Methods Nailfold of two patients with dermatomyositis were examined using dermatoscopy, (dermlite 3, 3 gen, USA.) MDA5 positivity was confirmed by ELISA.The findings were imaged using I pad mini (apple, USA). The images were compared to the patient with Jo-1, those with TIF1, or centromere.

Results Marked haemorrhages and enlarged capillaries were observed in almost all nailfolds of both hands, while only upto three nailfolds in patients with antibodies against Jo-1, TIF1, or centromere. However, loss of capillaries was not detected under the dermatoscopy at all, while these were detected in capillary scope in the literature in anti-MDA5 antibody positive patients.

Conclusions The results of the current study suggest that nailfold findings using dermatoscopy have a potential to diagnose the patients anti-MDA5 antibodies at their first visit, although there is a limitation in number of patient samples in this study. Likewise, the nailfold findings on dermatoscopy may provide visible information for the pathogensis of interstitial pneumonitis in these patients as well.

286 IDENTIFYING EXPOSURES TO CHEMICALS IN PATIENTS WITH SLE – "A NON-TARGETED EXPOSOME APROACH"

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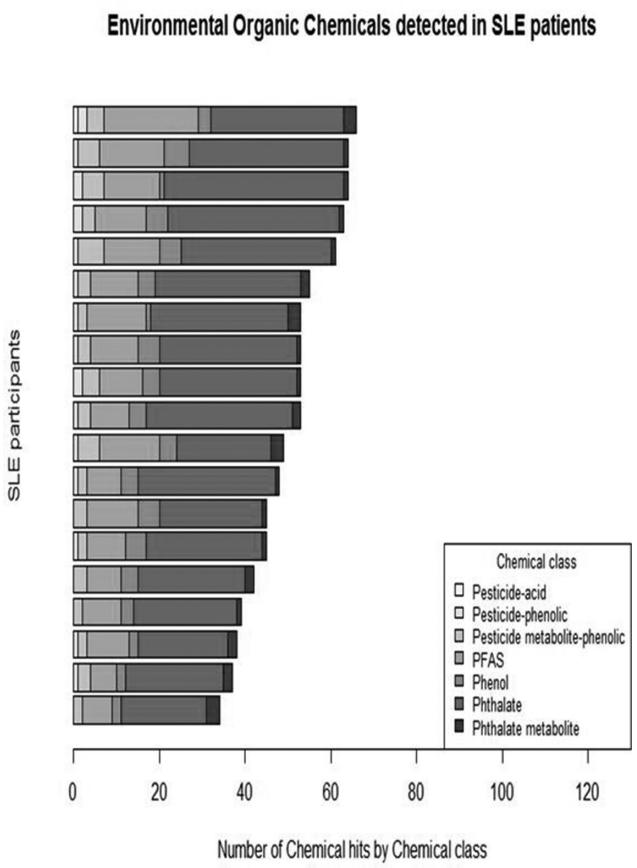
Background and aims Environmental exposures may play a substantial role in the pathogenesis of SLE. It recently became possible to identify and quantify a person's exposure to environmental chemicals ("the exposome") in a comprehensive fashion. This non-targeted approach has no a priori selection of chemicals. The goal of this study is to characterise multiple organic chemicals in a cohort of SLE patients and controls.

Methods Patients from the California Lupus Epidemiology Study and healthy controls were studied. Banked serum was analysed by Liquid Chromatography Quadruple Time-of-Flight Mass Spectrometry (**LC-QTOF/MS**). Data acquired by LC-QTOF/MS includes the molecular weights of all detected parent and daughter ions, as well as retention times and peak areas. This non-targeted screening allows rapid identification of potential hits. The results of the LC-QTOF/MS analysis are matched into a database of 740 potentially detected environmental organic chemicals [EOC].

Results We present preliminary data on 19 patients with SLE and 43 controls. 193 potential EOC hits were found in patients with SLE and 417 were found in controls. In SLE patients, the number of chemicals detected per participant ranged from 34–66, with an average of 50 hit matches. Pthalates and its metabolites were the most represented chemicals, with >50% of detected compounds in SLE. (Figure 1) Compounds of relevance include several endocrine disruptors such as Bisphenol A and Methoxyclor.

Conclusions Patients with SLE are exposed to a wide range of chemicals. LC-QTOF/MS can identify a wider range of potential chemical exposures in SLE, and aid in prioritising chemicals for further research and interventions.



Abstract 286 Figure 1 Environmental Organic Chemicals detected in SLE patients

287 RISK FACTORS FOR AND COMPONENTS OF METABOLIC SYNDROME: A STRUCTURAL EQUATION MODELLING ANALYSIS OF THE QUALITY OF LIFE OF PATIENTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS

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Background and aims This study assessed: (1) the relationships among the risk factors for and components of metabolic syndrome (MetS) and health-related quality of life (HRQOL), and (2) the effects of these variables on HRQOL in a hypothesised causal model using structural equation modelling (SEM) in patients with systemic lupus erythematosus (SLE).

Methods Of the 505 SLE patients enrolled in the Korean Lupus Network (KORNET registry), 244 had sufficient data to assess the components of MetS at enrollment. Education level, monthly income, corticosteroid dose, Systemic Lupus Erythematosus Disease Activity Index, Physicians' Global Assessment, Beck Depression Inventory, MetS components, and the Short Form-36 at the time of cohort entry were determined. SEM was used to test the causal relationship based on the Analysis of Moment Structure.

