and enrollment date. Diagnosis codes from the period between enrollment and the end of follow-up (disenrollment or 9/30/2015) were used to determine the presence of comorbidities. We assembled 57 chronic condition categories based on previously described 44 categories (England, B. ARD 2020). The 13 additional categories were added based on the SLICC/ACR damage index (SDI) or otherwise considered relevant to SLE. Two or more ICD-9 codes at least 30 days apart were used to define a comorbidity. We defined multimorbidity as the presence of ≥ 2 comorbidities (excluding SLE). Conditional logistic regression models were performed to estimate the prevalence of multimorbidity. The trajectory of multimorbidity in people with SLE (vs without SLE) was estimated utilizing generalized estimating equations. We looked at overall trajectory after index date, expanding the observation time one year before index date, and excluding silent conditions to mitigate surveillance bias (hypertension, hypothyroidism, etc.)

Odds ratios (OR) and estimates of the linear coefficient and 95% confidence intervals (CI) were reported.

Results A total of 34,893 SLE patients were matched to 34,893non-SLE comparators. Of these, 13,531 were incident cases. The mean age was 48 (SD 14.2) years, and 90.6% were female. 66.4% were White, 18.4% Black, 3.4% Asian, and 18.4% Hispanic. From enrollment to the index date, the mean observation time was 2.3 years (SD: 2.4) and 4.4 years (SD: 2.6) for the incident cohort. Multimorbidity was present in 72% of SLE vs. 47% of non-SLE subjects (OR 4.3; 95%CI: 4.1-4.5). Patients with SLE had 4.5 comorbidities compared to 2.4 for non-SLE subjects (OR: 1.91 (1.89-1.94).

Compared to baseline, multimorbidity increased among the incident cases, multimorbidity frequency was higher in incident SLE (vs non-SLE) throughout the follow-up compared to baseline (β: 1.85, 95%CI 1.79, 1.91). The rate of accrual chronic conditions was significantly higher in SLE than in non-SLE (figure 1A; β: 0.63; 95%CI: 0.60, 0.65). Patients with lupus had accelerated multimorbidity accrual after excluding silent conditions (figure 1B). Patients with SLE had increased multimorbidity even one year before SLE onset (figure 1C).

Conclusion In this nationwide commercial database insurance study, patients with SLE were four times more likely to suffer from multimorbidity than the general population. Trajectory analysis shows that multimorbidity progresses more rapidly in patients with SLE than those without SLE and may begin before SLE onset.
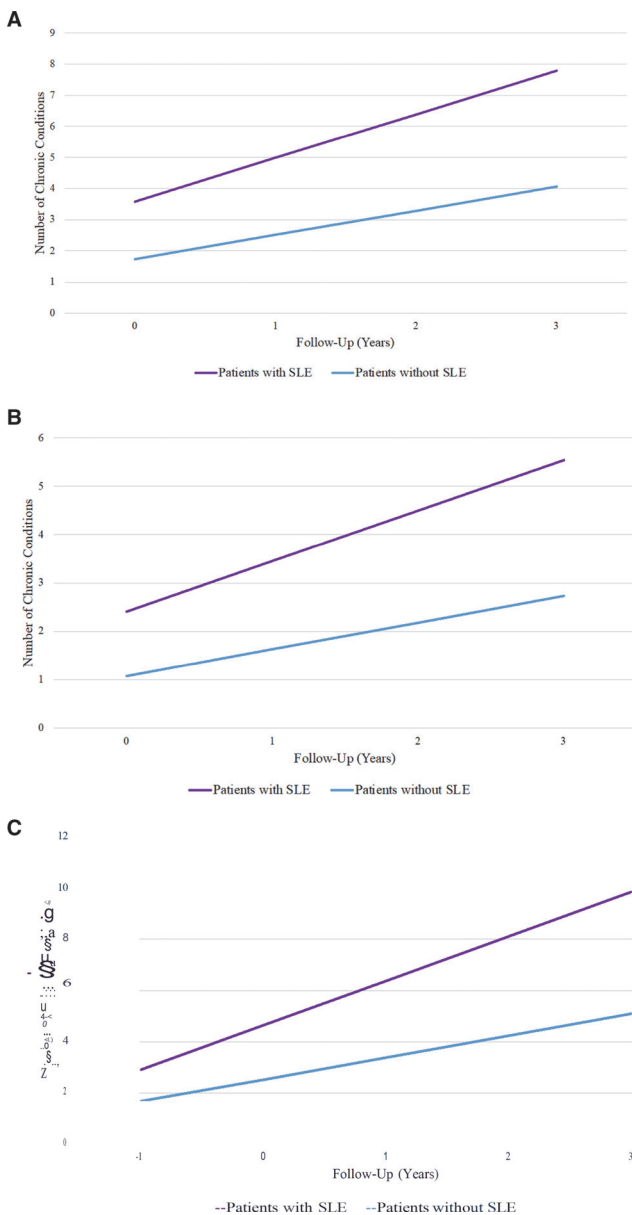
Abstract 626 Figure 1 Predicted burden of multimorbidity in incident SLE compared with patients without SLE after diagnosis. Panel A, primary analytical approach requiring 1 year in the data set without SLE diagnostic codes chronic conditions. Panel B, similar analytical approach removing silent conditions. Panel C, restricting the population to individuals with at least 2 years of data prior to index date and beginning follow-up at 1 years before the index date.

