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:

- [1] Kowal C, et al. *Immunity* 2004;21:179–88.
- [2] Mackay M, et al. *Lupus Sci Med* 2015;2:e000074.

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FRI0284 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 16 379 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

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FRI0285 DETECTION OF OLIGOCLONAL B-CELL POPULATIONS BY SPECTRATYPING ANALYSIS IN THE RENAL TISSUE OF PATIENTS WITH ACTIVE LUPUS NEPHRITIS

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Background: Previous studies have shown, using polymerase chain reaction (PCR), cloning, sequencing and analysis of rearranged immunoglobulin heavy-chain (Ig-V_H/D_H/J_H) genes, that clusters of clonally-related sequences are commonly found in the peripheral blood of patients with active lupus nephritis.

Objectives: Using an easy-to-perform method such as spectratyping analysis, to test the hypothesis that clonal B-cell populations are present in the renal tissue of lupus nephritis patients, induced perhaps as a result of local (auto)antigenic stimulation.

Methods: Genomic DNA extracted from renal biopsy samples from 18 patients with active lupus nephritis and 24 control patients with other (auto)immune-mediated glomerular diseases, as well as DNA from 25 paired peripheral blood samples, was subjected to multiplex PCR for the detection of Ig-V_H clonal rearrangement. PCR products were analysed by capillary electrophoresis according to the Biomed-2 standard guidelines for the definition of clonal B cell populations. Immunohistochemistry using the B-cell-specific L-26 antibody was also performed in available renal samples.

Results: Electrophoregrams of PCR products derived from patients with biopsy proven active lupus nephritis revealed the presence of oligoclonal B-cell populations among polyclonal B-cells in renal tissue of 6/18 patients. No associations with clinical or histology class were evident. Oligoclonal B-cell populations were also found in renal samples derived from patients with untreated focal segmental glomerulosclerosis (6 of 7), minimal change disease (1 of 3), membranous nephropathy (1 of 3) and IgA nephropathy (3 of 4), and not in patients with pauci-immune vasculitis (n=4) or membranoproliferative glomerulonephritis (n=3). Oligoclonal B-cell populations were not found in any of the paired peripheral blood samples derived from 13 patients having renal B-cell oligoclonality, suggesting the existence of local (auto)antigens leading to clonal expansion rather than B-cell transfer through peripheral circulation. Finally, spectratyping analysis identified polyclonal or oligoclonal B-cells in all renal tissues in the absence of detectable B-cells by immunohistochemistry in the same samples.

Conclusions: These novel findings show that spectratyping analysis can detect oligoclonal B-cell expansions in renal tissue from patients with active lupus nephritis and other (auto)immune-mediated glomerular diseases. Whether this standardised method can identify individual patients who could benefit from therapeutic B cell depletion deserves further study.

REFERENCE:

- [1] Sfikakis PP, et al. Clonal expansion of B-cells in human systemic lupus erythematosus: evidence from studies before and after therapeutic B-cell depletion. *Clin Immunol.* 2009 Jul;132(1):19–31.

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FRI0286 RANK-L IS EXPRESSED BY SALIVARY GLAND EPITHELIAL CELLS IN PRIMARY SJOGREN'S SYNDROME: A NOVEL ACTOR IN ECTOPIC LYMPHOID STRUCTURE NEOGENESIS

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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 syndrome¹ (pSS). TLOs are mimicking secondary lymphoid organs (SLOs) architecture and strikingly share common features with lymph nodes.² 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 precocious steps of lymph nodes development,³ notably through a stromal cell expression, 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 target tissue of pSS.

Methods: Stromal cells and RANK-L expression were analysed in TLOs from salivary glands by immuno-fluorescence 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-α) 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 Venules (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