Table 2. Clinical assessments across MBDA score categories.

	CDAI		SJC		vdHS	
	MBDA	aMBDA	MBDA	aMBDA	MBDA	aMBDA
MBDA Category						
Low	14.6 (10.9)	13.9 (9.9)	2 (1, 5)	2 (1, 5)	9 (1, 33.5)	9 (3, 32)
Moderate	13.2 (10.0)	14.4 (11.4)	2 (0, 5)	3 (0, 6)	10 (4, 49)	10 (2, 53)
High	18.4 (12.3)	17.7 (11.8)	4 (1, 8)	5 (2, 7)	20.5 (5, 70.5)	18 (4, 73)

Conclusion: Leptin-adjustment of the MBDA score reduced bias related to excess adiposity in women with RA. Adjustment results in lower MBDA scores in women with greater adiposity, and higher MBDA scores in women and men with lesser adiposity. The aMBDA may reduce misclassification due to excess adiposity and improve identification of active disease among patients with lower adiposity. High aMBDA scores among men with low adiposity may reflect severe disease or excess comorbidity in this group.

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Figure. Impact of Adjustment on MBDA Score by FMI Z-Score Quartile.

Disclosure of Interests: Joshua Baker Grant/research support from: Myriad RBM, Consultant of: Bristol-Myers Squibb, Burns-White LLC, Jeffrey Curtis Grant/research support from: AbbVie, Amgen, Bristol-Myers Squibb, Corrona, Janssen, Lilly, Myriad, Pfizer, Regeneron, Roche, UCB, Consultant of: AbbVie, Amgen, Bristol-Myers Squibb, Corrona, Janssen, Lilly, Myriad, Pfizer, Regeneron, Roche, UCB, David Chernoff Employee of: Myriad, Michael George Grant/research support from: Bristol Myers Squibb, Consultant of: AbbVie
DOI: 10.1136/annrheumdis-2020-eular.2221

FRI0573

VALIDATION OF FOUR SCREENING TOOLS FOR PSORIATIC ARTHRITIS IN CHINESE PATIENTS WITH PSORIASIS: A MULTICENTER STUDY

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Background: Psoriatic arthritis (PsA) is a chronic inflammatory arthropathy affecting 6–30% of patients with skin or nail psoriasis. If PsA is not identified early and managed appropriately, progressive joint damage with deformities and disability may occur. Preliminary efforts to develop screening tools for the identification of PsA have met with variable success. Whether the tools function well or not in Chinese patients remains unknown.

Objectives: We aimed to validate and compare the performance of 4 PsA screening tools in Chinese psoriasis patients.

Methods: Consecutive psoriasis patients (dermatology cohort) attending dermatology clinics without previous diagnosis of inflammatory arthritis and consecutive newly diagnosed PsA patients (rheumatology cohort) attending rheumatology clinics were invited to complete the questionnaires: early arthritis for psoriatic patients (EARP), psoriatic arthritis screening and evaluation (PASE), psoriasis and arthritis screening questionnaire (PASQ), and psoriasis epidemiology screening tool (PEST). Receiver operating characteristic (ROC) curves were utilized to calculate diagnostic accuracy, least absolute shrinkage and selection operator (lasso) and binary logistic regressions to identify the most discriminative questions.

Results: In this multicenter study, 379 patients in the dermatology cohort and 72 in the rheumatology cohort were recruited. In the dermatology cohort, 7.9% (30/379) were newly diagnosed with PsA. The EARP and PASQ tools demonstrated better discriminating ability for identifying PsA from psoriasis patients (yielded sensitivities/specificities were: 93.3%/92.3% and 90.0%/90.5%, while optimal cut-off values were: 3 and 5, respectively), and the good performance of EARP and PASQ was further confirmed in the rheumatology cohort. However, all these tools demonstrated low sensitivities (about 30%) with regard to screening the axial PsA. Based on the questions, a risk prediction model of PsA was established.

