Table 1. Validation of LDF according to the OMERACT filter

	TRUTH				DISCRIMINATION				FEASIBILITY
	Face	Content	Construct	Sensitivity in situations of change			Sensitivity in situations of no change		
				HC vs SSc	PRP vs SRP	LcSSc vs DcSSc		In clinical trials	
Basal	ND	NA	PV	PV	V	PV	PV	V	ND
Cold challenge	ND	V	ND	PV	V	ND	PV	ND	ND
Heat challenge	ND	V	PV	PV	V	PV	PV	ND	ND
PORH kinetics	ND	ND	ND	V	PV	V	ND	ND	ND
amplitude	ND	ND	ND	PV	PV	UV	ND	ND	ND

Conclusion: This systematic review emphasizes the very preliminary validation status of LDF in the assessment of the FBP in SSc. No single application method has emerged as fully validated according to the OMERACT filter.

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Only those studies which were found of good quality according to the Good Methods Checklist were considered and only the results where p-values were given were considered in this table. OMERACT= Outcome Measures in Rheumatologic Clinical Trials; HC= healthy controls; PRP= primary Raynaud's phenomenon; SRP= secondary Raynaud's phenomenon due to systemic sclerosis; LcSSc: limited cutaneous disease; DcSSc: diffuse cutaneous disease; PORH= post-occlusive reactive hyperaemia; NA= not applicable; ND= no data; V= valid if agreement exists among studies; PV= partially valid if disagreement exists among studies; UV= invalid if agreement about insignificant results exists.

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AB1330

SOLUBLE VASCULAR CELL ADHESION MOLECULE-1 AS AN INDEPENDENT MARKER FOR ENDOTHELIAL ACTIVATION IS ELEVATED IN ACTIVE RHEUMATIC DISEASES: A MULTIVARIATE ANALYSIS

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Background: CRP and/or ESR are often unreliable indicators of disease activity. Serum markers of endothelial activation may be promising alternatives. We have recently shown that soluble vascular cell adhesion molecule-1 (sVCAM-1) is elevated in patients with positive antinuclear antibodies [1]. We also have described similar findings in another cohort of patients with a variety of rheumatic diseases [2] and now report a multivariate analysis of these data.

Objectives: CRP, ESR, age, disease and gender were correlated to sVCAM-1.

Methods: Cross-sectional study with 230 patients with rheumatoid arthritis (RA), ankylosing spondylitis (AS), psoriatic arthritis (PsA) and different vasculitides (VASC). Disease activities were determined using DAS28, BASDAI, BVAS, RF, ACPA, CRP or ESR. Treatment regimens were subgrouped for conventional DMARDs (cDMARDs) or sets of biologics (bDMARDs). sVCAM-1 (ng/ml) was determined in the serum by ELISA and data were compared to age- and gender-matched healthy controls (HC).

Results: Significant (p

0.05) overexpression of sVCAM-1 as compared to HC were found in the following groups and subgroups (subgroup data not shown): **RA** (n=136): 1.26-fold and in subgroups with bDMARDs, female gender, age >50 years, and RF≥15 IU/ml. **AS** (n=34): 1.71-fold and in subgroups with bDMARDs, age ≤50 years, female gender, CRP <3 mg/dl, and ESR<20 mm/h. **VASC** (n=25): 2.52-fold and in subgroups with cDMARDs, BVAS ≤10 and >10, disease duration ≤120 months, age ≤50 years, female and male gender, CRP ≤3 mg/dl, and ESR ≤20 mm/h. **PsA** (n=35): no significant changes. Linear regression analysis showed that CRP and ESR but not sVCAM-1 were correlated to each other (r=0.637, p<0.001). In addition, multiple linear regression showed that sVCAM-1 was independently

associated with age and disease (RA, AS, VASC). However, sVCAM-1 had no impact on CRP, ESR and gender.

Conclusion: sVCAM-1 is an objective disease marker in patients with RA, AS and VASC. sVCAM-1 is not correlated with CRP and ESR and may thus provide additional information of disease activity. Prospective studies are needed to establish sVCAM-1 as a marker of rheumatic diseases, especially in vasculitis.

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AB1331

URINE METABOLIC PROFILE IN RHEUMATOID ARTHRITIS DEVELOPMENT

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Background: Rheumatoid arthritis (RA) is a chronic inflammatory disease characterized by increased mortality and associated with metabolic disorders including dyslipidaemia, insulin resistance and cachexia. Since the metabolomic profile is known to vary in response to different inflammatory conditions, metabolome analysis could substantially contribute to diagnosis and prognosis.

Objectives: To analyse the urine metabolic profile and assess its correlation with body composition parameters and disease activity of RA patients.

Methods: Seventy-nine RA patients, according to ACR/EULAR 2010 classification criteria, aged between 40 and 70 years, were recruited and followed for 12 months. Disease activity, body composition, fatigue and urine metabolome were measured. Body composition was assessed by total body dual-energy x-ray absorptiometry (DXA) for measurement of appendicular lean mass index (ALMI). Disease activity was assessed by Disease Activity Score-28 with erythrocyte sedimentation rate (DAS28-ESR). Fatigue as assessed by the Functional Assessment of Chronic Illness Therapy (FACIT). Nuclear Magnetic Resonance spectroscopy (NMR) measurements were performed to evaluate the profile of metabolic changes during the 12mo follow-up, resulting in the identification of 48 metabolites in urine collected at the baseline and after one year. Frequency analysis, Pearson Correlation and Multivariate data analysis with orthogonal projections to latent structures (OPLS) method were performed and a statistical significance was considered as p<0.05.

Results: The study population was characterized by the majority of women (86.7%), mean age 56 years old, mean disease duration of 8 years, around 80% with positive anti-CCP and RF. There was a significant increase of citric acid, creatinine, L-serine and urea during the follow-up, metabolites that are involved in the muscular-related metabolism. There was no substantial variation in the DAS28-ESR (baseline: 3.8, after