Results: 712 (out of 33,793) transcripts were overexpressed in kidneys from diseased mice (age > 6 months). These transcripts were significantly enriched in the following pathways: response to type I interferons, antigen processing and presentation, activation and regulation of B cells, complement activation, and regulation of cytotoxicity mediated by T cells.

Proportions of renal CD8 T cells with an effector phenotype were significantly increased in the kidneys from 6 months and older compared to younger mice, and compared to paired spleens. Proportions of renal effector CD8 T cells correlated significantly with transcripts involved in interferon signature, adaptive immune responses, cytotoxic T cells, chemotaxis, and correlated negatively with pathways associated with renal tubular cell functions.

Finally, we found a correlation between biological parameters of kidney function (plasma urea, albuminuria) and transcripts involved in pro-fibrotic pathways, chemokines and adaptive immune responses.

Conclusion: Our results confirm the link between the presence of activated immune effectors in the kidney and renal outcomes in a mouse model of SLE, similar to our previous observations in human LN, and warrant further functional studies on the role of kidney-infiltrating T and B cells in this model.

Acknowledgement: This research was funded in part by grants from Fonds de la Recherche Scientifique – FNRS, Fondation Roi Baudouin and Fondation Saint-Luc.

Disclosure of Interests: None declared

DOI: 10.1136/annrheumdis-2019-eular.5417

AB0187

CAN ARTIFICIAL INTELLIGENCE REPLACE MANUAL SEARCH FOR SYSTEMATIC LITERATURE REVIEW ON CUTANEOUS MANIFESTATIONS IN PRIMARY SJÖGREN'S SYNDROME?

Laure Orgeolet^{1,2}, Nathan Foulquier¹, Laurent Misery¹, Pascal Redou¹, Jacques-Olivier Pers¹, Valerie Devauchelle-Pensec¹, Alain Saraux¹. ¹CHU Brest, Brest, France; ²CHU Brest, Dermatology, Brest, France

Background: Manual systematic literature reviews are becoming increasingly challenging due to the sharp rise in publications. The task is particularly daunting when the study topic is complex.

Objectives: The primary objective of this literature review was to compare manual and in-house computer software retrieval of publications on the cutaneous manifestations of primary Sjogren's Syndrome (pSS). The secondary objective was to evaluate the prevalence of cutaneous manifestations in pSS.

Methods: We compared manual searching and searching with the in-house computer software BIBOT (1) designed for article retrieval and analysis. Both methods were used for a systematic literature review on a complex topic i.e., the cutaneous manifestations of pSS. Articles published in French or English between 1 January 1990 and 30 May 2018 were sought.

Results: The manual search retrieved 855 articles and BIBOT 1042 articles. In all, 202 articles were then selecting by applying exclusion criteria. Among them, 155 were retrieved by both methods, 33 by manual search only, and 14 by BIBOT only. Further selection was performed by reading the 202 articles, of which 54 were deemed relevant, including 23 providing data on the prevalence of one or more cutaneous signs in a cohort of patients with pSS. Cohort sizes and the nature and prevalence of cutaneous manifestations varied across publications. In all, 52 cutaneous manifestations were reported, of which the most common were cutaneous vasculitis (561 patients), xerosis (651 patients), and annular erythema (215 patients).

Conclusion: Agreement was good between the two methods. BIBOT was faster and automatically classified the articles in a chart. Combining the two methods retrieved the largest number of publications. The prevalence of cutaneous manifestations in patients with pSS varied considerably across studies. The advanced machine learning techniques used in artificial intelligence hold promise for literature reviews.

REFERENCES

- [1] Foulquier N, Redou P, Le Gal C, Rouvière B, Pers J-O, Saraux A. Pathogenesis-based treatments in primary Sjogren's syndrome using artificial intelligence and advanced machine learning techniques: a systematic literature review. *Hum Vaccin Immunother* 2018;14:2553-2558.

Disclosure of Interests: Laure Orgeolet: None declared, Nathan Foulquier: None declared, Laurent Misery: None declared, Pascal Redou: None declared, Jacques-Olivier Pers: None declared, Valerie Devauchelle-Pensec Grant/research support from: Roche-Chugai, Speakers bureau: MSD, BMS, UCB, Roche, Alain Saraux Consultant for: Roche SAS, Speakers bureau: Chugai Pharma France

DOI: 10.1136/annrheumdis-2019-eular.3981

AB0188

MOLECULAR NETWORKS IN MONOCYTES FROM SYSTEMIC LUPUS ERYTHEMATOSUS PATIENTS RELATED TO THEIR PHYSIOPATHOLOGY. MODULATORY EFFECTS OF ANTI-DSDNA ANTIBODIES AND MOLECULAR MECHANISMS UNDERLYING IN VIVOSTATIN TREATMENT

