of smaller marker panels, we have developed anti-MVP into\nprototypic bead-based ELISA format.\nResults Discovery and validation experiments using the Navi-\ngAID SLE array showed that anti-MVP antibodies occurred\nwith frequencies of 15%–30% in three different SLE cohorts\nat a specificity of 97%. Exploratory testing of multi-marker\npanels consisting of anti-MVP in combination with anti-\ndsDNA, anti-ribosomal P and anti-SmD yielded a 6% increase\nin sensitivity at 98% without loss of specificity. Multivariate\ndata projection methods revealed that anti-MVP is detected in\na subset of SLE patients with little overlap to established\nmarker. A bead-based ELISA was developed for measuring\nanti-MVP antibodies and showed good correlation with Lumim\nexus data (R=0.88) indicating successful platform transfer.\nConclusions Anti-MVP autoantibodies represent a useful\nmarker in SLE and, in combination with established markers,\noptimises the strategy for autoantibody testing. Furthermore,\nalthough more studies are needed, our findings suggest a pre-\nviously undescribed linkage of type I IFN and autoantibody\ntargets in SLE.

Background and aims Systemic Lupus Erythematosus (SLE) is\nknown for its multifaceted clinical features and complex\nimmune disturbance. Numerous studies have proven that cer-\ntain autoantibodies are linked to specific clinical manifesta-\ntions. However, the diversity of possible associations makes\nfor the uniqueness of each case of SLE. The goal of our study\nwas to analyse the link between clinical presentation and auto-\nantibody titers in Romanian patients with SLE.\nMethods We conducted an observational study of 48 adult\npatients with SLE hospitalised in the Rheumatology Depar-\ntment of the Clinical Rehabilitation Hospital. Venous blood\nsamples were drawn to measure antinuclear antibody levels as\nwell as anti-dsDNA, anti-ssDNA, anti-Sm, anti-U1RNP, anti-\nSSA, anti-SSB and anti-nucleosome antibody titers (ELISA).\nClinical presentation, biochemical tests, SLEDAI score values\nand urinalysis were extracted from patients’ charts. Patient\ncharacteristics were included in a database and analysed using\nIBM SPSS Statistics v20.\nResults We found statistically significant correlations (p<0.05)\nbetween cutaneous manifestations and anti-Sm, anti-U1RNP,\nanti-SSA, anti-SSB and anti-nucleosome antibodies. Kidney\ninvolvement correlated with anti-Sm, anti-U1RNP and anti-\nnucleosome antibodies (p<0.05). Joint involvement was\nstrongly associated with the presence of anti-U1RNP antibod-\nies (p=0.001). Haematological abnormalities were significantly\n correlated with anti-dsDNA, anti-U1RNP, anti-SSA and anti-\n SSB antibodies (p<0.05), while ESR and CRP levels were\nonly associated with anti-U1RNP antibodies (p=0.03). Further-\nmore, SLEDAI scores correlated with anti-dsDNA and anti-\nnucleosome antibody titers (p<0.05).\nConclusions Our data support the relationship between auto-\nantibody titers, disease activity and severity of clinical changes\nin Romanian patients with systemic lupus erythematosus.

Background The Integrin-alpha-M (ITGAM) rs1143679 SNP\nhas been associated with susceptibility to SLE and lupus nephe-\nritis (LN) in oriental Chinese and Thai populations. We have\npreviously found 13 ITGAM SNPs in linkage disequilibrium (LD)\nthat were associated with susceptibility to SLE, but found no\nassociation with rs1143679.\nAim To determine associations of ITGAM SNPs with SLE sub-\nphenotypes and autoantibodies.\nMethods We studied 248 patients fulfilling the 1997 ACR\nrevised criteria for SLE. SLE-associated ITGAM SNP alleles\nwere identified using custom-designed Immunochip arrays and\ngPLINK 1.062 software, with Bonferroni corrections for multi-\nple comparisons. Associations of SLE-related ITGAM SNPs\nwith SLE subphenotypes (malar or discoid rash, serositis,\nmouth ulcers, arthritis, haematological, renal or neurological\ninvolvement) and autoantibodies to dsDNA, Ro, RNP or Sm\ndetermined with chi-square and Fisher’s tests and logistic\nregression.\nResults All 13 SLE susceptibility ITGAM SNPs as well as the\nuncommon rs1143679 SNP (n=11) were associated with LN\n(Table 1). The strongest association was with rs2359661\n(p=0.002, uncorrected). Subjects with these SNPs were less\nlikely to have discoid rash. There was a trend towards an\nassociation with anti-Sm. Logistic regression models for 11\nSNPs retained the factors LN, discoid rash and anti-Sm, sug-\ngesting strong LD for these SNPs.\nConclusions This study demonstrated novel ITGAM SNP asso-\nciations with LN and confirmed the association of rs1143679\nwith LN. Most associated SNPs were in the regulatory region\nof ITGAM bearing promoter/enhancer histone marks and have\nbeen associated with expression levels in several cell types,\nsuggesting modulation of levels of ITGAM expression to\nimpact these subphenotypes.

Background and aims Human toll-like receptors (TLRs) partici-\npate in the innate response and signal the activation of adap-\ntive immunity. TLRs play a vital role in sensing infection. A\ncommon 23 bp insertion/deletion polymorphism at 5’UTR of\nTLR2 gene has been shown to affect TLR2 expression and\nplasma levels of pro-inflammatory molecules. We hypothesised