showed the most satisfactory performance across external cohorts, LASSO also performed well and yielded a parsimonious model that may be easier and more efficient to use as a risk assessment tool in practice. Data from additional external cohorts from the US and abroad will be obtained in the future for further validation and refinement of our APO prediction models.

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Trial Registration ClinicalTrials. gov Identifier: NCT00198068

Lay summary Nearly 20% of pregnancies in patients with Systemic lupus erythematosus (SLE) result in an adverse pregnancy outcome (APO); early identification of women with SLE who are at high risk of APO is vital. We previously explored several regression and machine learning methods to predict APO using data from the PROMISSE Study, a large multi-center, multi-ethnic/racial study of APO in women with mild/moderate SLE and/or aPL. We sought to determine which of the best performing algorithms in PROMISSE continued to perform well using data from other SLE pregnancy cohorts in the US and abroad. Most models showed satisfactory performance across cohorts in the ability to differentiate patients who did and not have an APO using variables measured early in pregnancy, indicating their potential for use in clinical practice to manage pregnant SLE patients.

Abstract 604 Table 1 Patient demographics by SLE Pregnancy Cohort

	Development	External validation data sets		
	PROMISSE	Bronx, NY	NYC, NY	Pisa, Italy
	n=385, 71 APOs	n=96, 23 APOs	n=62, 16 APOs	n=152, 28 APOs
	event rate=18.4%	event rate = 24.0%	event rate = 25.8%	event rate=18.4%
Maternal age , years	31 (28,34)	29 (24,34)	33 (29,33.5)	32 (28,36)
Non-Hispanic White (%)	49.3	0.0	27.4	98.7
Platelet count, x 10^9 cells/L	243 (204,296)	235 (209,259)	228 (188,274)	204 (188, 238)
Diastolic BP, mmHg	67 (60,73)	72.5 (63,79)	70 (64,75)	70 (61,75)
LAC + (%)	8.1	19.1	22.6	15.9
PGA > 1 (%)	10.6	4.4	11.1	7.9
SLE disease activity score	2 (0,4)	1.5 (0,2)	2 (0,5)	2 (0,4)
Low C3 (%)	20.2	27.6	24.2	52.6
aCL IgG + (%)	6.1	2.1	9.7	11.8
aCL IgM + (%)	1.8	0.0	16.1	1.3
Current glucocorticoid use (%)	39.7	50.5	23.1	58.9
Current anti hypertensives use (%)	8.6	12.6	4.8	5.3
Current hydroxychloroquine use (%)	64.7	54.3	84.6	63.4

Data are summarized as median (IQR), unless otherwise indicated; BP=blood pressure

Abstract 604 Table 2 AUC (95% CI) of all algorithms based on internal and external assessments

	Development	External Validation data sets		
	PROMISSE	Bronx, NY	NYC, NY	Pisa, Italy
LASSO	0.77 (0.71,0.83)*	0.60 (0.46,0.73)	0.63 (0.47,0.80)	0.66 (0.53,0.79)
Support vector machine	0.77 (0.70,0.84)*	0.61 (0.47, 0.74)	0.58 (0.41, 0.74)	0.73 (0.63,0.83)
Random Forest	0.77 (0.71,0.83)*	0.68 (0.55,0.81)	0.57 (0.46,0.80)	0.67 (0.56, 0.79)
Super Learner	0.78 (0.72,0.84)*	0.66 (0.53,0.79)	0.63 (0.43,0.76)	0.71 (0.56, 0.81)

*Based on 5x10-fold cross-validation

605 THE SYSTEMIC LUPUS ERYTHEMATOSUS INTERNATIONAL COLLABORATING CLINICS (SLICC), AMERICAN COLLEGE OF RHEUMATOLOGY (ACR), AND LUPUS FOUNDATION OF AMERICA (LFA) DAMAGE INDEX REVISION – ITEM GENERATION PHASE

