NETosis-derived bioproducts were further evaluated by multiplex assay and specific commercial kits, respectively. Besides, miRNomes were identified using next-generation sequencing. Clinical significance of the biomolecules analyzed was explored by correlation/association studies with immunological and CV-risk features.

Results: A significant relationship among the incidence of CVD (i.e. thrombosis or cardiac involvement) and the positivity for anti-dsDNA antibodies was recognized in the first SLE cohort. Accordingly, in the second SLE cohort, significantly impaired micro-vascular endothelial function (identified by reduction of hyperemia post-occlusion area), increased atherogenic index and pathologic increase in the CIMT were assessed in patients positive for anti-dsDNA in relation to anti-dsDNA negative patients. Around a 65% of SLE patients displayed a sustained positivity for anti-dsDNA antibodies for more than 7 years. These patients showed a distinctive and specific molecular profile compared with patients that had remained negative for anti-dsDNA, including increased inflammatory profile (IL1B, IL2, IL6, IL17, EOTAXIN, FGF, GM-CSF, IFN γ , IP10, RANTES, TNF), enhanced oxidative status (lipoperoxides), and higher NETosis (nucleosomes, elastase). Levels of those biomolecules were closely interconnected and associated to their regulatory miRNAs, which accordingly exhibited differential expression in SLE anti-dsDNA(+) vs anti-dsDNA(-) patients. Finally, the frequency for positivity of anti-dsDNA significantly correlated both with markers of endothelial dysfunction and with the presence of atheroma plaques in SLE patients, pointing at the direct involvement of anti-dsDNA-Abs in the development of these processes.

Conclusion: 1. Positivity for anti-dsDNA antibodies confers a specific molecular profile linked to an enhanced CV-risk in SLE patients. 2. Moreover, the sustained positivity for anti-dsDNA antibodies fosters the establishment of an atherothrombotic status in these autoimmune patients.

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AB0137 DIVERSITY ANALYSIS OF INTESTINAL FLORA IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS

Z. Mingxing¹, X. F. Yin¹. ¹The Second Hospital of Shanxi Medical University, Taiyuan, China

Background: Systemic lupus erythematosus (SLE) is a multiple systemic autoimmune disease and its pathogenesis is still not fully understanding. In recent years, there has been reports on the relationship between SLE and intestinal flora.

Objectives: To study the diversity and the intestinal flora intestinal microbes in patients with SLE and further provide new ideas for clinical treatment.

Methods: The stool samples of 28 patients with SLE and 125 normal healthy adults were collected. The 16S rRNA in the specimen was sequenced using the Roche/45 high-throughput sequencing platform, and the differences between the two groups were compared at the level of the phylum and genus.

Results: In SLE patients, as the picture show, the levels of fusobacteria, proteobacteria and TM7 were significantly higher ($P<0.05$) and the number of firmicutes was significantly decreased ($P<0.05$) than that of healthy controls at the phylum level. The percentage of bifidobacterium, collinsella, enterococcus, leuconostoc, streptococcus, bilophila were significantly higher ($P<0.05$) and the number of lachnospira, roseburia, gemmiger, devosia, desulfovibrio were significantly decreased ($P<0.05$) than that of healthy participants at the genus level.

Figure 1. the differences between patients with SLE and normal healthy adults were compared at the level of the phylum

Figure 2. the differences between patients with SLE and normal healthy adults were compared at the level of the genus

Conclusion: The diversity of intestinal flora in patients with SLE altered from that of normal population. The differences are likely to be one of the pathogenesis of lupus, which might provide theoretical foundation for the regulation of intestinal flora to treat autoimmune diseases such as lupus.

Disclosure of Interests: None declared

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AB0138 INCREASED CD38 EXPRESSION LEVELS ON IMMUNE CELL SUBSETS IN SYSTEMIC LUPUS ERYTHEMATOSUS

L. Ostendorf^{1,2}, P. Enghard^{2,3}, P. Durek², F. Heinrich², M. F. Mashreghi², G. R. Burmester¹, A. Radbruch², F. Hiepe^{1,2}, T. Alexander^{1,2}. ¹Charité – Universitätsmedizin Berlin, Department of Rheumatology and Clinical Immunology, Berlin, Germany; ²Deutsches Rheuma-Forschungszentrum (DRFZ), Berlin, Germany; ³Charité – Universitätsmedizin Berlin, Department of Nephrology, Berlin, Germany

Background: Plasma Cells (PCs) are implicated in the pathogenesis of Systemic Lupus erythematosus (SLE) and their targeting proved a promising treatment modality. As there is a monoclonal therapeutic antibody targeting CD38 licensed for clinical use in multiple myeloma, plasma cell depletion via CD38 seems to represent a promising path in SLE treatment. While CD38 is highly expressed on plasmacells, it is present on the surface of subsets of T and B lymphocytes as well as myeloid cells.

Objectives: Here we aim to identify the differential expression of CD38 on peripheral blood leukocytes in SLE compared to healthy controls (HC) investigate the function of CD38+ T lymphocytes

Methods: We performed flow cytometry to investigate the expression of CD38 on peripheral blood mononuclear cells of SLE patients (n=36) and HCs (n=20). We additionally analyzed the expression of T lymphocytes within the urine of patients with lupus nephritis as well as the skin of SLE patients. We investigated the