classification of the disease by pathological conditions. However, the association with MFG-E8 expression and clinical features of SLE patients is not fully understood.

**Objectives:** To clarify the clinical significance of MFG-E8 in SLE, we analysed the correlation between the expression level of MFG-E8 in circulating phagocytic leukocytes and clinical parameters of the patients.

**Methods:** A multi-centre, exploratory and prospective SLE cohort was established. Among SLE patients who visited our division from May 2015 to March 2017 and satisfied the 1997 revised criteria, patients with one or both of BILAG A or B, or with SLEDAI-2K ≥ 4 and clinical symptoms were defined as active SLE. These patients were then matched with randomly selected patients by age, gender, history of nephritis, and daily glucocorticoid dose as an inactive SLE group. Age and sex matched healthy controls (HC) were also recruited. The expression level of MFG-E8 in monocytes and its concentration in serum of the patients were measured by FACS and ELISA, respectively. The clinical parameters of the patients were collected from their clinical records.

**Results:** A total of 108 cases were enrolled, consisting of 36 active (mean age: 44.2±18.6, female: 80.6%, nephritis: 69.7%), 38 inactive SLE and 24 HC cases. The absolute number and the proportion of MFG-E8 positive-monocytes to total monocytes were significantly higher in the active SLE group (p<0.01), whereas serum MFG-E8 level showed no significant difference among the group. Importantly, the proportion was also significantly correlated with SLEDAI-2K, serum levels of anti-dsDNA antibody and complement and C1q (table 1). Notably, elevated proportion of MFG-E8-positive monocytes to total monocytes was observed in the patients with cutaneous or musculoskeletal involvement or leukocytopenia. In addition, the proportion of MFG-E8-positive monocytes to total monocytes significantly decreased from the baseline in active SLE patients after 6 months treatment and increased concordantly with disease activity in 6 refractory cases. Then we further analysed the accuracy to discriminate between active and inactive SLE patients and found that the proportion of MFG-E8 monocytes showed significant accuracy of disease activity, which is equivalent to serum levels of anti-dsDNA antibody, complement and C1q, by receiver operating characteristic curve analysis (figure 1).

**Conclusions:** Our study indicate that the proportion of MFG-E8-positive monocytes to total monocyte in peripheral blood was positively associated with disease activity of SLE and may be a novel mechanistic biomarker to determine the disease activity.

**REFERENCES:**

**Disclosure of Interest:** None declared

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Conclusions: This is the first report of increased BBBP in SLE subjects that is specific to the hippocampus; a region that we have previously reported to have abnormal resting metabolism in SLE subjects. These data, including the abnormal NP testing, support the murine model of autoantibody-mediated cognitive impairment following disruption of the BBB. The results also suggest that DCE-MRI may be an effective, non-invasive tool to measure BBBP and its role in neuropsychiatric SLE pending confirmatory studies with increased sample size.

REFERENCES:

Disclosure of Interest: None declared


FR10284

ALTERED PATTERNS OF HISTONE ACETYLATION POINT TO MECHANISMS OF TRANSCRIPTIONAL DYSREGULATION IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS

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Background: Systemic lupus erythematosus (SLE) is a chronic autoimmune disease designated by a heterogeneous course and systemic nature. It arises as a result of complex pathways, as well as the interaction of genetic and environmental factors, leading to the altered reactivity of the immune system that culminates in autoantibody formation. Epidemiological studies have shown an important role of the genetic component in the emergence of SLE and genome-wide association studies have identified more than 50 SLE-associated risk loci, pointing to a complex genetic background.

Objectives: The aim of the study was to further elucidate the genetic mechanisms influencing the development of SLE.

Methods: We performed chromatin immunoprecipitation experiments to ascertain the levels of histone acetylation in peripheral blood mononuclear cells collected from 5 recent onset and treatment naive SLE patients compared to 5 age and gender matched controls.

Results: The analysis revealed 16379 significantly enriched genomic regions in control patients compared to 39 204 significantly enriched genomic regions in SLE patients. Among the SLE specific regions several pathways were significantly enriched including the adaptive immune system pathway, cytokine signaling in immune system, disease of immune system and inflammation mediated by chemokine and cytokine pathway.

Conclusions: The collective data point to a significant alteration of histone acetylation patterns in SLE patients possibly mediated by the DNA specific autoantibodies. The results of the study offer additional insight into the genetics of SLE pointing to putative mechanisms of transcriptional dysregulation.

Disclosure of Interest: None declared


FR10285

DETECTION OF OLIGOCLAND B-CELL POPULATIONS BY SPECTRATYPING ANALYSIS IN THE RENAL TISSUE OF PATIENTS WITH ACTIVE LUPUS NEPHRITIS

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Background: Tertiary Lymphoid Organs (TLOs) are observed in target tissues of various immune-mediated inflammatory diseases (IMIDs) such as salivary glands in primary Sjögren’s syndrome (sS). TLOs are mimicking secondary lymphoid organs (SLOs) architecture and strikingly share common features with lymph nodes. SLOs organogenesis is coordinated by a complex stromal network that has not been fully characterised in TLOs yet. Although RANK-L (Receptor Activator of NF-κB Ligand) has been recently involved as a pivotal cytokine in precoce stages of lymph nodes development, its contribution in TLOs neogenesis remains unclear.

Objectives: To characterise stromal cells subsets within TLOs arising in the salivary glands and to determine whether RANKL is expressed or not in the the target tissue of pSS.

Methods: Stromal cells and RANK-L expression were analysed in TLOs from salivary glands by immunofluorescence on frozen sections in the NZB/NZW F1 mouse model and in minor salivary gland biopsies of patients fulfilling 2016 ACR-EULAR Sjögren’s syndrome criteria and by flow- cytometry after enzymatic digestion of NZB/NZW F1 salivary glands. RANK-L expression has also been assessed by Real Time quantitative Polymerase Chain Reaction (RT-qPCR) and immunofluorescence on primary cultures of salivary gland epithelial cells (SGEcs) with or without IL-1b or Interferon alpha (INF-a) stimulation.

Results: Most of SLOs stromal cells populations: Fibroblastic Reticular Cells (FRCs), Follicular Dendritic Cells (FDCs), Lymphatic Endothelial Cells (LECs), Blood Endothelial Cells (BECs) and High Endothelial Veinules (HEVs) were identified in salivary TLOs of both NZB/NZW F1 mice and patients with pSS. FRCs were the dominant subset in salivary TLOs and their proportion correlated with the degree of lymphocytic infiltration (r=0.7 ; p=0.007). In SLOs, RANK-L was mainly expressed by MRCs, whereas, none of them could be detected in salivary TLOs. However, despite the absence of MRCs in TLOs, RANK-L was still expressed by...