

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 bead-based ELISA was developed for measuring anti-MVP antibodies and showed good correlation with Lumindex 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.

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AUTOANTIBODIES DICTATE CLINICAL MANIFESTATIONS IN PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS

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Background and aims Systemic Lupus Erythematosus (SLE) is known for its multifaceted clinical features and complex immune disturbance. Numerous studies have proven that certain autoantibodies are linked to specific clinical manifestations. However, the diversity of possible associations makes for the uniqueness of each case of SLE. The goal of our study was to analyse the link between clinical presentation and autoantibody titers in Romanian patients with SLE.

Methods We conducted an observational study of 48 adult patients with SLE hospitalised in the Rheumatology Department of the Clinical Rehabilitation Hospital. Venous blood samples were drawn to measure antinuclear antibody levels as well as anti-dsDNA, anti-ssDNA, anti-Sm, anti-U1RNP, anti-SSA, anti-SSB and anti-nucleosome antibody titers (ELISA). Clinical presentation, biochemical tests, SLEDAI score values and urinalysis were extracted from patients' charts. Patient characteristics were included in a database and analysed using IBM SPSS Statistics v20.

Results We found statistically significant correlations ($p<0.05$) between cutaneous manifestations and anti-Sm, anti-U1RNP, anti-SSA, anti-SSB and anti-nucleosome antibodies. Kidney involvement correlated with anti-Sm, anti-U1RNP and anti-nucleosome antibodies ($p<0.05$). Joint involvement was strongly associated with the presence of anti-U1RNP antibodies ($p=0.001$). Haematological abnormalities were significantly correlated with anti-dsDNA, anti-U1RNP, anti-SSA and anti-SSB antibodies ($p<0.05$), while ESR and CRP levels were only associated with anti-U1RNP antibodies ($p=0.03$). Furthermore, SLEDAI scores correlated with anti-dsDNA and anti-nucleosome antibody titers ($p<0.05$).

Conclusions Our data support the relationship between autoantibody titers, disease activity and severity of clinical changes in Romanian patients with systemic lupus erythematosus.

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

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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.

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ASSOCIATION OF TLR2 (23BP INS/DEL) POLYMORPHISM WITH SYSTEMIC LUPUS ERYTHEMATOSUS (SLE) AND P. FALCIPARUM MALARIA: A STUDY IN MALARIA ENDEMIC AREA OF ODISHA, INDIA

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Background and aims Human toll-like receptors (TLRs) participate in the innate response and signal the activation of adaptive immunity. TLRs play a vital role in sensing infection. A common 23 bp insertion/deletion polymorphism at 5'UTR of TLR2 gene has been shown to affect TLR2 expression and plasma levels of pro-inflammatory molecules. We hypothesised

Abstract 269 Table 1 Associations of ITGAM SNPs with SLE subphenotypes & auto-antibodies (n=248)

SNP	Allele	Lupus nephritis		Discoid rash		Anti-Sm	
		OR (95% CI)	p	OR (95% CI)	p	OR (95% CI)	p
rs4561481	G	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs8051304	C	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs889551	A	1.39 (1.09-1.77)	0.008	0.57 (0.36-0.91)	0.03	1.65 (1.02-2.65)	0.04
rs4889640	C	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs889549	C	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs11645526	A	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs8057320	C	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs7193943	G	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs11865830	G	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs3764327	T	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.54 (0.96-2.47)	0.07
rs7196256	T	1.41 (1.10-1.81)	0.006	0.57 (0.36-0.90)	0.02	1.51 (0.94-2.43)	0.10
rs3815801	C	1.39 (1.08-1.78)	0.009	0.58 (0.36-0.91)	0.03	1.43 (0.90-2.28)	0.14
rs2359661	A	1.46 (1.13-1.89)	0.002	0.59 (0.37-0.93)	0.03	1.36 (0.85-2.16)	0.23
rs1143679	A	1.67 (1.34-2.08)	0.03	0.39 (0.06-2.58)	0.46	0.35 (0.05-2.28)	0.30

(uncorrected p-values shown)

that a mutation at 5'UTR region of TLR2 gene could be associated with susceptibility/resistance to SLE and malaria. We performed a hospital based case-control study on SLE patients residing in *P. falciparum* endemic areas.

Methods Two hundred female SLE patients and age and sex, matched healthy controls were enrolled. 120 *P. falciparum* infected patients including 50 uncomplicated cases and 70 severe malarial patients were included. TLR2 (23bp ins/del) polymorphism was typed by polymerase chain reaction (PCR). 20% samples were randomly sequenced for validation of PCR results.

Results The mean age and disease duration of SLE patients were 27.44 and 2.91 years respectively. Prevalence of mutants (ins/del+del/del) of TLR2 gene polymorphism were significantly lower in SLE patients compared to healthy controls ($p=0.02$; $OR=0.54$). Distribution of TLR2 variants were comparable among different clinical phenotypes of SLE. The TLR2 5'UTR mutants were associated with elevated TNF alpha, IL1 beta and IL6 compared to the wild genotypes. Mutants were more prevalent in severe malaria patients than uncomplicated cases ($p=0.05$; $OR=2.31$).

Conclusions TLR2 5'UTR 23bp ins/del variants are associated with development of severe disease in *P. falciparum* malaria but possibly an evolutionary mechanism to protect SLE patients against severe malaria in endemic areas

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CIRCULATING TREGS AND TH17 CELLS PERCENTAGES IN CLASS IV DIFFER FROM OTHER CLASSES OF LUPUS NEPHRITIS

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Background and aims Lupus nephritis (LN) is a severe complication of systemic lupus erythematosus. T lymphocytes with regulatory properties (Tregs) play a role in preventing autoimmunity, are involved in LN pathogenesis and may also determine glomerular lesions in LN. Their potential use as LN biomarkers is investigated.

The aim of our study was to assess the relationship between repeated measurements of Tregs proportions, histopathology classes and five-year clinical outcomes in LN patients with different disease duration and activity.

Methods Forty eight LN patients were followed-up for 5 years. Their mean age, disease duration and activity (SLEDAI) at baseline was 41.1 years, 9.8 years and 8.3 points, respectively. Their blood was collected twice: at baseline and after 6 months. Populations of Tregs and Th17 cells were analysed by