Methods PBMCs were collected from 46 SLE patients and 48 healthy controls. The mRNA expression of ANKRD44 and IFN-inducible genes was detected by real time PCR. The mRNA expression of ANKRD44 was measured at different time points in Raw264.7 cells during IFN stimulation. ANKRD44 was knocked down by using siRNA. The activation of IFN signaling pathway were examined by western blotting at different time points in Raw264.7 cells.

Results The mRNA expression levels of ANKRD44 were decreased in PBMCs from SLE patients compared to healthy controls. The expression of ANKRD44 was downregulated when stimulating by poly(I:C) or IFN in Raw264.7 cells. Knockdown of ANKRD44 up-regulated the expression of IFN-inducible genes (such as IFIT3 and CCL2). Consistently, knockdown of ANKRD44 promoted the phosphorylation of STAT1, STAT2, JAK1 and TYK2 stimulated by IFN in Raw264.7 cells.

Conclusions Our study indicates that ANKRD44 functions as a negative regulator in type I IFN signaling pathway. Decreased expression of ANKRD44 constitutes one of the mechanisms for dysregulated IFN response in SLE, which may play important roles in the pathogenesis of Lupus.

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CLASSIFICATION OF SYSTEMIC LUPUS ERYTHEMATOSUS PATIENTS: THE 2018 EULAR/ACR CRITERIA VS THE 1982/1997 ACR CRITERIA. A COMPARATIVE STUDY IN TWO MULTICENTER MULTIETHNIC COHORTS

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Background The 2018 EULAR/ACR criteria for the classification of patients with systemic lupus erythematosus (SLE) has been a work in progress over the last five years. They have been presented and proposed over the last couple of years being their goal to improve the sensitivity and specificity of the previously published SLE criteria. The aim was to determine the sensitivity of the 2018 EULAR/ACR criteria using two well-defined lupus cohorts.

Abstract 83 Table 1 Comparison of baseline demographic and clinical characteristics by whether the patients met 2018 EULAR/ACR -based diagnosis at the same time, earlier, or later than diagnosis based on 1982/1997 ACR criteria

	EULAR/ACR criteria met at the same time as 1982/1997 ACR criteria	EULAR/ACR criteria met earlier than the 1982/1997 ACR criteria	EULAR/ACR criteria met later than the 1982/1997 ACR criteria,	p-value*
	n=344	n=41	n=173	
US cohort				
DEMOGRAPHIC				
Race or ethnicity, n (%)				
Hispanic (Texan)	82 (23.8)	11 (26.8)	21 (12.1)	<0.0001
African-American	159 (46.2)	18 (43.9)	46 (26.6)	
Caucasian	73 (21.2)	5 (12.2)	65 (37.6)	
Hispanic (Puerto Rican)	30 (8.7)	7 (17.1)	41 (23.7)	
Gender, n (%)				
Female	307 (89.2)	33 (80.5)	160 (92.5)	0.0725
Male	37 (10.7)	8 (19.5)	13 (7.5)	
Age at enrollment, mean (SD)	34.8 (12.4)	34.4 (13.1)	37.5 (12.6)	0.0604
CLINICAL				
SLAM score at enrollment, mean (SD)	10.0 (6.3)	8.9 (5.7)	8.3 (4.9)	0.0093
Latin American cohort				
	n=556	n=71	n=329	
DEMOGRAPHIC				
Race or ethnicity, n (%)				
Mestizo	190 (34.2)	43 (61.4)	135 (41.2)	0.0003
African-Latin-American	68 (12.2)	6 (8.6)	29 (8.8)	
Caucasian	289 (52.0)	21 (30.0)	154 (47.0)	
Other	9 (1.6)	0 (0.0)	10 (3.1)	
Gender, n (%)				
Female	497 (89.4)	62 (87.3)	301 (91.5)	0.4500
Male	59 (10.6)	9 (12.7)	28 (8.5)	
Age at enrollment, mean (SD)	29.8 (12.8)	30.4 (11.6)	29.5 (11.7)	0.8580
CLINICAL				
SLEDAI score at enrollment, mean (SD)	10.9 (7.9)	9.3 (7.7)	10.7 (8.2)	0.3500

