**LSO-075** PERFORMANCE OF CONVENTIONAL CARDIOVASCULAR RISK SCORES IN IDENTIFYING SUBCLINICAL ATHEROSCLEROSIS IN SYSTEMIC LUPUS ERYTHEMATOSUS

Gayathri Ms*, Chengappa Kavadichanda, Nived Haridas, Jaiweer Singh, Christina Mary Maraiselvam, Ashwinyi Gopal, Molly Mary Thabah, Vir Singh Negi. Clinical Immunology, Jawaharlal Institute of Postgraduate Medical Education and Research, India; Nephrology, Stanley Medical College and Hospital, India; Undergraduate Trainee, Jawaharlal Institute of Postgraduate Medical Education and Research, India; Clinical Immunology, All India Institute of Medical Sciences, Bhilaspur, India

10.1136/lupus-2023-KCR.115

**Background** Cardiovascular disease (CVD) is a major cause of mortality in systemic lupus erythematosus (SLE). The role of conventional risk scores which look at cardiovascular events, in assessing subclinical atherosclerosis in SLE is not fully established. This study aims to assess performance of QRESEARCH database risk score-3 (QRISK3), systemic coronary risk evaluation (SCORE) and WHO (World Health Organization) CVD scores in subclinical atherosclerosis and determine clinical associations of the same.

**Methods** This is a single center cross-sectional analytical study which enrolled 79 patients with SLE (without CVD) and 76 healthy controls. Demography, disease activity, autoantibodies, steroid dose were noted. Subclinical atherosclerosis (carotid plaque or abnormal carotid intima media thickness cIMT) and CVD risk (QRISK3, SCORE and WHO scores) were assessed. Agreement between scores was determined using kappa coefficient.

**Results** Subclinical atherosclerosis was seen in 52% SLE (abnormal cIMT-47% and plaque- 8%) and 53% healthy controls. Demography, disease activity, autoantibodies, steroid dose were noted. Subclinical atherosclerosis (carotid plaque or abnormal carotid intima media thickness cIMT) and CVD risk (QRISK3, SCORE and WHO scores) were assessed. Agreement between scores was determined using kappa coefficient.

**Conclusion** Sensitivity of conventional CVD scores in detecting subclinical atherosclerosis was very poor in SLE with QRISK3 and WHO score having good specificity. Hence, until further scores are validated, screening for subclinical atherosclerosis using carotid ultrasound remains gold standard.

**LSO-107** ASSOCIATION OF HYPERTENSION WITH HIGHER CHRONICITY INDEX SCORES AMONG PATIENTS WITH LUPUS NEPHRITIS

Peter Paolo Daleon*, Wendell Oliver Española, Sandra Navarra. Internal Medicine – Section of Rheumatology, University of Santo Tomas Hospital, Philippines

10.1136/lupus-2023-KCR.117

**Background** Kidney biopsies provide useful information to guide management in lupus nephritis (LN). Standard histopathology report includes ISN/RPS class, as well as Activity Index (AI) and Chronicity Index (CI) scores representing inflammation and fibrosis, respectively. We analyzed the clinical attributes associated with histopathologic class, AI and CI scores in patients with LN.

**Methods** We reviewed the medical records of LN patients seen at the University of Santo Tomas (UST, Manila Philippines) who underwent kidney biopsies from 2015 to 2022. Correlations between SLE disease characteristics at time of biopsy with ISN/RPS class, AI and CI scores were analyzed using Pearson correlation coefficient.

**Results** Of 44 patients (95.5% females), 13 and 29 patients had Class III and Class IV LN respectively, 1 each with coexisting Class V. Two patients had pure Class V, there were no patients in the other classes. Mean age was 25.1±10.3 years at LN diagnosis, with average disease duration of 2.4 ±3.7 years from diagnosis to biopsy. 70.5% had mild to moderate disease (SLEDAI<12) at biopsy. Average serum creatinine was 1.4±0.87 mg/dL, eGFR 71.8±37.7 mL/min, UPCR 2.6±1.4, and SLEDAI 10.6±4.4. Of renal parameters, only hypertension was associated with higher CI (r=0.417, p=0.002); although there was a trend for higher UPCR (r=0.144, p=0.176) and serum creatinine (r=0.221, p=0.075)

**LSO-106** RISK FACTORS ASSOCIATED WITH THE DEVELOPMENT OF CARDIOVASCULAR EVENTS IN A MULTIETHNIC ASIAN SYSTEMIC LUPUS ERYTHEMATOSUS COHORT

Hwee Siew Howe*. Rheumatology, Allergy and Immunology, Tan Tock Seng Hospital, Singapore

10.1136/lupus-2023-KCR.116

**Background** Objective: To determine the risk factors associated with the development of cardiovascular events (CVE) in a multi-ethnic Asian cohort of Singapore Systemic Lupus Erythematosus (SLE) patients.
correlating with higher AI, this was not statistically significant. Extra-renal features of oral ulcers (rs=−0.368, p=0.007), arthritis (rs=−0.461, p=0.001), and serositis (rs=−0.301, p=0.023) were associated with lower CI scores. There was no correlation of individual disease parameters with ISN/RPS class.

