and placebo (3 times daily), for 3 months. Anti-ds DNA serum levels were measured by ELISA and urine protein were measured by urine albumin creatinine ratio (UACR).
Results After supplementation for 3 months, this study showed that decreased of anti-dsDNA serum levels in the supplementation group was significantly greater than in the placebo group. The decreased of UACR in the supplementation group was also significantly greater than the placebo group.
Conclusions Adding curcumin on vitamin D supplementation can decrease anti-dsDNA serum levels and proteinuria greater than vitamin D supplementation plus placebo in SLE patients with hipovitamin D.

258 THE EFFECT OF ADDING CURCUMIN ON VITAMIN D3 SUPPLEMENTATION ON CYTOKINES BALANCE, IN SLE PATIENTS WITH HYPOVITAMIN D

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Background and aims Vitamin D has important roles in the regulation of the immune system in Lupus. Seventy percent of lupus patients in Indonesia are experienced hypovitamin D. Curcumin is a natural VDR ligand and has sinergic effect with vitamin D. This study was aimed to determine the effect of adding curcumin on vitamin D supplementation on IFN-γ/IL-4 ratio and IL-17/TGF-β ratio, in SLE patients with hipovitamin D.
Methods This was a randomised controlled trial, double blind study. Forty SLE patients with hypovitamin D were studied, that randomised into two groups: 20 patients (supplementation group) received vitamin D (cholecalciferol 1200 IU daily) with curcumin 20 mg (three times daily); and 20 patients (placebo group) was given vitamin D (cholecalciferol 1200 IU daily) and placebo (3 times daily), for 3 months. Cytokines serum levels (IFN-γ, IL-4, IL-17, TGF-β,) were measured by ELISA.
Results After supplementation for 3 months, this study showed that decreased of IFN-γ/IL-4 ratio in the supplementation group was significantly greater than in the placebo group. The decreased of IL-17/TGF-β ratio in the supplementation group was also significantly greater than the placebo group.
Conclusions Adding curcumin on vitamin D supplementation can decrease IFN-γ/IL-4 ratio and IL-17/TGF-β ratio than vitamin D supplementation plus placebo in SLE patients with hipovitamin D.

259 THE EFFECT OF VITAMIN D3 SUPPLEMENTATION ON THE ANTI-DSDNA LEVELS AND URINE PROTEIN IN SLE PATIENTS WITH HYPOVITAMIN D

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Background and aims Vitamin D has important role in the regulation of the immune system in Lupus. 71% of lupus patients in Indonesia experienced hypovitamin D. This study was aimed to determine the effect of vitamin D supplementation on the levels of anti ds dna and degree of urine protein in lupus patients with hypovitamin D.
Methods Thirty nine SLE patients with hypovitamin D were studied, that randomzed into two groups: 20 patients was given vitamin D and 19 patients received placebo for 3 months. Anti-ds DNA levels were measured by ELISA and urine protein were measured by dipstick method.
Results Anti-dsDNA levels in the supplement group before and after giving vitamin D were 226.84±82.11 vs 191±72.55 (p=0.00), and the placebo group were 233.69±66.52 vs 227.72±61.21 (p=0.077). The degrees of urine protein in the supplement group before and after treatment were 24 vs 12 U/ml (p=0.003) and the placebo group were 16 vs 10 U/ml (p=0.070).
Conclusions Vitamin D supplementation plays a role on decreasing the levels of anti ds-DNA and urine protein in SLE patients with hypovitamin D.

260 THE EFFECT OF VITAMIN D3 SUPPLEMENTATION ON THE DISEASE ACTIVITIES AND DEGREE OF FATIQUE IN SLE PATIENTS WITH HYPOVITAMIN D

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Background and aims Vitamin D has important roles in the regulation of the immune system in Lupus. 71% of lupus patients experienced hypovitamin D in Indonesia,. This study was aimed to determine the effect of vitamin D supplementation on the degree of disease activity and degree of fatigue in SLE patients with hypovitamin D.
Methods Thirty nine SLE patients with hypovitamin D were studied, that randomised into two groups: 20 patients was given vitamin D and 19 patients received placebo for 3 months. Disease activity is determined by the SLEDAI scores and the degree of fatigue is determined by the FSS (Fatigue Severity Scale).
Results This study showed that supplementation of vitamin D 1200 IU per day increased 6:55±1:27 ng/cc of 25 (OH) D. The decreased of SLEDAI scores in the supplementation group were greater than the placebo group (6.45±3:07 vs 0.17 ±1.63), p=0.000. The decreased of Fatigue Severity Scale in the supplementation group also greater than the placebo group (2.27±0.73 vs 0.005±0.62.), p=0.000.
Conclusions Vitamin D supplementation plays a role on improving the activity of the disease (SLEDAI score) and the condition of fatigue (FSS) in SLE patients with hypovitamin D.