Poster

627 EFFECT OF IMMUNOSUPPRESSION ON COVID VACCINATION

[1]Michelle Petri, [1]Daniel Joyce, [1]Kristin Haag, [1]Andrea Fava, [1]Daniel W Goldman, [2]Diana Zhong, [3]Shaoming Shao, [3]Aaron Milstone, [4]Laurence S Magder. [1]*Johns Hopkins University School of Medicine, Department of Medicine, Division of Rheumatology;* [2]*Johns Hopkins University School of Medicine, Department of Medicine, Division of Infectious Diseases;* [3]*Johns Hopkins University School of Medicine, Department of Pediatrics. Division of Infectious Diseases;* [4]*University of Baltimore School of Medicine, Department of Epidemiology and Biostatistics*

Background The risk of COVID-19 infection is increased in patients with systemic lupus erythematosus (SLE), and immunosuppressive medications including corticosteroids impact the risk. Furthermore, immunosuppressive medications may reduce the effectiveness of COVID-19 vaccination. Consensus documents have suggested management strategies on handling immunosuppressive medications to increase vaccine efficacy, but the benefit of such strategies has not been proven.

Methods We collected information on COVID infection, COVID vaccination history, and COVID antibodies in the Hopkins Lupus Cohort, a longitudinal cohort with structured quarterly visits. A cohort of healthcare workers was used for comparison. SARS-CoV-2 IgG was measured by ELISA (Euroimmun). Outcome measures included: SARS-CoV-2 antibody IgG levels after vaccination over time in both cohorts; and
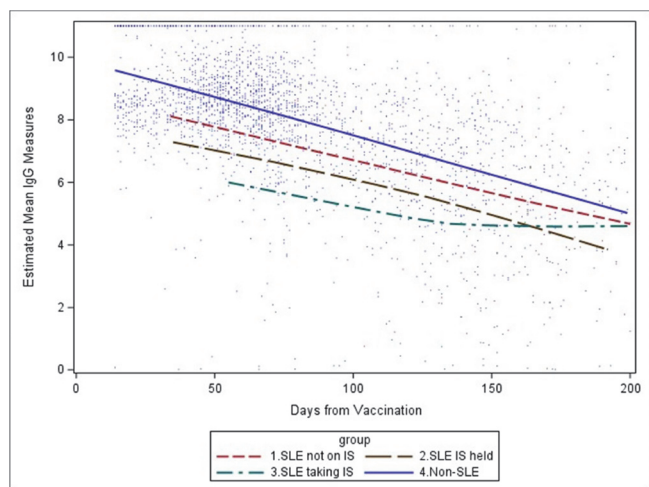
Abstract 627 Figure 1 Mean antibody level by time since the second vaccination for each cohort. Estimated mean IgG measure over time since 2nd vaccination, by cohort and use of immunosuppressants (IS).

Abstract 627 Table 1 Estimated effect of treatment at time of vaccination on mean IgG based on a multivariable regression model

Treatment	Estimated effect on mean IgG (95% confidence interval)[1]	P-value[1]
Prednisone dose <10 mg/day (versus non-use)	-0.46(-1.44, 0.51)	0.35
Prednisone dose >= 10 mg/day (versus non-use)	-1.25 (-3.52, 1.02)	0.28
Mycophenolate mofetil dose > 1000	-2.38 (-3.57, -1.19)	<0.0001
Tacrolimus use	-1.49 (-2.60, -0.37)	0.0092
Belimumab use	-2.29 (-4.13, -0.45)	0.015
Anti-hypertensive medication use	-0.58 (-1.18, 0.020)	0.058

[1]Estimated effect and p-value based on a multivariable GEE model, adjusting for sex, time since vaccination, time since vaccination squared, and all other treatments on the table.

effect of immunosuppressive medications on post-vaccine IgG levels in SLE patients.

