**Results** Bulk flow sorted cell populations (CD45, epithelial) from kidney samples can separate LN from controls based on gene expression. IFN stimulated genes were differentially expressed in renal CD45 LN cells. Analysis of single cells sorted from 4 LN kidney biopsies revealed major differences in infiltrates composition, with 2 samples demonstrating a high percentage of B cells (average of 18% compared to no B cells in the other 2 samples) and CD4 T cells (18% vs 8%), and low percentage of CD8 T cells (9% vs 23%). A high transcriptomic lupus interferon signature was detected in urine CD45 cells. Distinct infiltrates and distinct expression profiles were detected across patients.

**Conclusions** The PEARL-Phase 0 project shows the feasibility of single cell isolation and transcriptomic analysis from LN kidney and urine. Analyses at a bigger scale in the two next phases of the project will accelerate discovery of new therapeutic targets and identification of biomarkers to guide therapeutic decisions in lupus nephritis and integrate the treatment effect.

### 265 THE EXPRESSION OF SIGLEC-10 IS ELEVATED ON B LYMPHOCYTES AND ASSOCIATED WITH DISEASE ACTIVITY IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS

J Bo miao*, P Dan, L Xiaochong, H Zhiming, Z Li, Y Zijing, H Lan. xi’an jiaotong university, First Affiliated Hospital, xi’an, China

**Background and aims** Siglec-10 (sialic acid-binding immunoglobulin-like lectins-10) is a member of Siglecs family and known to be expressed on B cells to regulate immune tolerance. This study aimed to investigate the expression of Siglec-10 on B cells of SLE and evaluate anti-inflammatory and immunosuppressive drugs impact on the expression of Siglec-10 on B cells in vitro.

**Methods** Peripheral blood mononuclear cells (PBMC) were obtained from patients with SLE (n=57) and healthy donors (n=30). Flow cytometry was performed to examine the expression of Siglec-10 on B cells. The potential association of these measures with the values of SLE disease activity index (SLEDAI) score was also analysed. In vitro cultivation of PBMC with Dexamethasone sodium phosphate and chloroquine phosphate, the expression of Siglec-10 on B cells were detected by flow cytometry after 16 hour.

**Results** The expression of Siglec-10 on B cells was significantly increased in SLE patients compared with normal controls (p<0.001). Moreover, it was positively correlated with SLEDAI (OR=0.277, p<0.05) and elevated in non-treatment patient than patients after anti-rheumatic treatment (p<0.05).

**Conclusions** The results from this study imply that Siglec-10 may play a potential role in progression and pathogenesis of SLE, which may represent a therapeutic target in SLE patients.
of smaller marker panels, we have developed anti-MVP into prototypic bead-based ELISA format. **Results** Discovery and validation experiments using the NavigAID SLE array showed that anti-MVP antibodies occurred with frequencies of 15%-30% in three different SLE cohorts at a specificity of 97%. Exploratory testing of multi-marker panels consisting of anti-MVP in combination with anti-dsDNA, anti-ribosomal P and anti-SmD yielded a 6% increase in sensitivity at 98% without loss of specificity. Multivariate data projection methods revealed that anti-MVP is detected in a subset of SLE patients with little overlap to established marker...A head-based ELISA was developed for measuring anti-MVP antibodies and showed good correlation with Lumix data (R=0.88) indicating successful platform transfer. **Conclusions** Anti-MVP autoantibodies represent a useful marker in SLE and, in combination with established markers, optimises the strategy for autoantibody testing. Furthermore, although more studies are needed, our findings suggest a previously undescribed linkage of type I IFN and autoantibody targets in SLE.

**269** SINGLE NUCLEOTIDE POLYMORPHISMS (SNPS) OF INTEGRIN-ALPHA-M (ITGAM) ARE ASSOCIATED WITH LUPUS NEPHRITIS (LN) IN AN ASIAN SYSTEMIC LUPUS ERYTHEMATOSUS (SLE) COHORT

1M Chan*, 1WG Lau, 1TY Lian, 1KO Kong, 2CY Yu, 1YW Song, 1HH Cheng, 1Leung, 1B Tsao, 1HS Howe, 1Tan Tock Seng Hospital, Rheumatology Allergy and Immunology, Singapore, Singapore; 2The Research Institute at Nationwide Children’s Hospital, Centre for Molecular and Human Genetics, Columbus, USA; 3Seoul National University, Rheumatology, Seoul, Republic of Korea; 4University of California Los Angeles, Rheumatology, Los Angeles, USA

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**Background** The Integrin-alpha-M (ITGAM) rs1143679 SNP has been associated with susceptibility to SLE and lupus nephritis (LN) in oriental Chinese and Thai populations. We previously found 13 ITGAM SNPs in linkage disequilibrium (LD) that were associated with susceptibility to SLE, but found no association with rs1143679.

**Aim** To determine associations of ITGAM SNPs with SLE subphenotypes and autoantibodies.

**Methods** We studied 248 patients fulfilling the 1997 ACR revised criteria for SLE. SLE-associated ITGAM SNP alleles were identified using custom-designed Immunochip arrays and gPLINK 1.062 software, with Bonferroni corrections for multiple comparisons. Associations of SLE-related ITGAM SNPs with SLE subphenotypes (malar or discoid rash, serositis, mouth ulcers, arthritis, haematological, renal or neurological involvement) and autoantibodies to dsDNA, Ro, RNP or Sm were determined with chi-square and Fisher’s tests and logistic regression.

**Results** All 13 SLE susceptibility ITGAM SNPs as well as the uncommon rs1143679 SNP (n=11) were associated with LN (Table 1). The strongest association was with rs2359661 (p=0.002, uncorrected). Subjects with these SNPs were less likely to have discoid rash. There was a trend towards an association with anti-Sm. Logistic regression models for 11 SNPs retained the factors LN, discoid rash and anti-Sm, suggesting strong LD for these SNPs.

**Conclusions** This study demonstrated novel ITGAM SNP associations with LN and confirmed the association of rs1143679 with LN. Most associated SNPs were in the regulatory region of ITGAM bearing promoter/enhancer histone marks and have been associated with expression levels in several cell types, suggesting modulation of levels of ITGAM expression to impact these subphenotypes.