* Estimated from a Pearson's Chi-square test and analysis of variance for categorical and continuous variables, respectively

Methods Patients from two well-defined multiethnic and multi-center lupus cohorts, one from the US and the other from Latin America were included. SLE was defined in the US cohort using the 1982/1997 ACR criteria and as diagnosed by the physician for the Latin American cohort although more than 95% of these patients also achieved the 1982/1997 ACR criteria. For these analyses the 1982/1997 ACR criteria were used as the gold standard. Demographics and disease activity at baseline were compared in order to determine differences between those patients who achieved the EULAR/ACR criteria before, at the same time or after than 1982/1997 ACR criteria.

Results Five-hundred and fifty-eight patients out of 640 from the US cohort and 956 out of 1047 from the Latin American cohort achieved the EULAR/ACR criteria. The sensitivity of the EULAR/ACR criteria in the US cohort was 87.2% and in the Latin American cohort was 91.3%; in the US cohort, 41 (7.3%) achieved the EULAR/ACR criteria earlier, 344 (61.6%) at the same time and 173 (31.0%) later than the ACR criteria; for the Latin American cohort these numbers and percentages were 71 (7.4%), 556 (58.2%) and 329 (34.4%), respectively. Patients who achieved the EULAR/ACR criteria earlier were less likely to be Caucasian; disease activity (measured with the SLAM: systemic lupus activity measure for the US cohort, and with the SLEDAI: Systemic Lupus Erythematosus Disease Activity Index for the Latin American cohort) did not differ between the groups. These data are depicted in table 1.

Conclusions The sensitivity of the 2018 EULAR/ACR criteria against the 1982/1997 ACR criteria (gold standard) was high (87.2% for the USA and 91.3% for the Latin American cohort). While the large majority of patients were classified at the same time (58.2% to 61.6%) with both criteria, about one third were classified later and a small proportion (about 7%) were classified earlier with the 2018 EULAR/ACR criteria. Further examination of the 2018 EULAR/ACR criteria is warranted.

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COMPARATIVE STUDY IN SLE PATIENTS WITH AND WITHOUT RENAL INVOLVEMENT BY LABEL FREE PROTEOMIC ANALYSIS OF URINE

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Background Lupus nephropathy (LN) is an important cause of morbidity and mortality in patients with Systemic Lupus Erythematosus (SLE). Considering that renal biopsy is a specialized technique and not risk free, a proteomics study is proposed to determine biomarkers that may help us to differentiate patients diagnosed with SLE with and without renal involvement.

Methods We selected 12 patients with SLE and renal involvement and 14 patients with SLE without renal involvement. There were no differences between groups according to race, gender and age. The patients were classified as moderate (<500), mild (150–500) or normal (<150) level of proteinuria in the urine. A 24 hour urine sample was obtained for analysis. Proteomic analysis was conducted by label free nLC MS/MS analysis.

Results The Principal Component Analysis (PCA) revealed differences between samples from patients who have high level of proteinuria in 24 hours and patients who do not have renal involvement. Interestingly, patients with mild proteinuria correlated better with patients without renal involvement than with the severe proteinuria group. A total of 292 proteins (identified with at least two peptides with a FDR<1%) were quantified and further considered in the analysis. Consistent with the nature of the sample, the Gene Ontology (GO analysis) of the whole list of identified proteins revealed the presence of extracellular (277 proteins, p=2.25E-171) and secretion-related proteins (49 proteins, p=1.1E-09), among others. Proteins related to defensive processes were prominent among them.

Interestingly, clear differences were detected between the three subgroups of samples. The Students T-test analysis reflected the differential presence of 147 proteins (p<0.01) between patients with and without renal involvement, being 17 more abundant in the urine of the patients with renal damage, whereas 130 showed the opposite pattern. The subset of proteins whose abundance increases upon renal damage is comprised of typical highly-abundant serum proteins. In addition, differences between most closely related groups (mild proteinuria and no renal affection) revealed differences that may be useful for a better stratification of patients.

Conclusions A different protein pattern is observed between the groups of patients, so in a more detailed study we may indicate if some of these can serve as prognostic markers for this type of patients.

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