patients with SLE occurred after the age of 40 compared to those with diabetes mellitus (DM).

Methods Incident SLE patients aged over 40 years and age-sex matched (1:4:4) controls with DM or general population were identified from the nationwide claims database in Korea between 2008 and 2018. We defined CVD risk as ischemic heart disease, stroke, and cardiac death. The incidence rate (IR), incidence rate ratio (IRR), and adjusted hazard ratio (HR) of CVDs were calculated using generalized estimating equation models.

Results We identified 4,272 SLE, 17,003 DM, and 17,088 general population patients aged over 40 years. Their mean age was 53.1 (±9.7) and 87.1% of them were female. The IR per 1,000 person-years (PYs) of CVDs for SLE, DM, and general population were 16.8, 11.7, and 5.7, respectively. Compared to general population, patients with SLE (IRR 3.27, 95% CI 2.78–3.85) and DM (IRR 2.77, 95% CI 2.02–2.56) showed higher CVD risk compared to general population. Increased risk of CVDs in SLE patients was highest in their forties (IRR 4.13, 95% CI 3.06, 5.59). After adjusting confounders, the CVD risk of SLE (HR 1.99, 95% CI 1.66–2.38) was higher than DM (HR 1.39, 95% CI 1.22–1.58) patients.

Conclusions Older onset SLE patients had increased CVD risk compared to general population. Even after adjustment for confounders, older onset SLE patients showed higher CVD risk than DM patients in Korea.

LSO-103 CHILDHOOD-ONSET SYSTEMIC LUPUS ERYTHEMATOSUS: LONG-TERM OUTCOMES IN A LARGE MULTI-ETHNIC ONTARIO COHORT

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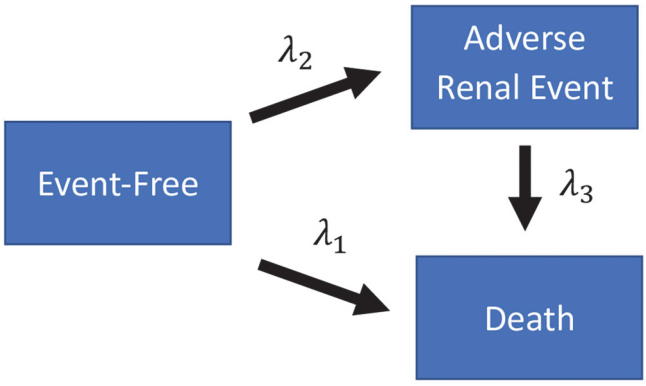
10.1136/lupus-2023-KCR.95

Background The long-term morbidity and mortality of childhood-onset SLE (cSLE) after transition to adult care is not well-documented. The present study aims to fill this knowledge gap by analyzing outcomes in a large province-wide cSLE cohort. Our objectives were to: 1) determine all-cause and cause-specific mortality rates, adverse renal event rates, cardiovascular event and cancer rates; and 2) determine baseline characteristics associated with higher rates of transition between 3 different states: event-free, adverse renal event, and death.

Methods Clinical data were abstracted for cSLE patients diagnosed between January 1990 and March 2011 after contacting all pediatric and adult rheumatologists and nephrologists in Ontario. Data were linked to administrative healthcare databases at ICES to determine the outcomes of interest. We examined descriptive summaries of major outcomes including death, end-stage kidney disease [ESKD] requiring chronic dialysis and renal transplant, cardiovascular events and cancer. We used a multi-state Cox model to determine baseline characteristics associated with higher rates of transition between the 3 states (figure 1).



Abstract LSO-103 Figure 1

Results There were 37 deaths in a cohort of 601 patients at a mean follow-up time of 14 years. The all-cause mortality rate was 3.43 per 1000 person-years. The rates for ESKD requiring chronic dialysis and renal transplant were 5.34 and 2.16 per 1000 person-years, respectively. The rates for any type of cardiovascular event and cancer were 6.32 and 3.13 per 1000 person-years, respectively. The multi-state model indicated that the non-white ethnic group (HR, 2.15; 95% CI, 1.14–4.08) and the presence of renal involvement at baseline (HR, 2.15; 95% CI, 1.17–3.95) were significantly associated with higher rates of transition from event-free to adverse renal event.

Conclusions In this large multi-ethnic cSLE cohort, ethnicity was associated with adverse outcomes including renal events and death. Further analyses will help inform risk for adverse outcomes to improve clinical care for the highest risk patients.

Short oral presentation session 10: SLE genetics & omics

LSO-053 ELEVATED EXPRESSION OF HSA_CIRC_0000479 IN NEUTROPHILS CORRELATES WITH FEATURES OF SYSTEMIC LUPUS ERYTHEMATOSUS

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Background Accumulating evidence suggests that differentially expressed circular RNAs (circRNAs) play critical roles in immune cells of SLE patients. Hsa_circ_0000479 has been studied in the field of cancer and infection, whereas a few researches in autoimmune disease. The aim of this study was to discuss the roles and clinical value of hsa_circ_0000479 in SLE.

Methods Reverse-transcription real-time quantitative polymerase chain reaction (RT-qPCR) was conducted to detect the expressions level of hsa_circ_0000479 in PBMCs (HC: n = 8; SLE: n = 8) and in neutrophils (HC: n = 45; SLE: n = 80). The relationships between hsa_circ_0000479 levels in neutrophils and the clinical features and laboratory parameters in SLE were analyzed.

Results The expressions level of hsa_circ_0000479 in SLE patients were higher than that in healthy controls. Even the expressions of hsa_circ_0000479 of neutrophils were significant obvious than that of PBMCs of patients with SLE. Moreover, the expressions level of hsa_circ_0000479 on neutrophils in SLE patients were negatively related to absolute neutrophils count (r = -0.323, P = 0.004) and complement 3 (C3) (r = -0.346, P = 0.002), whereas positively correlated with anti-dsDNA (r = 0.394, P = 0.001) and anti-nucleosome antibodies (r = 0.384, P = 0.001). Additionally, the increased level of hsa_circ_0000479 was associated with several clinical manifestations, including mucocutaneous vasculitis involvement, anemia, arthritis, lupus nephritis, neuropsychiatric involvement, and pulmonary involvement of SLE.

Conclusions Hsa_circ_0000479 in neutrophils probable was one of factors which involved in the pathogenesis and had potential clinical value in SLE.

LSO-054 GENETIC FINE MAPPING OF INDEPENDENT VARIANTS IN MHC REGION ASSOCIATED WITH PREDISPOSITION AND CLINICAL FEATURE OF SYSTEMIC LUPUS ERYTHEMATOSUS IN HAN CHINESE POPULATION

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10.1136/lupus-2023-KCR.97

Background The association between major histocompatibility complex (MHC) regions and systemic lupus erythematosus (SLE) has been widely established.

Methods To refined the most significant independent MHC loci with SLE susceptibility and clinical manifestations in Chinese Han population, we conducted stepwise conditional analysis 7,342 SLE cases and 7,185 control subjects of Chinese Han population based on the genotyped MHC region in Genome-wide association studies data by the Han-MHC reference panel in 1000 Genomes Project phase 3. Meta-analysis was performed in part of those independent loci with other ethnic populations from published studies. The correlation between the independent variants and SLE clinical feature was assessed by chi-square test.

Results A total of 1427 HLA variants significantly associated with SLE were identified(P<5×10–8): amino acid residue at position 233 in HLA-DRB1 (P=2.99×10–4, OR 0.81), HLA-DRB1*15:01(P=2.46×10–5, OR 1.37) and rs3135393 (P=1.74×10–4, OR 0.71) contributing the strongest signal. Stepwise conditional analysis revealed 20 independent variants including 15 novel loci with most strongly statistically association signal.

