**LUPUS NEPHRITIS: HISTOLOGICAL FEATURES AND LONG TERM OUTCOMES IN A LARGE SINGLE-CENTRE COHORT**

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**Background:** In Systemic Lupus Erythematosus (SLE) patients the incidence of lupus nephritis (LN) is about 40% [1]. The rate of progression to end stage renal disease (ESRD) is 4.3-10.1% [2] and renal involvement is a strong predictor of morbidity and mortality.

**Objectives:** To describe clinical, histological features and renal outcomes of LN patients included in our single-center registry reporting data from more than 30 years. Moreover, we examined the correlation between clinical features at LN diagnosis and therapeutic lines used during the course of a 24 years follow-up.

**Methods:** A total of 71 patients were diagnosed with LN from 1989 to 2020. Demographic features and laboratory abnormalities (serum creatinine, 24 hours urine protein, urinary sediment, ds-DNA) at the time of LN diagnosis and at last available follow-up, were evaluated. We also examined renal biopsy performed and the histological classes (proliferative vs non-proliferative). We considered the increase number of therapeutic lines adopted as a negative prognostic factor in response to therapy.

**Mean (SD) or median (IQR) were used according the variable distribution.**

**Results:** Among 71 patients with LN, 63 (88.7%) were females and 8 (11.3%) males, with a F/M ratio of 6. Median SLE duration was 180 (162) months. The median age at the onset of nephritis was 28 (19.5) years and occurred in median after 12 (60) months from SLE diagnosis.

Sixty patients underwent a biopsy: the histology showed class III or IV proliferative glomerulonephritis in 49 patients (81.6%) and a non-proliferative class in 11 (18.3%) (p < 0.0001). Median serum creatinine value, 24 hours urine protein, urinary sediment at LN onset are reported in Table 1. Induction therapy was performed with cyclofosfamide in 14.5% of cases, mycophenolate in 61.5% and a maximum of 6 lines with a median value of 1.

Overall, the median follow-up was 180 (111) months and 30 (21.3%) patients had at least 120 months of follow-up. Median serum creatinine value, 24 hours urine protein, urinary sediment at eGFR last available follow-up are reported in Table 1.

Three patients underwent dialysis and 3 kidney transplantation. Eight patients underwent a re-biopsy: 7 (87.5%) had a proliferative class and 1 (12.5%) had a membranous class (p=0.01). Median serum creatinine value, 24 hours urine protein, urinary sediment at biopsy are reported in Table 1. In re-biopsied subgroup patients, induction therapies were cyclofosfamide in 50% of cases, mycophenolate in 12.5%, cyclosporine A in 25% and azathioprine in 12.5%.

There were not statistically significant differences among the age on LN onset, the time from renal onset to the onset of the disease and the number of therapeutic lines adopted (Figure 1).

**Conclusion:** Among patients with LN the proliferative classes are the most common. At the 15-year follow-up 2.1% had renal transplantation and 2.1% dialysis. We did not detect any association between age at diagnosis, time from renal impairment and the number of therapeutic lines.

**REFERENCES:**


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**CHANGING EXPRESSION PROFILES OF LONG NONCODING RNAS, MICRNAS, MRNAS AND CIRCULAR RNAS IN LABIAL SALIVARY GLANDS OF PRIMARY SjÖGRÉN’S SYNDROME (PSS)**

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**Background:** Primary Sjögren’s syndrome (pSS) is a relatively common autoimmune disease characterized by oral and ocular dryness. An increasing number of studies have revealed that long non-coding RNA (IncRNA), mRNA, miRNA and circular RNA (circRNA) contributes to the pathogenesis of autoimmune diseases.

**Objectives:** To explore IncRNA, miRNA, mRNA and circRNA expression profiles in labial salivary glands (LSGs) in pSS patients and their biological functions in the regulation of pSS.

**Methods:** The expression of 75,550 IncRNAs, 2,318 miRNA, 20,292 mRNA and 6,877 circRNAs were determined in the LSG of six pSS patients and six healthy controls using microarray experiments. Validation was performed in pSS patients and controls using real-time PCR. LncRNA-miRNA co-expression and gene-pathway networks were constructed using bioinformatics software.

**Results:** A total of 599 IncRNAs (upregulated: 279, downregulated: 320), 78 mRNAs (upregulated: 26, downregulated: 52), 615 miRNAs (upregulated: 590, downregulated: 25) and 160 mRNAs (upregulated: 110, downregulated: 50) were differentially expressed in the LSGs of pSS patients. Five of these IncRNAs were validated using real-time PCR. IncRNA HCP5, IncRNA SNHG5, IncRNA IFI44L, IncRNA CMPK2 were significantly upregulated and IncRNA TTYH1 were downregulated in pSS. GO

**Disclosure of Interests:** None declared

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