Alejandra M. Patiño-Trives¹, Pérez Sánchez Laura¹, María Galindo-Izquierdo², María Luque-Tévar¹, Alejandro Ibañez-Costa¹, Iván Arias de la Rosa¹, María del Carmen Abalos-Aguilera¹, Pedro Seguí Azpilcueta¹, Nuria Barroja Puerto¹, Eduardo Collantes Estevez¹, María A. Aguirre¹, Carlos Perez-Sanchez¹, Chary Lopez-Pedraza¹. ¹IMBIC/Reina Sofia Hospital/University of Cordoba, Cordoba, Spain; ²Hospital 12 de Octubre, Madrid, Spain

Objectives: 1. To characterize the mRNAs and microRNAs transcriptomes of monocytes from systemic lupus erythematosus (SLE) patients and their association with the pathophysiology of the disease. 2. To evaluate the role of anti-dsDNA antibodies in the regulation of these processes. 3. To investigate the molecular mechanisms involved in the efficacy of Fluvastatin in preventing the atherothrombotic risk.

Methods: Monocytes from peripheral blood of 81 SLE patients and 40 healthy donors (HD) were purified by negative immunomagnetic selection. Then, gene expression microarray (Agilent G4112F platform) and nCounter microRNA expression arrays (Nanostring) were performed. Functional categorization of altered genes and miRNAs was made using IPA software, and interaction networks were identified. Genes and miRNAs integrating the networks were validated in the whole cohorts by RT-PCR. Predicted miRNA-mRNA interactions were tested by microRNA over-expression or inhibition experiments. Serum and cellular inflammatory and oxidative profiles were evaluated by multiplex assay, PCR and specific commercial kits, respectively; phosphorylation status of intracellular proteins was analyzed by PathScan array. To evaluate the clinical significance of the parameters analyzed, correlation and association studies were performed. Mechanistic studies were developed to typify the specific effects of the anti-dsDNA antibodies on monocytes. Besides, the beneficial effects of ex vivo Fluvastatin treatment on the monocyte molecular profiles were assessed.

Results: Microarray identified 553 altered genes in SLE monocytes. Relevant biofunctions and disorders on which these genes were involved included inflammatory, immunological, cardiovascular, neurological, renal and reproductive disease. Analysis of miRNA profiles showed altered expression of 35 miRNAs in SLE monocytes. Sixty-one genes were inversely correlated and predicted as CVD-related target genes of 26 differentially expressed miRNAs. Transfection studies confirmed the relationship between specific miRNAs and their identified target genes.

Association of these genes and miRNAs with the anti-dsDNA positivity, early atherosclerosis and nephropathy, along with correlations with disease activity (SLE-DAI), activation of some intracellular signaling proteins, and levels of serum inflammatory and oxidative markers were demonstrated. *In vitro* studies demonstrated the specific modulation of several genes/miRNAs by anti-dsDNA, along with the increase of prothrombotic and proinflammatory mediators, the induction of apoptosis and the phosphorylation of intracellular proteins participating in renal and CVD-related signaling pathways. Besides, treatment of HD-monocytes with SLE patients' serum after Fluvastatin supplementation prevented the proinflammatory altered gene/miRNA profiles induced by serum from those patients before treatment.

Conclusion: 1. Gene and microRNA expression profiles allowed the identification of relevant genes and pathways altered in monocytes of SLE patients, associated with the pathogenesis of the disease, and modulated by anti-dsDNA. 2. Specific microRNA-miRNA regulatory networks control the biological processes and factors related to the CV pathology in SLE, which are prevented by Fluvastatin treatment.

Acknowledgement: Funded by ISCIII, PI15/01333, PI18/00837 and RIER RD16/0012/0015 co-funded with FEDER.

Disclosure of Interests: None declared

DOI: 10.1136/annrheumdis-2019-eular.7142

AB0189

DECREASED URINE SEMAPHORIN 3A SECRETION PREDICTS THE EXTENT OF RENAL DAMAGE IN SYSTEMIC LUPUS ERYTHEMATOSUS PATIENTS

Doron Rimar¹, Merav Lidar², Nasrin Eiza³, Elias Toubi³, Amal Silawy¹, Gleb Slobodin¹, Itzhak Rosner¹, Michael Rosenbaum¹, Abid Awisat¹, Nina Boulman¹, Lisa Kaly¹, Shira Ginsberg¹, Nizar Jiries¹, Zahava Vadasz³. ¹Bnai Zion Medical Center, Rheumatology, Haifa, Israel; ²Sheba Medical Center, Rheumatology, Ramat Gan, Israel; ³Bnai Zion Medical Center, Division of Allergy and Clinical Immunology, Haifa, Israel

Background: Semaphorins are a family of proteins, involved in axon-guidance, malignancy spread and angiogenesis. Semaphorin 3A (sema3A) is recognized also as "immune semaphorin", it is expressed on regulatory T cells and has been