type of glomerulonephritis that the patient presents to direct treatment. Considering that it is a specialised technique and not risk free, a proteomics study is proposed to determine biomarkers that help us to differentiate patients diagnosed with SLE with and without renal involvement.
Objectives: To determine if there is a different pattern of proteins between patients diagnosed with SLE with and without renal involvement.
Methods: We selected 12 patients diagnosed with SLE with renal involvement and 14 patients diagnosed with SLE without renal involvement. There were no differences between groups according to race, gener and age. The patients were classified as high, low or negative level of proteinuria in the urine. A 24 hour urine sample was obtained for analysis.
Results: We have done a Principal Component Analysis (PCA) where we can see differences between samples from patients who have high level of proteinuria in 24 hours and patients who have not renal involvement. Patients with positive proteinuria but not high level are a little confuse figure 1.
A total of 292 proteins (identified with at least two peptides with a FDR<1%) were quantified and further considered in the analysis. The Student's T-test analysis reflected the differential presence of 147 proteins (p<0.01). Of these, 130 were less abundant in the urine of the patients with renal damage, whereas 17 showed the opposite pattern, being more abundant in the patients with affected renal function.
Consistent with the nature of the sample, the Gene Ontology (GO analysis) of the whole list of identified proteins revealed the presence of extracellular (277 proteins, p=2.25E-171) and secretion-related proteins (49 proteins, p=1.1E-09), among others. Proteins related to defensive processes were prominent among them. Interestingly, the subset of proteins whose abundance increases upon renal damage is comprised of typical highly-abundant serum proteins. These proteins render a large number of peptides, suggesting they are very abundant. This protein pattern may reflect the higher albuminuria characteristic of patients with affected renal function. On the other hand, a number of proteins became significantly less abundant upon renal damage. The presence of highly abundant serum proteins in the urine of patients with compromised renal function may explain this phenomenon, since this will provoke a dramatic reduction in the relative abundance of the proteins already present in their urine.



Abstract AB1373 – Figure 1

Conclusions: A different protein pattern is observed between the two groups of patients, so in a more detailed study we can indicate if some of these can serve as prognostic markers for this type of patients.
Disclosure of Interest: None declared
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AB1374 PERFORMANCE OF EQ-5D, RAPID-3 AND HADS SCALES IN THE ASSESSMENT OF QUALITY OF LIFE AND FUNCTIONAL STATUS IN PATIENTS WITH ERYTHEMA NODOSUM

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Background: Erythema nodosum (EN) is the typical example of a mostly *septal panniculitis* with no vasculitis. Sarcoidosis and streptococcal infection are considered to be the most common etiological factors. There are no special scales available for practitioners to assess the efficacy of EN treatment in spite of high disease prevalence in general population. Sensitivity, specificity and validity of EQ-5D, RAPID-3 and HADS questionnaires have been demonstrated in other rheumatic diseases.
Objectives: The aim of this study is to evaluate the psychometric properties of EQ-5D, RAPID-3 and HADS scales in EN patients.
Methods: The study included 47 patients (45 females, 2 males) aged 37,6 ±11,2 y with mean EN duration 2,5[1; 6] months who were on the record at V. A. Nasonova Research Institute of Rheumatology during 2013–2017 yy. All patients filled in EQ-5D, RAPID-3 and HADS questionnaires at baseline (first visit) and 12 months later. The sensitivity of the questionnaires was assessed by comparing obtained scores with patient's response to therapy until achievement of nodular regression at the time of dynamic examination. The construct validity was determined using a correlation analysis with "external criteria", such as presence of artralgia/arthritis, palpatory tenderness of nodules assessed with VAS scale, ESR and CRP levels.
Results: Complete nodular regression was achieved in 39 patients. Positive post-treatment changes (nodular regression) correlated with improved EQ-5D (EQ-5D-index – p=0,005, EQ-5D-VAS – *p*=0,009) and HADS-anxiety subscale – p=0,02. No significant association was found for other questionnaires with *p* value=0,11 for RAPID-3 and p=0,69 for HADS-depression scale. Moderate correlation was established at control visit after 12 months (Mo12) between EQ-5D-index and nodular tenderness to palpation (r=–0,49, p=0,0001), between EQ-5D-index and ESR value (r=–0,55, p=0,0016), as well as between general health status assessed by VAS and nodular tenderness to palpation at baseline visit (r=–0,56, p=0,0001), indicating close association of data obtained by these assessment tools with objective physical and laboratory findings. There was also moderate correlation between functional RAPID-3 scores and nodular tenderness to palpation at Mo12 (r=0,37, p=0,0172) and ESR level (r=0,52, p=0,0002). These data demonstrate close association of assessment scales performance with objective health status. Moderate correlation was established for HADS-depression subscale scores with nodular tenderness to palpation in 12 moth after initiation of treatment (r=0,41, *p*=0,0077) and CRP value (r=0,34, p=0,025). There were no additional statistically significant correlations for RAPID-3 and HADS subscales with clinical and laboratory findings.
Conclusions: EQ-5D questionnaire is a valid and sensitive tool for assessment of quality of life in EN patients.
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