Conclusion: The prevalence rate of undiagnosed PsA in the patients with psoriasis is 7.9%. Both EARP and PASQ tools show better favorable trade-off between sensitivity and specificity than PASE and PEST, while all the 4 tools are not sensitive to identify axial PsA.

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Acknowledgments: This project was supported by grants from National Natural Science Foundation of China (81771746 and 81471604).

Disclosure of Interests: None declared

DOI: 10.1136/annrheumdis-2020-eular.2698

FRI0574

RENAL TISSUE EPIGENETIC BIOMARKERS' CHARACTERIZATION IN PATIENTS WITH LUPUS NEPHRITIS AS PARAMETERS OF DISEASE ACTIVITY, REMISSION AND FLARE

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Background: Epigenetic factors such as non-coding RNA (miRNA) have been shown to be deregulated in Systemic Lupus Erythematosus (SLE). In particular, in mouse model (1), different miRNAs have been associated with lupus nephritis (LN), one of the most severe manifestations of the disease.

Objectives: The aim of the study was to evaluate the expression of miR-155 and miR-34a in renal tissue as biomarkers of organ involvement and inflammatory tissue activity in patients with LN.

Methods: Thirty-two LN patients with active renal involvement were enrolled (age: 32.2 ± 9.2 years). The nephritic onset of the disease (early-SLE) was present in 13 patients (41%), while 19 patients (59%) showed a renal involvement during the follow-up (long-SLE). Clinical, laboratory and demographic data were collected for each patient. Disease activity was recorded using SLEDAI-2K and renal activity, using the total SLEDAI-2K fraction including the items related to the renal involvement. Ultrasound-guided renal biopsy has been performed for each patient for the definition of the nephritic class according to the ISN / RPS classification of 2003 revised in 2018(2). The expression of miR-155 and miR-34a in renal tissue was carried out by extraction of total RNA from paraffin-preserved biopsies and after a retrotranscription protocol was evaluated using SYBR® Green-based real-time PCR by relative quantification considering the ΔCt (Ct miRNA- Ct housekeeping gene)(3).

Results: MiR-155 and miR-34a expression in renal tissue were comparable in the different histological classes. Dividing patients on the base of nephritic onset, patients with early SLE showed lower expression of miR-155 (ΔCt 12.8 ± 10.8) and miR-34a (ΔCt 14.6 ± 9.9) than patients with long-SLE (miR-155: ΔCt 6.1 ± 8.7 $p = 0.02$; miR-34a: ΔCt 7.1 ± 9.0 $p = 0.03$). Furthermore, a direct correlation was observed between the expression of miR-155 and miR-34a ($r = 0.91$, $p < 0.001$). Considering patients with early-SLE, the expression of miR-34a was slightly significant in patients who had relapsed (ΔCt 8.2 ± 11.4 vs ΔCt 18.4 ± 7.9 $p = 0.08$), although no correlation emerged between the expression of miR-155 and miR-34a both at the time of the biopsy and with the disease activity indices. At the histological evaluation, miR-155 and miR-34a were more expressed in Early-SLE patients who had wire loop lesions (miR-155: ΔCt 19.5 ± 7.7 vs ΔCt 7.3 ± 9.6 $p = 0.05$; miR-34a: ΔCt 21.7 ± 1.1 vs ΔCt 8.8 ± 9.7 $p = 0.05$) possibly associated with a greater activation of the inflammatory component.

Conclusion: MiR-155 and miR-34a may represent tissue biomarkers of inflammatory activation in patients with LN in particular the higher expression of these miRNA in Long-SLE patients could indicate a possible role of these biomarkers in renal involvement in patients with SLE with later renal onset. The increased expression of miR-34a could give indications of a disease recurrence suggesting a closer monitoring of the patient.

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Disclosure of Interests: None declared

DOI: 10.1136/annrheumdis-2020-eular.5507

FRI0575

BIOMARKER ANALYSIS FROM THE RISE-SSC STUDY OF RIOCIQUAT IN EARLY DIFFUSE CUTANEOUS SYSTEMIC SCLEROSIS (DCSSC)

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Background: RISE-SSc (NCT02283762) was a multicenter, double-blind, Phase IIb study of riociguat in early dcSSc. Primary endpoint was change in mRSS from baseline to Wk 52.