Results The average age of the 244 patients was 40.7±11.8 years. The SEM results supported the good fit of the model (χ^2 = 71.629, p=0.078, RMSEA 0.034, CFI 0.972). The final

model showed a direct negative effect of higher socioeconomic status and a positive indirect effect of higher disease activity on MetS, the latter through corticosteroid dose. MetS did not directly impact HRQOL but had an indirect negative impact on it, through depression.
Conclusions In our causal model, MetS risk factors were related to MetS components. The latter had a negative indirect impact on HRQOL, through depression. Clinicians should consider socioeconomic status and medication and seek to modify disease activity, MetS, and depression to improve the HRQOL of SLE patients.

288 CIRCULATING PROLACTIN LEVEL IN SYSTEMIC LUPUS ERYTHEMATOSUS AND ITS CORRELATION WITH DISEASE ACTIVITY: A META-ANALYSIS

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Background and aims Prolactin has an immune stimulatory effect and may promote autoimmunity by encouraging the development of antigen presenting cells expressing MHC class II and co-stimulatory molecules and modulating IFN-γ secretion. This study aimed to evaluate the relationship between circulating prolactin level and systemic lupus erythematosus (SLE), and to establish a correlation between plasma/serum prolactin levels and SLE activity.
Methods We performed a meta-analysis comparing the plasma/serum prolactin levels in patients with SLE to controls, and examined correlation coefficients between circulating prolactin level and SLE disease activity.
Results Twenty-five studies with a total of 1056 SLE patients and 426 controls were included. Prolactin levels were significantly higher overall in the SLE group than in the control group (SMD=0.987, 95% CI=0.512–1.463, $p=4.7x10^{-5}$). Stratification by ethnicity showed significantly elevated prolactin levels in the SLE group in Asian, Latin American, and mixed populations (SMD=0.813, 95% CI=0.137–1.490, p=0.018; SMD=0.981, 95% CI=0.307–1.655, p=0.004; SMD=1.469, 95% CI=0.443–2.495, p=0.005, respectively), but not in the European population. Meta-analysis of correlation coefficients showed a significantly positive correlation between circulating prolactin level and SLE activity (Correlation coefficient=0.379, 95% CI=0.026–0.487, $p=4.0x10^{-9}$).
Conclusions Our meta-analysis demonstrated that circulating prolactin levels are higher in patients with SLE and that a significantly positive correlation exists between prolactin levels and SLE activity.

289 APPLICATIONS OF PROTEIN MICROARRAY FOR SALIVA DIAGNOSTICS IN AUTOIMMUNE DISEASES

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Background and aims Many reports suggest that saliva could be a source of biomarkers capable of detecting certain diseases. However, very few studies conducted to profile autoantibody isotypes in the saliva of autoimmune diseases.This study was performed to establish protein microarray for saliva diagnostics and to identify distinct profiles of salivary autoantibody in patients with systemic lupus erythematosus (SLE).
Methods We constructed antigen microarrays with canonical antigens of SLE as well as cytokines to characterise autoantibodies in matched saliva and serum derived from 17 SLE patients and 13 healthy controls. The autoantibody IgG and IgA isotypes were assayed.The Axon Scanner and GenePix Pro 7.0 were used to determine median fluorescence intensities (MFI) of features and background. Data were analysed using MultiExperiment Viewer and Significance Analysis of Microarray (SAM) algorithm.
Results The dynamic range of detection on the array was 1–10^4 ng/mL for commercial Abs spiked into saliva. We observed a high degree of specificity for its target antigen. IgG Ab reactivity against specific antigens was found mainly in serum, while IgA Ab reactivity to given antigens was predominant in saliva. SAM identified 7 antigens including BAFF, Ro60, U1-A and Sm/RNP that were significantly more reactive to IgA Ab in the saliva of SLE patients than in healthy controls (false discovery rate <0.01). The hierarchical clustered heat-map successfully placed SLE patients into close subgroups.
Conclusions Protein microarrays facilitate detection of autoantibody in human saliva as well as serum. Saliva profiling revealed that elevated IgA autoantibody reactivity to several targets including BAFF was associated with SLE compared with controls.

290 INVESTIGATION OF DATA CAPTURE TECHNOLOGY ON CLINICAL PHENOTYPE DISTRIBUTION OF 4150 PATIENTS WITH SLE

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Background and aims To set up the data base of Systemic Lupus Erymatosus using data capture technology (Hitales platform).
Methods Using Optical Character Recognition, Artificial Intelligence, Natural language processing technology to transfer the medical records into structured data which can be easily and freely explored. The medical records are acquired from admitted medical histories of department of Shanghai Renji Hospital.
Results Totally 4150 cases of admitted SLE patients in Dept. of Rheumatology Shanghai Renji Hospital from 2010–2015 were enrolled. The clinical patterns can be easily visualised. 3729 were females and 375 males; The average age was 36.2 ±14.1, with SLEDAI scores of 6.9±5.6. The most items frequently counted in SLEDAI were proteinuria (37.6%), low complement (33.7%) and rash (29.2%). Compared to female patients, male patients were tendency to have protenuira (48.4% vs.36.6%, p<0.01), hematuria (25.8% vs.19.7%, p<0.01). Disease activity evaluated by SLEDAI were highest in summer, however the highest cost in hospital were in winter. 47.0% (1948/4150) patients with lupus nephritis did renal biopsy. The majority pathology type was type IV (27.4%), while 23.6% for type V and 12.1% for V+IV. The most common features counted AI and CI were glomerular cell proliferation (89.6%) and interstitial fibrosis (62.4%) respectively.