(DAS28-CRP <2.7) in this study. The CT of metacarpophalangeal (MCP) and proximal interphalangeal (PIP) joints of 2nd to 5th fingers was bilaterally visualized and measured at the middle portion of MCP and PIP joints from a longitudinal dorsal view, with approximately 90 degrees flexion. In addition, JSN of finger were scored by van der Heijde- modified Sharp method for patients who had a hand X-ray within 2 months.

Results: CT in MCP joints ranged from 0.0 to 1.1 mm (median 0.5 mm), and CT in PIP ranged from 0.0 to 0.6mm (median 0.3mm), respectively. The sum of total CT from 8 fingers ranged from 4.0 to 9.4 mm (median 6.9 mm), and there was a significant difference in total CT, but not in JSN score, between male and female patients (7.4 versus 6.7, p=0.006; and 11 versus 10, p=0.899, respectively). CT was well correlated with JSN (ρ=-0.589, p<0.001; ρ=-0.595, p<0.001 for MCP joints andρ=-0.448, p<0.001 for PIP joints), and both CT and JSN were significantly correlated with disease duration (ρ=-0.282, p=0.002, andρ=0.286, p=0.005, respectively). Notably, CT of MCP, but not of PIP, was inversely correlated with disease duration (ρ=-0.328, p<0.001). Height was correlated with CT (ρ=0.244, p=0.008), but not with JSN (ρ=-0.057, p=0.589). CT and JSN were not correlated with age, functional disability, and seropositivity.

Conclusions: A direct visualization and quantification of finger joint CT, especially MCP joints, by US is valid and useful in RA.

Disclosure of Interest: None declared

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SAT0662 EVALUATION OF ANTI-DOUBLE STRANDED DNA ANTIBODIES IN THE MONITORING OF SYSTEMIC LUPUS ERYTHEMATOSUS

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Background: Systemic lupus erythematosus (SLE) is a chronic autoimmune rheumatic disease characterized by the production of pathogenic autoantibodies. Amongst these antibodies, those directed to dsDNA are routinely used to monitor disease activity and are components of the SELENA-SLEDAI index to score severity of SLE disease. Because the predictive value of anti-dsDNA is dependent on the sensitivity and robustness of the assays used, the choice of anti-dsDNA is crucial in the clinical laboratory and clinical research setting.

Objectives: The objective was to compare four anti-dsDNA assays for their performance characteristics of SLE disease activity.

Methods: A cohort of 36 subjects with active SLE presenting with classical complement activation were enrolled and followed monthly for 1 year. At each study visit blood was collected, serum isolated and frozen until analysis. A total of 371 specimens were collected. Disease activity was scored on the day of each study visit according to the SELENA-SLEDAI method excluding anti-dsDNA or complement components (non-serological [ns] SELENA-SLEDAI). All specimens were tested using four different anti-dsDNA kits; QUANTA Lite, QUANTA Flash, a high Avidity anti-dsDNA ELISA, and the *Crithidia luciliae* indirect immunofluorescence assay (CLIFT) (Inova Diagnostics, San Diego, CA). Study visits presenting with inactive disease (ns-SELENA- SLEDAI score=0) were compared to those presenting with active disease (ns-SELENA- SLEDAI>0). The longitudinal data were analyzed using linear mixed effect modeling with the ns-SELENA-SLEDAI as dependent variable and the anti-dsDNA titers as fixed effect predictors. Marginal R^2 was calculated for each assay.

Results: At enrollment the sensitivity of the QUANTA Lite and High Avidity anti-dsDNA both reached 64%; whereas anti-dsDNA positivity was 83% by QUANTA Flash and reached 96% by CLIFT. Study visits with active disease presented with several fold higher anti-dsDNA titers than those with inactive disease status (Table 1). Linear mixed effect modeling indicated that the decrease in ns-SELENA-SLEDAI scores were associated with significant reduction in titers of all three anti-dsDNA kits (Table 2). QUANTA Flash yielded highest marginal R^2 (0.112) (Table 2).