Objectives: Exploratory, descriptive analyses of riociguat target engagement and effects on disease biomarkers in RISE-SSc and their relationship with effects on the primary endpoint. All biomarker p-values are for information only.

Methods: Pts with dcSSc (duration ≤ 18 mo; modified Rodnan skin score [mRSS] 10–22 units) were randomized to riociguat 0.5–2.5 mg tid ($n=60$) or placebo ($n=61$). Biomarkers of target engagement (cGMP), inflammation and/or vascular/endothelial function (e.g. high-sensitivity C-reactive protein [hsCRP], soluble platelet endothelial cell adhesion molecule 1 [sPECAM-1], soluble E-selectin, chemokine ligand 4 [CXCL-4]), and fibrosis (e.g. alpha-smooth muscle cell actin [alphaSMA], pro-collagen mRNA expression) were measured in plasma, serum, and skin biopsies at baseline and Wk 14.

Results: Mean $\pm$ SD change from baseline in mRSS was -2.09 ± 5.66 ($n=57$) with riociguat and -0.77 ± 8.24 ($n=52$) with placebo ($p=0.08$). From baseline to Wk 14, plasma cGMP rose by mean (SD) 94% (78%) ($n=52$) with riociguat and 10% (39%) ($n=52$) with placebo (nominal $p<0.001$). Serum sPECAM-1 and CXCL-4 fell with riociguat vs placebo; changes in hsCRP or E-selectin differed little between groups (Fig 1). Pts with higher baseline sPECAM-1 showed larger mRSS reductions with riociguat vs placebo than pts with lower levels (nominal interaction $p=0.004$). In baseline skin biopsies, 34% and 31% of pts in the riociguat and placebo groups, respectively, had no alphaSMA-positive cells; other pts had +ve cells (alphaSMA counts 0.1–99.5, median 2.5), a potential indicator of higher disease activity. Pts with +ve baseline alphaSMA counts showed a reduction of mRSS with riociguat vs placebo (Fig 2). Skin collagen mRNA expression biomarkers in skin biopsies showed no differences between groups.

Conclusion: Primary study endpoint (change in mRSS) was not met. Plasma cGMP rose with riociguat, confirming engagement with the NO-sGC-cGMP pathway. Serum sPECAM-1 (marker of endothelial activation) and CXCL-4 (marker of progressive SSc) fell with riociguat; hsCRP and E-selectin did not. Some serum and skin biomarkers of higher disease activity at baseline were associated with a greater effect of riociguat on skin fibrosis.

Figure 1. Changes in selected serum biomarkers in riociguat and placebo groups from baseline to Week 14

Figure 2. Treatment difference (riociguat-placebo) for primary endpoint (change in mRSS from baseline to Week 52) according to baseline α SMA count

Acknowledgments: RISE-SSc was jointly funded by Bayer AG and Merck Sharp & Dohme Corp., a subsidiary of Merck & Co., Inc., Kenilworth, NJ, USA.

Disclosure of Interests: Oliver Distler Grant/research support from: Grants/Research support from Actelion, Bayer, Boehringer Ingelheim, Competitive Drug Development International Ltd. and Mitsubishi Tanabe; he also holds the issued Patent on mir-29 for the treatment of systemic sclerosis (US8247389, EP2331143)., Consultant of: Consultancy fees from Actelion, Acceleron Pharma, AnaMar, Bayer, Baecon Discovery, Blade Therapeutics, Boehringer, CSL Behring, Catent, ChemomAb, Curzion Pharmaceuticals, Ergonex, Galapagos NV, GSK, Glenmark Pharmaceuticals, Inventiva, Italfarmaco, iQvia, medac, Medscape, Mitsubishi Tanabe Pharma, MSD, Roche, Sanofi and UCB, Speakers bureau: