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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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($P<5\times10-8$): amino acid residue at position 233 in HLA-DRB1 ($P=2.99\times10-4$, OR 0.81), HLA-DRB1*15:01($P=2.46\times10-5$, OR 1.37) and rs3135393 ($P=1.74\times10-4$, 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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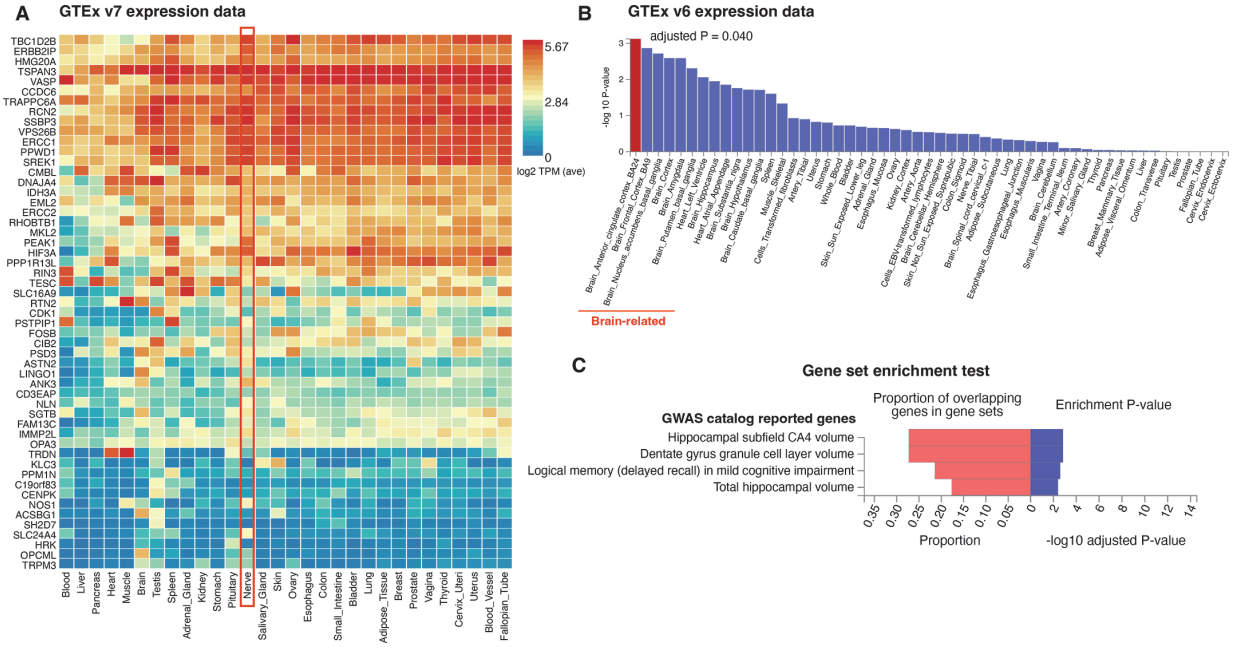
Background Despite recent advances in systemic lupus erythematosus (SLE) genetics, genetic contribution to development



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