[1]Burak Kundakci, [2]Ann E Clarke, [3]Sindhu R Johnson, [4]Hermine I Brunner, [5]Jiacai Cho, [6]Nathalie Costedoat-Chalumeau, [7]Ellen M Ginzler, [8]John G Hanly, [7]Abida Hasan, [9]Murat Inanç, [7]Naureen Kabani, [10]Kaitlin Lima, [11]Livia Lindoso, [12]Anselm Mak, [10]Rosalind Ramsey- Goldman, [13]Guillermo Ruiz-Irastorza, [11]Clovis A Silva, [14]Farah Tamirou, [11]Vitor C Trindade, [15]Évelyne Vinet, [1]Ian N Bruce, [2]Megan RW Barber*. *[1]Centre for Epidemiology Versus Arthritis, Faculty of Biology, Medicine and Health, The University of Manchester, Manchester, Manchester, UK; [2]Division of Rheumatology, Cumming School of Medicine, University of Calgary, Calgary, Alberta, Canada; [3]Division of Rheumatology, Department of Medicine, Schroeder Arthritis Institute, Krembil Research Institute, Toronto Western and Mount Sinai Hospitals; Institute of Health Policy, Management and Evaluation, University of Toronto, Toronto, Ontario Canada; [4]Division of Rheumatology, Cincinnati Children's Hospital Medical Center, University of Cincinnati, Department of Pediatrics; Cincinnati, Ohio, USA; [5]National University Health System (NUHS), Singapore, Singapore; [6]Cochin Hospital, Internal Medicine Department, Centre de référence maladies auto-immunes et systémiques rares d'île de France, Paris, France; [7]SUNY Downstate Health Sciences University, Department of Medicine, Brooklyn, NY, USA; [8]Division of Rheumatology, Queen Elizabeth II Health Sciences Center (Nova Scotia Rehabilitation Site) and Dalhousie University, Halifax, Nova Scotia, Canada; [9]Istanbul University Faculty of Medicine, Istanbul, Turkey; [10]Northwestern University Feinberg School of Medicine, Chicago, USA; [11]Faculdade de Medicina da Universidade de São Paulo (FMUSP), Brazil; [12]Division of Rheumatology, Department of Medicine, Yong Loo Lin School of Medicine, National University of Singapore, Singapore; [13]Autoimmune Diseases Research Unit, Biocruces Bizkaia Health Research Institute, Hospital Universitario Cruces, UPV/EHU, Barakaldo, País Vasco, Spain; [14]Rheumatology Department, Cliniques universitaires Saint- Luc, Brussels, Belgium; [15]McGill University Faculty of Medicine, Division of Rheumatology, Montreal, QC, Canada; *Designates presenting author*

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Background The SLICC, ACR and LFA embarked on a data- and expert-driven project to develop a revised systemic lupus erythematosus (SLE) organ damage index (SDI). The methodological approach includes 5 phases: updating the construct of damage (I), item generation (II), item reduction (III), item weighting and threshold determination (IV), and the assessment of validation and reliability (V). In phase I, a consensus statement was developed to define the construct of damage in SLE[1]. In the Item Generation phase, we aimed to develop and agree on a candidate list of items that reflect the construct of damage in SLE and are appropriate to be included in a new damage index including consideration of relevant items from adult, paediatric and young adult SLE. In this analysis, we compare the two approaches to initial item generation that were employed in a parallel process, namely a literature review and a Delphi exercise.

Methods Item generation included a literature review and 3-part Delphi exercise. A group of lupus experts conducted a

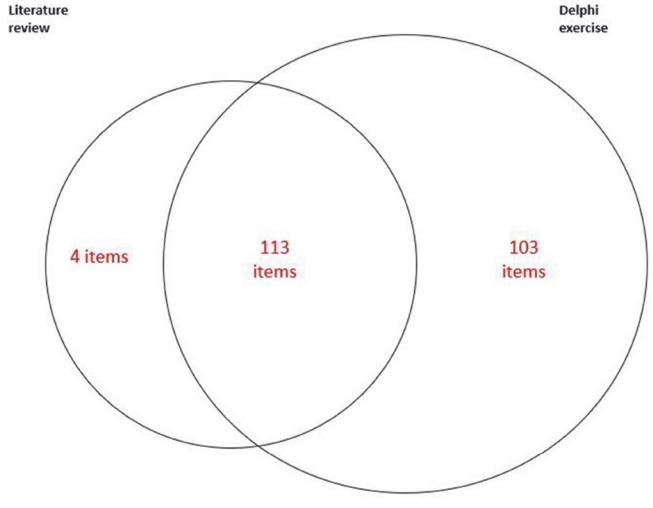
literature review to identify items that reflect the construct of damage in SLE and grouped the items into organ domains. Each domain was reviewed by paediatric rheumatologists.

Snow-ball sampling was used among SLICC members, asking them to nominate 3-4 SLE experts considering a range of clinical expertise, equality, diversity and inclusiveness factors, and the global nature of SLE research. The LFA, Lupus UK, Lupus Europe and Lupus Canada were also asked to nominate 4-6 patient/carer representatives to participate in the Delphi exercise. Participants were asked to nominate items that should be included in a revised damage index based on the updated construct definition1 using a free-text option in Delphi exercise.

