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 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 up to 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 pathogenesis of interstitial pneumonitis in these patients as well.

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. Phthalates 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 Methoxychlor.

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.
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.

Conclusions The 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.

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 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^-10). 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=0.233–0.487, p=0.001). 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.

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.

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, Ros60, U1-A and SmRNP 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.