Table 1. Anti-dsDNA antibody and disease activity

Anti-dsDNA		Inactive Disease 0 (n=141)	Active disease 1+ (n=230)	*p* value
QUANTA Flash	Titers (units)	72 (30–134)	170 (56–813)	<0.001
	Percent positive (>35 Units)	72%	86%	<0.001
High Avidity	Titers (units)	36 (12–170)	129 (47–775)	<0.001
	Percent positive (>30 Units)	56%	77%	<0.001
QUANTA Lite	Titers (units)	343 (106–624)	545 (293–879)	<0.001
	Percent positive (>301 Units)	53%	74%	<0.001
CLIFT	Titers (units)	1:160 (1:80 – 1:320)	1:320 (1:160–1:320)	<0.001
	Percent positive (>1:10)	99%	97%	0.26

Titers are presented as median inter-quartile range.

Table 2. Linear Mixed model effects of anti-dsDNA with ns-SELENA-SLEDAI scores

Assay	Intercept + Estimate SE	*p* value	Marginal R^2
QUANTA Flash	3.3±0.5 + 0.0011±0.001	<0.001	0.112
High Avidity	2.8±0.8 + 0.0023±0.0011	0.001	0.082
QUANTA Lite	2.9±0.6 + 0.0037±0.001	0.022	0.037
CLIFT	3.3±0.8 + 0.0031±0.003	0.28	0.006

Conclusions: These preliminary data indicate that anti-dsDNA antibodies determined by QUANTA Flash have value in monitoring SLE disease activity.

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SAT0663 TWO-STEP ALGORITHM FOR EARLY DIAGNOSIS OF OSTEOARTHRITIS BASED ON PLASMA DAMAGED AMINO ACIDS PROVIDES SIMPLE AND LOW COST SCREENING TEST

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Background: Currently, magnetic resonance imaging techniques have been developed for evaluation of cartilage damage in early-stage osteoarthritis (eOA). These imaging techniques have approximately 70% sensitivity and 90% specificity compared to reference diagnosis by arthroscopy. They require expensive instrumentation, time and facilities. In searching for biomarkers for clinical diagnosis we found that the proteolysis of damaged (oxidised, glycated and nitrated) proteins gives a unique pattern in the plasma of arthritic patients with the severity of the disease – trace level oxidised, glycated and nitrated amino acids. In this study we developed a two-step algorithm using these analytes as features.

Objectives: The objective was to distinguish between the following four groups: healthy control, eOA, early stage rheumatoid arthritis (eRA) and other inflammatory joint disease (non-RA).

Methods: Four algorithm types were tested for performance using random forests, multiclass logistic regression, multi-class sparse logistic regression and support vector machines. In all cases, the diagnostic algorithms were trained on the training data set, before being used to predict the disease class for each sample in the test data set. A two-stage approach was taken: (i) to distinguish between disease and healthy control; and (ii) to distinguish between eOA, eRA and non-RA. The area under the curve of the receiver operating characteristic plot (AUROC) statistic was used as measure of performance

Results: Random forest was the best-performing method. Application of two algorithms consecutively gave the best diagnostic outcome. The AUROC (sensitivity/specificity) values for disease/health were: eOA, 0.99 (0.92/0.91); eRA, 0.96 (0.89/0.90) and non-RA, 0.77 (0.73/0.72) for the training set and test set validations. A random outcome is 0.50. For typing arthritis, eOA, eRA and non-RA, AUROC values were in the range 0.68–0.98, 0.77–0.93 and 0.62–0.91 for training set and test set cross-validations and test set validation, respectively. A random outcome is 0.33.

Conclusions: A two-step algorithm approach based on trace level damaged amino acids gave better diagnostic performance that MRI for detecting and typing eOA. It is low cost and suitable for rollout as a clinical screening test.

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SAT0664 IS THERE AN EARLY ULTRASONOGRAPHIC PATTERN IN SALIVARY GLANDS IN BOTH PRIMARY AND SECONDARY SJOGREN SYNDROME?

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Background: Sjogren Syndrome (SS) affects mainly exocrine glands. Ultrasonography (US) demonstrates specificity and sensibility in major salivary glands (SG) evaluation. Recent data confirm US might be used as primary evaluation technique for its ability to show structural alterations of parenchyma [1].

Objectives: To assess the gray scale (GS) parenchymal inhomogeneity of major SG in patients with established primary and secondary SS and correlate with clinical and biological data.

Methods: Consecutive patients with SS were recruited and SG US was performed. Inhomogeneity of glandular parenchyma was quantified binary on each gland. ESSDAI and ESSPRI scores were calculated. Statistics was performed with SPSS.