Results We established a group of 146 individuals (mean age 50.6 ranging from 28 to 79 years; 60.3% females; 58.9% white; clinical experience from 1 to 51 years) from 35 countries, broadly representative of the lupus research and patient community. There were 135 medical doctors, 2 allied health professionals and 9 patients. Of 135 medical doctors, 120 were rheumatologists, 7 internists, 5 nephrologists, 2 dermatologists, and 1 immunologist. The response rate after the first round Delphi exercise was 97.9%.

All items in the original SDI were nominated in both processes. Item generation yielded approximately 2,600 items. After rationalising for repetition, redundancy, and harmonisation of synonyms, 220 unique items were identified across 14 organ systems. The literature review proposed 4 (1.8%) unique items, 103 (46.8%) unique items were from the Delphi only and 113 (51.4%) items appeared in both exercises (figure 1).

Conclusion Using a combined data-driven and expert/patient-based approach, items and domains that comprise damage in SLE have been expanded. Just over half of all items were nominated by both approaches. However, the Delphi exercise which included a wide and diverse group of contributors, provided a large number of unique items for further consideration. Our data confirms the value of large group exercises early in such a process to maximise the scope of new items to consider for a revised index.



Abstract 605 Figure 1 Number of candidate items for the revised organ damage index from literature review and the first round Delphi exercise.

REFERENCE

1. Johnson, S. R *et al*. Evaluating the construct of damage in SLE. *Arthritis Care Res*. 2021.

Lay Summary The SLICC/ACR Damage Index (SDI) (published in 1996) is widely used in clinical studies and trials to measure the long-term complications that can occur in lupus patients, such as cataracts, fractures, and kidney failure. Higher scores are associated with poorer quality of life, as reported by patients. A number of drawbacks have also been found with the SDI. We need to better understand and measure the impact of these complications from a patient and doctor's perspective to get a much deeper understanding of how SLE affects people. We used two methods to generate new items to include in an updated SDI. First, we used the medical literature to identify possible complications of lupus. Then, we asked a large group of lupus experts and patients to nominate complications. The process generated approximately 2,600 items. After removing redundant suggestions, 220 unique items were identified. The literature review proposed 4 (1.8%) unique items, 103 (46.8%) unique items were from the large group only and 113 new (51.4%) items appeared in both exercises. Our data shows the value of large group exercises that include patient representatives, to maximise the scope of new items to consider for a revised index.

606 CELL-SPECIFIC HUMAN ENDOGENOUS RETROVIRUS EXPRESSION, HOST GENE EXPRESSION AND SLE PHENOTYPES

[1]Zachary Cutts, [2]Sarah Patterson, [3]Lenka Maliskova, [2]Chun Jimmie Ye, [2]Maria Dall'Era, [2]Jinoos Yazdany, [4]Lindsey A Criswell, [5]Chaz Langelier, [1]Marina Sirota*, [4]Cristina Lanata*. *[1]Bakar Computational Health Science Institute, University of California, San Francisco; [2]Russell/Engleman Rheumatology Research Center, Department of Medicine, University of California, San Francisco, San Francisco, CA, USA4; [3]Institute for Human Genetics, University of California, San Francisco; [4]National Human Genome Research Institute, National Institutes of Health, Bethesda, MD, USA; [5]Division of Infectious Diseases, Department of Medicine, University of California, San Francisco, San Francisco, CA, USA*

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Background/purpose Human endogenous retroviruses (HERVs) and long interspersed nuclear elements (LINEs) make up 5-8% and 21% of the human genome. Their expression may contribute to production of type I interferon and the generation of autoantibodies. The objective of this study was to detect

HERVs and LINEs in 4 cell-types in SLE patients and characterize their relationship to host gene expression and SLE phenotypes.

Methods Peripheral blood mononuclear cells were isolated from 120 deeply-phenotyped SLE participants. Cells were sorted utilizing magnetic beads (CD14+ monocytes, B cells, CD4+ T cells, and NK cells) and STEM cell technologies for a total of 480 samples. Libraries were sequenced on a HiSeq4000 PE150. Trimmed fastq files were aligned to GRCh38 release 104 using default settings with STAR to generate alignment files. Alignment files were converted to gene counts using featureCounts. Raw counts from *Telescope* were normalized using DESeq2 and summed per patient; patients were then separated into tertiles based on the summed counts for HERVs and LINEs. DESeq2 was used to perform differential gene expression analysis using gene counts from featureCounts, comparing the third to the first tertile. Gene set enrichment analysis was performed using genes with adjusted