Conclusions This study demonstrated a significant correlation of hypertension with higher chronicity index scores among LN patients. Extra-renal disease activity features of oral ulcers, arthritis and serositis had lower CI scores. Aside from early aggressive management of active LN, strict sustained blood pressure control must be reinforced throughout the disease course in order to prevent renal damage.

**Short oral presentation session 14: SLE precision medicine**

**LSO-076 UNDERSTANDING THE GENETIC ARCHITECTURE OF SLE FROM THE PERSPECTIVE OF ASSOCIATIONS FROM 14 OTHER AUTOIMMUNE DISEASES**

Wanling Yang*, Xiao Dang, Yong-Fei Wang. Paediatrics and Adolescent Medicine, University of Hong Kong, Hong Kong

10.1136/lupus-2023-KCR.118

Background Genetic factors play key roles in the pathogenesis of systemic lupus erythematosus (SLE). In the last one and half decade, genome-wide association studies (GWAS) have seen enormous successes, revealing nearly 200 associated loci. However, for large number of loci, the causal variant(s), the association mechanism(s) are unclear. For some, the target gene(s) are unknown or controversial. Lack of functional understanding is the major challenge for translating genetic findings into clinical applications.

Methods In this study, we compared the association signals for SLE with the associations from 14 other autoimmune diseases, using linkage disequilibrium and conditional analyses to identify the shared and specific association signals. We annotated these signals using genomic resources such as eQTL, histone marks, chromatin accessibility, TF binding, and promoter interaction. Relevant cell types and signaling networks are constructed and compared among these diseases.

Results Analyzing the association signals between SLE and other autoimmune diseases and genomic annotations allow us to have a better grip on the causal genes and association mechanisms. Specific associations are identified for SLE even when the locus is shared with other diseases, including in IKZF1, ETS1, IL12A, DUSP22, IL12RB2, and CD40. Specific target genes, distinct cell types and signaling networks are detected for SLE. The differences suggested by these analyses raise intriguing questions on the shared and unique mechanisms of these autoimmune diseases.

Conclusions Genetic analysis and genomic annotations of associated loci for SLE in comparison with associations with 14 other autoimmune diseases facilitate the identification of the causal genes and the association mechanisms for SLE. The signals that are shared, or SLE-specific, or lack thereof shed new light on this prototype autoimmune disease from different angles.

**LSO-077 IDENTIFICATION OF AN INTERFERON 5-GENE SIGNATURE SCORE AS A PHARMACODYNAMIC AND POTENTIAL PREDICTIVE BIOMARKER FOR DEUCRAVACITINIB TREATMENT IN A PHASE 2 TRIAL IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS**

1Chun Wu*, 2Yanhua Hu, 3Mary K Crow, 4Amit Saxena, 5Christina Amiens, 6Coburn Hobar, 7Adrian Coles, 8Ian M Catlett. 1Informatics and Predictive Sciences, Bristol Myers Squibb, USA; 2Rheumatology, Hospital for Special Surgery, Weill Cornell Medical College, New York-Presbyterian Hospital, USA; 3Medicine, Division of Rheumatology, NYU Grossman School of Medicine, USA; 4Arthritis and Clinical Immunology, Rheumatology, Oklahoma Medical Research Foundation, USA; 5Medicine, University of Oklahoma Health Sciences Center, USA; 6Clinical Development, Bristol Myers Squibb, USA; 7Global Biometrics and Data Sciences, Bristol Myers Squibb, USA; 8Translational Medicine, Bristol Myers Squibb, USA

10.1136/lupus-2023-KCR.119

Background Tyrosine kinase 2 (TYK2) mediates cytokine pathways (eg, Type I IFN) linked with SLE pathogenesis. Deucravacitinib is a first-in-class, oral, selective, allosteric TYK2 inhibitor approved for the treatment of adults with plaque psoriasis. Deucravacitinib was efficacious in a phase 2 SLE trial. We developed a customized IFN 5-gene signature score, assessed the pharmacodynamic effects of deucravacinib on the IFN score, and evaluated the score’s association with SLE disease activity and clinical response in the phase 2 trial.

Methods Patients were randomized equally to placebo or deucravacitinib (3 mg BID, 6 mg BID, or 12 mg QD). Deucravacitinib was administered for 12 weeks. The main endpoint was the change from baseline in a 51-gene IFN signature score. The IFN score was calculated using a machine-learning approach. An IFN 5-gene signature score was also assessed. The score was calculated using a machine-learning approach. The score was calculated using a machine-learning approach. The score was calculated using a machine-learning approach. The score was calculated using a machine-learning approach.

Results An IFN 5-gene signature score (MX1, HERC5, IFIT1, RSAD2, and BAFF) and anti-dsDNA levels, and IFN-low subgroups; however, clinical response by IFN score was inconsistently improved (table 1). IFN-regulated gene expression performs well as a pharmacodynamic biomarker to confirm deucravacitinib mechanism of action and to aid in phase 3 dose selection.