Results: Twenty one (42.85% primary SS, 90.47% female) consecutive patients were included. Mean age was 53.66+/-12.99 years and disease duration 5.33+/-3.74 years. Antibody SSA/SSB presence was found in 85.7% (18/21). ESSDAI mean was 8.67+/-8.9 (0–29), ESSPRI 10.13+/-5.59 (0–20). There were no differences regarding ESSDAI and ESSPRI in the two groups (primary and secondary SS). Right parotid gland showed alterations in 71.4% patients (77%

with primary SS, 66% with secondary SS). Frequently inhomogeneity was found in all major SG (33%, 22% left and right submandibular, 77%, 44.4% left and right parotid glands) in primary SS. Both submandibular glands were symmetrically involved ($p<0.02$). Duration of disease was negatively correlated to inhomogeneity of right parotid gland ($p<0.02$).

Conclusions: Inhomogeneity in major SG in GS US was found in the majority of patients with primary and secondary SS. The symmetrical involvement of submandibular glands was significant. The inhomogeneity appears in the early period of diagnosis. No major differences were found between two groups.

References:

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SAT0665 DOES PATIENTS' OPINION OF REMISSION IN RHEUMATOID ARTHRITIS OVERLAP US "TRUE" REMISSION?

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Background: Patients describe RA remission as the absence of any symptoms or return to normality. Ultrasound (US) in RA remission patients did not exactly overlap clinical evaluation of remission in previous studies (residual synovitis frequently described). US tenosynovitis evaluation and scoring seemed to better follow clinical remission scores than synovitis in RA [1].

Objectives: To verify with US/clinical evaluations if patients' reported remission is "true" remission, and if and which clinical and US scores are lowest possible in that cohort.

Methods: Forty-eight RA patients were enrolled in this pilot study between 2015–2017 according to their positive answer to the question "Are you feeling free of symptoms, like before RA started for you?"; the enrollment was regardless of the treatment they were on. Written informed consent was obtained. Clinical evaluation of tender and swollen joints was performed the same day with US evaluation of 24 joints and 26 tendon sites and with lab CRP evaluation, blinded from one another. DAS28 and SDAI were calculated after, counting VAS=1, for both physician and patients.

Results: Mean patients age was 58, 35/48 (72.9%) patients were also in remission per DAS28 criteria. Except for CRP value, no other variables (tender, swollen joints, RF, CCP, remission duration) were significantly different in the group with overlapping DAS28 remission. Considering 1.00 as the "ideal" situation (absolute overlapping of US remission and remission felt by patients), the closest was PD scoring in tenosynovitis of the ankle and feet (100%) and the furthest was GS scoring of synovitis in superior and inferior limbs (mean 17.1%)-table 1. Although residual synovitis and tenosynovitis in remission RA patients did not exhibit a statistically significant difference, PD tenosynovitis in both upper and lower limbs was found in less than 10% of patients. This confirms the results from our previous cohort [1], that tenosynovitis better overlaps RA remission than synovitis.

Table 1. Prevalence of US remission in patients with clinical remission – bootstraping for CI

MSUS Remission	DAS28 remission	SDAI Remission
PD Tenosynovitis	94.3 (5.7–100)	90.9 (77.3–100)
GS Tenosynovitis	57.1 (40.0–74.3)	54.5 (36.4–72.7)
PD Synovitis	62.9 (45.7–80.0)	59.1 (36.4–77.3)
GS Synovitis	17.1 (5.7–31.7)	13.6 (0–31.8)
PD Lower limb tenosynovitis	100 (100)	100 (100)
GS Lower limb tenosynovitis	91.4 (82.9–100)	86.4 (72.7–100)

Conclusions: The way patients perceive their disease activity is not related to either DAS28, SDAI scores or to objective US assessment of joints and tendons (GS or PD). However, PD signal especially in tendons sheaths seems to be absent in patients having a normal life, according to their own opinion. Consequently, patients in remission could benefit from US evaluation on any machine, regardless of its costs and Doppler settings. GSUS synovitis/tenosynovitis can be residual finding and does not imply any dissatisfaction in patients' health. An ongoing cohort of active RA patients is currently conducted to explore the validity of this conclusion in these cases, too.

References:

[1] Vlad V et al. Tenosynovitis US scoring systems follow synovitis and clinical scoring systems in RA and are responsive to change after biologic therapy. Med Ultrason 2015 Sep;17(3):352–60.

