297 HYPERPROLACTINAEMIA ASSOCIATION WITH LUPUS NEPHRITIS DISEASE ACTIVITY

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Background and aims Prolactin has been found to be associated with immune regulation in SLE. The aim of this study is to determine the correlation between high prolactin level in comparison with IL – 6 with lupus nephritis disease activity in UKMMC.

Methods In this cross-sectional study, the analysis was conducted in SLE patients who attended Nephrology clinic in UKMMC from August 2015 till February 2016

Results Out of 43 patients with lupus nephritis, 27.9% of the patients had raised serum prolactin. The median of serum prolactin level at 0 min was 19.91 ng/ml (IQR: 15.95–22.65) for active lupus nephritis that was significantly higher as compared to the median of serum prolactin level 14.34 ng/ml (IQR: 11.09–18.70) for patients in remission (p=0.014). The serum prolactin level was positively correlated to SLEDAI (rho_s : 0.449, p=0.003) and UPCI level in lupus nephritis patients (rho_s : 0.241, p=0.032). Assessment of serum IL-6 levels found that the active lupus nephritis patients were having a higher median level of 65.91 pg/ml (21.96–146.14) compared to in remission level of 15.84 pg/ml (IQR: 8.38–92.84), (p=0.039). ROC curve analysis of serum prolactin 0 min and serum prolactin 30 min and IL-6 level for prediction of SLE diseases activity provide the cutoff value of serum prolactin 0 min was 14.63 ng/ml with sensitivity 91.7% and specificity 58.1% and AUC of 0.74 (p=0.015).

Conclusions Baseline fasting serum prolactin level was found to be a sensitive biomarker for evaluation of lupus nephritis disease activity.

298 IDENTIFICATION OF PLASMACYTOID DENDRITIC CELL INDUCED PROTEINS AS POTENTIAL BIOMARKERS FOR JNJ-56022473

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Background and aims Plasmacytoid dendritic cells (pDC) are potent producers of IFNα, we investigated what additional soluble factors are produced by pDCs and the effect of pDC depletion with JNJ-56022473 (JNJ-473), a novel antibody against CD123. We then investigated which of these factors are elevated in SLE patient sera to determine potential biomarkers.

Methods pDCs were isolated from healthy donor (HD) PBMC (n=6) which were stimulated with CpGc (TLR9) and imiquimod (TLR7) then analysed by RNAseq. PBMC from SLE and HD were also treated with isotype or JNJ-473 before stimulation with CpGc for 24 hour. Culture supernatant, SLE (n=33) and HD sera (n=34) was analysed by bead-based multiplex assay (Myriad U.S.A).

Results TLR9 and TLR7-agonism induced the regulation of thousands of genes, many of which were different IFNα-subtypes. Transcripts of many other secreted proteins such as MCP-2/CCL8, IP-10/CXCL10, ITAC/CXCL11 and MIP-3β/CCL19 were also upregulated. Proteins of these were also found to be significantly increased in SLE sera compared to HD.

Depleting pDCs with JNJ-473 in SLE and HD PBMC cultures reduced production of many CpGc-induced proteins including IFNα, MCP-2/CCL8, IP-10/CXCL10, ITAC/CXCL11 and MIP-3β/CCL19. RNAseq of SLE PBMC treated with JNJ-473 before CpGc stimulation, confirmed significantly decreased expression of MCP-2/CCL8, IP-10/CXCL10 and ITAC/CXCL11.

Conclusions We found that pDC depletion with JNJ-473 was able to prevent TLR9-induced production of IFNα and various other soluble proteins which are elevated in the sera of SLE patients. We propose that these soluble factors could be useful biomarkers to determine the effectiveness of pDC depletion and the modulation of IFN in SLE.

299 DIFFERENTIAL ABUNDANCE OF MIRNAS CIRCULATING IN PERIPHERAL BLOOD OF PATIENTS WITH CLASS IV LUPUS NEPHRITIS

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Background and aims Among the organs involved in-the SLE, we can highlight the renal damage, as the largest contributor to mortality in SLE patients is estimated that nearly-50% of SLE develop kidney disease in the first years of diagnosis. Class-IV lupus-nephritis (LN-IV) is the class of lupus nephritis most common in Colombian-patients with systemic-lupus-erythematosus. MicroRNAs are important molecules involved in the pathogenesis of LN. The aim of this study was to evaluate the relative abundance of circulating microRNAs in peripheral-blood of Colombian-patients with LN class IV.

Methods an observational case-control, cross-sectional. Patients-diagnosis by biopsy class IV lupus-nephritis was compared with patients without nephritis, and healthy-individuals was raised. These were extracted venous blood, which total RNA, which was subsequently sequenced. it was Compared Against the miRBase and Ensembl database. Differential gene expression analysis was Carried Out with edgeR and Functional analysis functional analysis was done with DIANA-miRPath. Was used as variables of selection Fold-Change(≥ 2 o ≤ -2) and False-Discovery-Rate (0.05).

Results We identified 24 circulating microRNAs with diference abundace that LNN or CTL, two of these microRNAs miR-107-3p and miR375-3p are described for first time to lupus nephritis.

Conclusions This changes in the abundace of miRNA, it implies alterations in the miRNAs-mRNA regulatory network in the pathogenesis of LN preceding the clinical onset of the disease. The findings thus contribute to understanding the