Results 228 SLE patients received COVID-19 vaccine: 10 had 1 dose of Johnson & Johnson; 94 had 2 doses of Moderna; and 124 had 2 doses of Pfizer. Of these, 98 patients had no history of COVID infection and at least 1 visit within 210 days before the vaccine series and at least one visit after the vaccine series. SLE patients on immunosuppressive medications had lower post-vaccine IgG levels than SLE patients who were not; but both groups had lower levels than healthcare workers (figure 1). Holding mycophenolate for one week after vaccine increased post-vaccine IgG levels significantly. In multiple variable models, mycophenolate mofetil, tacrolimus, and belimumab all significantly reduced antibody response to vaccination (table 1).

Conclusion SLE patients, regardless of background immunosuppressive therapy, had lower vaccine IgG levels than healthcare workers. Belimumab, tacrolimus and mycophenolate use significantly reduced IgG response to vaccine. Holding mycophenolate for one week improved vaccine efficacy, providing clinical benefit on vaccine response, without leading to clinical flares.

MODULAR GENE ANALYSIS REVEAL DISTINCT MOLECULAR SIGNATURES FOR CUTANEOUS LUPUS PATIENT SUBSETS

[1]Jane L Zhu, [2]Ly Tran, [2]Miles Smith, [2]Frank Zheng, [3]Ling Cai, [2]Judith James, [2]Joel Guthridge, [1]Benjamin F Chong. [1]University of Texas at Southwestern Medical Center, Department of Dermatology, Dallas, TX, USA; [2]Oklahoma Medical Research Foundation, Arthritis and Clinical Research Immunology Program, Oklahoma City, OK, USA; [3]University of Texas at Southwestern Medical Center, Quantitative Biomedical Research Center, Department of Population and Data Sciences, Dallas, TX, USA

Background Cutaneous lupus erythematosus (CLE) is a heterogeneous autoimmune disease with clinical sequelae such as itching, dyspigmentation, and scarring. However, studies investigating the molecular heterogeneity of CLE patients are lacking. We applied a previously described modular analysis approach to assess the molecular heterogeneity of CLE patients.

Methods Whole blood transcriptomes of RNA sequencing data from a racially and ethnically diverse group of CLE patients (n=62) were used to calculate gene co-expression module scores. An unsupervised cluster analysis and K-means clustering based on these module scores were then performed. We used Fisher's exact tests and Kruskal Wallis tests to compare characteristics between patient clusters.

Results Six unique clusters of CLE patients were identified from the cluster analysis (figure 1). We observed that seven inflammation modules were elevated in two CLE patient clusters.

Additionally, these clusters were characterized by interferon, neutrophil and cell death signatures, suggesting that inter-
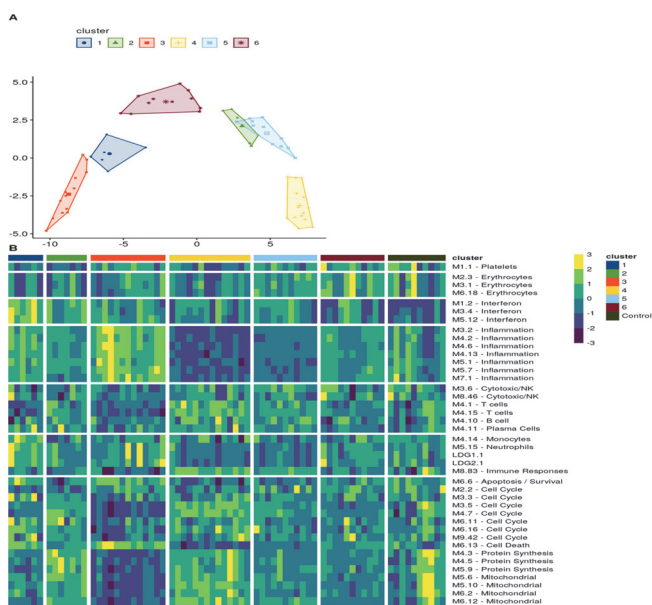
Abstract 801 Figure 1 Clustering of CLE patients based on gene expression module scores. (A) Random forest and k-mean clustering using expression module scores identified six molecularly distinct CLE patient subsets. Each point on this plot represents a patient. (B) Heat map of expression module scores of the six CLE patient subsets was shown. Modules were grouped by primary function. Boxes were color-coded by relative activation of modules. Purple represented less activation and yellow represented more activation.