collectively suggest that the loss of ATM activation in monocytes may contribute to the disease process of SSc, and is possibly due to DNA damage and oxidative stress.

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AB0191 ANTI-SSA AND ANTI-JO1 LEVELS IN INTERSTITIAL LUNG DISEASE RELATED TO IDIOPATHIC INFLAMMATORY MYOPATHIES

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Background: The lung is the most frequently involved extramuscular organ in idiopathic inflammatory myopathies (IIMs); the most common form of lung involvement is interstitial lung disease (ILD). Some autoantibodies are strongly associated with ILD and with specific phenotypes and prognosis of ILD. Among myositis-specific auto-antibodies (MSAs), antibodies against aminoacyl-tRNA-synthetases (AsAb) are the strongest predictive factors for ILD, and anti-Jo-1 is the most common AsAb. Among myositis-associated auto-antibodies (MAAs), anti-SSA/Ro52 is frequently found in sera of patients with IIM and ILD, often associated with anti-Jo-1. The coexistence of anti-SSA/Ro52 and anti Jo-1 seems to be related to a more severe and extensive pulmonary fibrosis with higher score in HRCT compared with the patients with only anti-Jo-1 antibodies. Furthermore, some reports suggest that presence of anti-Jo-1 could be a biomarker for good prognosis¹. The significance of antibodies levels for the prognosis of ILD in IIMs was not widely investigated.

Objectives: To investigate the relationship between antibody levels and clinical manifestations, laboratory data, pulmonary function tests (PFTs), disease activity indices in ILD associated to IIMs.

Methods: Among 130 IIMs admitted to Rheumatology Unit of Bari from January 2010 to January 2018, we retrospectively examined 49 patients (40 F; 22 PM, 25 DM, 1 IBM; mean age at ILD onset 51 years, range: 23–83) because of ILD defined by high resolution computed tomography (HRCT). Clinical manifestations, laboratory data, HRCT pattern, PFTs (FVC, FEV1 and DLCO), therapy, disease activity as Manual Muscle Test (MMT-12), Health Assessment Questionnaire (HAQ), Physician Global Assessment (PGA) at ILD onset, were obtained from medical records. Ferritin levels and autoantibodies were detected in serum samples collected at ILD onset. ANA were tested by IIF on HEp-2 cell substrates, MSAs (JO1, EJO, OJ, PL7, PL12, SRP, HMGCR, Mi2, TIF1γ, MDA5, NXP2, SAE) and MAAs (Ro52, Ku, PM/Scl 75–100, RNP, Scl70) by line-blot method. Anti-SSA and anti-Jo1 were also detected by CLIA method. Correlation analysis were run using parametric and non-parametric test according to data distribution.

Results: 45 of 49 (91,8%) patients were positive for MSAs and/or MAAs. 40 of 45 (88%) were positive at least one of MSAs. The double presence of MSAs and anti-Ro52 was observed in 21 of 40 (52,5%), showing anti-Jo1/SSA in most cases (15/21, 71,4%). Among all correlations studied between anti-Jo1 or anti-SSA levels and PGA or PFTs, we found a significantly correlation between anti-Jo1 and PGA (p=0,03, R=0,46). We didn't find significantly correlation between autoantibodies and ferritin serum levels.

Conclusions: These findings confirm that ILD was associated with autoantibodies positivity. Further studies in larger cohort need to investigate if autoantibodies levels have a prognostic role in global outcome. Unlikely some controversial works in literature, serum ferritin does not seem a biomarker of severity of lung involvement in IIMs.

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AB0192

DISCOVERY OF POTENTIAL SKIN BIOPSY BIOMARKERS FOR SYSTEMIC SCLEROSIS BY HIGH-THROUGHPUT PROTEOMIC APPROACHES

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Background: Systemic Sclerosis (SSc) is an autoimmune connective tissue rheumatic disease characterised by three main hallmarks; vasculopathy, immune system abnormalities and fibrosis. It is considered a multisystemic and heterogeneous disease as many organs of the body may be affected and symptoms vary among patients. Up to date, SSc is untreated and its etiology and pathogenesis remain unclear. Early prognosis and diagnosis of the disease are challenging.

Objectives: The aim of this study was to analyse the proteomic profile of SSc patients in order to gain insights into the mechanisms implicated in disease pathogenesis and also discover new biomarkers that would facilitate early prognosis, more accurate diagnosis and therapeutic targeting of SSc.

Methods: Human biopsies were obtained from ten affected and three non-affected skin areas of SSc patients and have been classified based on histological criteria. Biopsies were cryo-pulverised and proteins were extracted, purified, reduced, alkylated and digested by trypsin. Purified peptides were analysed on a Waters Synapt G2Si HPLC instrument operated in ion mobility mode using a UHPLC approach. Data were processed by the Progenesis Q1 and functional annotation analysis was carried out using multiple bioinformatics resources.

Results: Proteomic analysis led to the identification and quantification of approximately 1500 non-redundant proteins per sample. About 400 of these proteins, including interferons and interleukins, are differentially expressed between affected and non-affected samples. Functional annotation analysis of these proteins showed that they are involved in multiple pathways including, antigen processing and presentation, complement, ubiquitin mediated proteolysis and Notch signalling, which are known to be associated with autoimmune diseases and fibrosis.

Conclusions: Using a Mass Spectrometry-based proteomic approach for the analysis of SSc human skin biopsies, we identified a number of proteins that might be involved in the development and pathogenesis of SSc. Interestingly, some of these proteins are differentially expressed in specific histological groups and thus could be considered as potential biomarkers for specific SSc stages.

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AB0193

SEMAPHORIN4A INDUCES TH17 CYTOKINE PRODUCTION IN SYSTEMIC SCLEROSIS

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Background: Systemic sclerosis (SSc) is an autoimmune disease characterised by inflammation, vascular injury and excessive fibrosis in different organs. Different studies have shown that Th17 cells and Th17 cytokines (IL-17, IL-21 and IL-22) play a key role in the pathogenesis of the disease. Semaphorin 4A (Sema4A) is a transmembrane protein that belongs to a large family of proteins initially described as ligands essential for neuronal development. Further studies have shown that they also play a role in other biological processes including the control of immune responses. Importantly, Sema4A has a critical role in the skewing of CD4⁺ T cells towards a Th17 phenotype. However, it is unknown if Sema4A contributes to the elevated number of Th17 cells observed in SSc patients.

Objectives: The aim of this study was to analyse the potential role of Sema4A as a regulator of Th17-skewing in SScs.

Methods: Plasma levels of Sema4A were measured by ELISA. Expression of Sema4A and its receptors PlexinB2, PlexinD1 and neuropilin-1 (NRP-1) was determined by (q)quantitative PCR, western blot and flow cytometry in monocytes and CD4⁺ T cells of healthy donors (HD) and SSc patients. Monocytes were stimulated with Poly IC (5 µg/ml) or CXCL-4 (5 µg/ml) and Sema4A expression