Disclosure of Interest: None declared

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SAT0666 SAMPLE SIZE FOR RA CLINICAL TRIALS USING ULTRASOUND OUTCOME MEASURES MAY BE REDUCED BY NOVEL JOINT SELECTION METHODS: A PILOT STUDY

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Background: Novel outcome measures selecting a reduced joint count for ultrasonography can be highly responsive in demonstrating the improvement in joint inflammation seen in rheumatoid arthritis (RA) patients on treatment [1].

Objectives: To determine whether the use of the novel methods can translate into smaller sample sizes for subject recruitment into RA clinical trials. Results from the existing methods are used for comparison.

Methods: 24 RA patients with treatment starts or escalation had clinical and ultrasound joint assessment at baseline and 3 months. The novel methods select joints based on (A) ultrasound joint findings (i.e. Individualized Ultrasound (IUS) method) or (B) a composite of ultrasound and clinical joint findings (i.e. Individualized Composite Ultrasound (ICUS) method). In contrast, the existing methods utilize pre-determined joint sites for ultrasonography. Scores at the relevant joints per patient are summed up to obtain the total inflammatory score (TIS). The effect size (ES) was measured as the mean change of the TIS divided by the standard deviation of the change in the TIS. Sample sizes were calculated from confidence intervals (CIs) on ES that reflect uncertainty in estimating ES. For a given CI on ES, sample sizes are computed as the minimum number of patients required to provide $\geq$80% power at α =0.05 for rejecting the null hypothesis (defined as no difference in the 3-month mean change in TIS comparing novel versus existing methods).

Results: Based on the 95% CI analysis, sample sizes using existing joint assessment methods in conjunction with the 12-joint approach ranged from 10 to 234. The corresponding sample sizes using the ICUS method with the 12-joint approach ranged from 7 to 39, and using the IUS method with the 12-joint approach ranged from 6 to 37. The corresponding sample sizes using the ICUS method with the 7-joint approach ranged from 6 to 24, and using the IUS method with the 7-joint approach ranged from 6 to 35.

Table 1. Summary statistics for novel versus existing methods on 3-month change in scores

Method/Approach	Sample Estimates				95% CI	
	Mean 3-month change in TIS	SD of change in TIS	Effect Size	Post-hoc Sample Size	Effect Size	Sample Size
ICUS/7-joint	0.61	0.54	1.13	9	0.61, 1.64	6, 24
ICUS/12-joint	0.87	0.91	0.96	11	0.46, 1.43	7, 39
IUS/7-joint	0.66	0.67	0.99	11	0.49, 1.47	6, 35
IUS/12-joint	0.91	0.94	0.97	11	0.47, 1.45	6, 37
Existing/7-joint	0.10	0.29	0.34	70	-0.07, 0.75	16, –[1]
Existing/12-joint	0.22	0.35	0.63	68	0.18, 1.06	10, 234

CI: Confidence Interval; SD: Standard Deviation. [1]Interval contains zero which corresponds to the null hypothesis, so upper limit cannot be calculated.

Conclusions: Our findings strongly suggest that novel ultrasound joint selection methods result in smaller sample size requirements compared to existing methods, and provide justification for larger studies to confirm these observations.

References:

[1] Tan YK et al. Novel Ultrasound Joint Selection Methods Using a Reduced Joint Number Demonstrate Inflammatory Improvement when Compared to Existing Methods and Disease Activity Score at 28 Joints. J Rheumatol. 2016;43:34–7.

Disclosure of Interest: None declared

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SAT0667 PRESEPSIN AND PROCALCITONIN ARE OF DIAGNOSTIC VALUE FOR BACTERIAL INFECTION IN PATIENTS WITH CONNECTIVE TISSUE DISEASES

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Background: Recently, presepsin (soluble CD14-subtype) and procalcitonin are reported as a good diagnostic markers of bacterial infection, especially sepsis. However, their utility in patients with connective tissue diseases (CTDs) has been unknown.

Objectives: To assess the diagnostic value of presepsin and procalcitonin in patients with CTDs.

Methods: We enrolled the consecutive patients with CTDs, who checked the level of procalcitonin and/or presepsin during January to September, 2016, retrospectively. We divided two groups; the infection group and non-infectious group. Infection was diagnosed by symptoms, micro-bacterial methods and the good response to antibiotics. The data analysis were assessed using IBM SPSS statistics 22.