Meta-analysis of different ethnic groups confirmed 3 alleles shown consistent role to disease predisposed effects in multiple races and HLA-DQB1*03:01 present slightly different in different race. In a sub-phenotype comparative analysis, a link between 7 alleles, 5 amino acid residue and 3 SNP of HLA independent variant were detected strongly signal with different clinical manifestations of SLE.

Conclusions Our study emphasized the genetic value of the MHC region in the predisposition and its clinical feature of SLE in Chinese Han population. This funding provided a new perspective for early diagnosis, prevention, intervention among autoimmune diseases.

LSO-055 GENETIC CONTRIBUTIONS TO NEUROPSYCHIATRIC SYSTEMIC LUPUS ERYTHEMATOSUS

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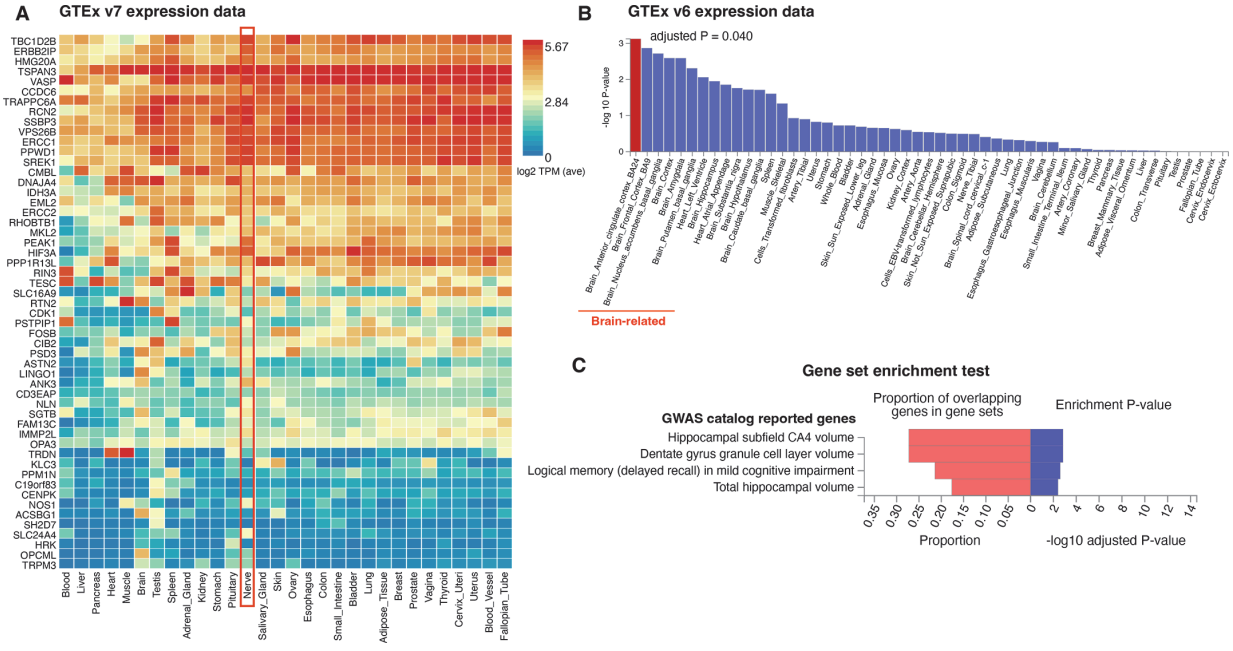
10.1136/lupus-2023-KCR.98

Background Despite recent advances in systemic lupus erythematosus (SLE) genetics, genetic contribution to development



Abstract LSO-055 Figure 1 Functional analyses for genetic risk loci of NPSLE. Tissue implicated by genetic associations with NPSLE from (A) GTEx data expression data v7, (B) GTEx data expression data v6. (C) Result of gene set enrichment test using genetic associations with NPSLE