261 LONG-TERM EFFECTS OF OF HYDROXYCHLOROQUINE ON METABOLISM OF SERUM LIPIDS AND LEFT VENTRICULAR STRUCTURE AND FUCTION IN PATIENTS OF SYSTEMIC LUPUS ERYTHEMATOSUS

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Background and aims To observe the effects of long term hydroxychloroquine treatment on blood lipid and left ventriclar function of systemic lupus erythematosus(SLE) patients.
Methods 72 patients with SLE were randomly divided into two groups: Hydroxychloroquine treatment group(n=36)and non-hydroxychloroquine group(n=36). The level of blood lipid, left ventricular end-diastolic diameter (LVEDD), left ventricular end-systolic diametef (LVESD), interventricular septum thickness(IVST), *left ventricular* posterior wall thickness (LVPWT), fractional shortening rate(FS), left ventricular ejection fraction(LVEF), E/A were mearsured before, 6 month, 12 month and 2 years after the treatment.
Results The long term applies of hydroxychloroquine can bring statistically different of TC, TG, LDL and HDL to SLE patients. LVEDD, LVWPT and E/A were statistically different ($p<0.05$) before and after hydroxychloroquine were used.
Conclusions The long term applies of hydroxychloroquine can improve the lipidic metabolism and left ventricular function in SLE patients.

Genetics, epigenetics, omics, biomarkers and personalised medicine in SLE and autoimmunity

262 UTILITY OF SERUM FERRITIN AS A MARKER OF DISEASE ACTIVITY IN CHILDHOOD SYSTEMIC LUPUS ERYTHEMATOSUS

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Background and aims To assess the usefulness of serum ferritin levels as a marker of disease activity and organ involvement in childhood systemic lupus erythematosus (cSLE) and to screen children with SLE for subclinical macrophage activation syndrome.
Methods Consecutive children who met the criteria of SLICC were enrolled. All patients interviewed and assessed for disease activity using SLE disease activity index (SLEDAI). Biochemical and serological tests including serum ferritin level and markers of disease activity and macrophage activation syndrome (MAS) including LDH, AST, triglyceride and CD25 were measured by standard laboratory procedure.
Results A total of 29 (24 female) SLE patients with a mean age of 10.9 (± 2.9) years and mean of disease duration of 4 (± 2.4) years were included. The most frequent manifestations were musculoskeletal in 25 patients followed by haematological in 15 then renal involvement in 13 patients. Twenty patients had active disease (SLEDAI >4). Serum ferritin level was correlated significantly with SLEDAI ($p<0.0001$) and markers of MAS (LDH, AST, triglyceride and CD25) and negative correlation with fibrinogen (p 0.02). Interestingly, serum ferritin was weakly correlated with ESR but no correlation with CRP and proteinuria. Two patients confirmed to have MAS.
Conclusions Serum ferritin is a simple and probably a good marker of disease activity and screening for MAS in cSLE.

263 UPDATE ON SLE-HLA ASSOCIATION: CONTRIBUTION OF ALLELE-SPECIFIC EXPRESSION IN ADDITION TO AMINO ACID CHANGES IN HLA ALLELES

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Background and aims A genetic contribution of the human leukocyte antigen (HLA) genes to SLE has been well documented (e.g., OR=1.65, Heritability explained by HLA=2%; *Nat Genet* 2016). To understand the association in HLA loci within the major histocompatibility complex (MHC) region in large cohorts genotyped for MHC SNPs, we developed an ethnicity-matched HLA reference panel (*PLoS One* 2014).
Methods Using the HLA imputation and various statistical approaches, we investigated HLA amino acid residues, HLA classical alleles and MHC SNPs simultaneously, and identified that the changes in amino acid positions 11, 13 and 26 of HLA-DRB1 explained the entire HLA association (*Nat Commun* 2014; *Nat Genet* 2016). Additionally, all the protein-coding HLA-DR beta genes (*HLA-DRB1*, *HLA-DRB3*, *HLA-DRB4* and *HLA-DRB5*) with similar functions were further investigated using imputation-based conditional regression and haplotype analyses. *HLA-DRB1* was solely associated with SLE and accounted for the associations of the other HLA-DR beta genes (*PLoS One* 2016). Finally, we measured allele-specific expression of *HLA-DRB1* in blood cells by RNA sequencing followed by an allele-specific read mapping method.
Results Strong allele-specific expression among *HLA-DRB1* classical alleles was observed, which caused relatively unequal expression of two heterozygous alleles in individuals. Disease association models, fitted by logistic regression including either the copy number or both the copy number and the relative expression of each allele as predictors, revealed that the SLE association was significantly better explained by adding the variables for the relative expression.
Conclusions These findings indicate that both the qualitative and quantitative effects of *HLA-DRB1* variants are driving SLE (Figure).

264 PEARL: PATHWAY EXPLORATION AND ANALYSIS IN RENAL DISEASE IN THE ACCELERATING MEDICINE PARTNERSHIP (AMP) LUPUS NETWORK

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Background and aims Despite treatments, a substantial proportion of lupus nephritis (LN) patients progress to end stage renal disease and death. Detailed transcriptomic analyses of LN kidneys may identify new therapeutic targets. Our goal is to demonstrate the feasibility of single cell and low-input transcriptomic analyses of LN kidney and urine cells.
Methods Cells from urine and renal biopsies performed for clinical diagnosis from inform-consented patients (1 class III, 3 class IV+V, 1 class V) and 1 control (healthy part of tumour nephrectomy) were isolated, frozen, sorted and analysed by RNAseq.