Results: (1) There were 3212 gene was regulated in LN kidney (Fold change>1.5, $FDA < 0.05$, compared with healthy control. DCBLD2, NPNT, CPVL, RGS5, LRRN4 were found to have the leading correlation with eGFR slope of LN patients by using random forest method. (2) In the independent cohort, we validate that the mRNA and protein level of DCBLD2, NPNT, CPVL, RGS5, LRRN4 was significantly evaluated in tubulointerstitial component in LN kidney, compared with healthy controls ($p < 0.05$), and also significantly correlated with eGFR slope [LRRN4($r = -0.715$, $P < 0.0001$, DCBLD2($r = -0.620$, $P < 0.0001$, CPVL($r = -0.517$, $P = 0.004$, RGS5($r = -0.489$, $P = 0.008$, NPNT($r = -0.412$, $P = 0.016$]. In addition, the mRNA level of LRRN4 and DCBLD2 in kidney was correlated with SLEDAI score($r = 0.611$ and $r = 0.512$, respectively, $P < 0.001$ and serum C3 level ($r = 0.501$, $r = 0.435$, $P < 0.05$). LRRN4 mRNA level also significantly associated with tubulointerstitial fibrosis scoring($r = 0.432$, $P < 0.05$); the protein of LRRN4 was expressed both in glomeruli and tubulointerstitial tissue. And IHC level of LRRN4 protein was significantly associated with eGFR slope ($r = 0.534$, $P < 0.05$ in LN patients).

Conclusion: LRRN4 in kidney may be used as a novel predictive biomarker of renal outcome in LN patients.

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THU0248

UTILITY OF A MOBILE PHONE BASED APPLICATION TO COLLECT PATIENT REPORTED OUTCOME INFORMATION FROM SUBJECTS WITH SYSTEMIC LUPUS ERYTHEMATOSUS

Brooke Williams¹, Bridget Muckian², Christine Peschken³, Richard Furie⁴, Elena Massarotti⁵, Vanja Sikirica⁶, Steven Gilbert⁶, Martin Hodge⁶, Peter Lipsky¹.

¹AMPEL BioSolutions, Charlottesville, VA, United States of America; ²Ampel BioSolutions, Charlottesville, VA, United States of America; ³University of Manitoba, Winnipeg, Canada; ⁴Northwell Health, Great Neck, NY, United States of America; ⁵Brigham and Women's Hospital, Boston, MA, United States of America; ⁶Pfizer, Boston, MA, United States of America

Background: Patient Reported Outcomes (PROs) can provide important data about the impact of a disease on an individual subject and/or the quality of the response to medication. However, in most circumstances, PRO information is collected only intermittently and usually at the point of care or treatment. The development of mobile technology to collect PRO data provided the opportunity to acquire this information more frequently, in real time, and in the subject's normal environment.

Objectives: To test the utility of a smart phone application (app) to collect PRO information in subjects with systemic lupus erythematosus (SLE).

Methods: A smart phone app was developed that collects data from a number of PRO instruments, including FACIT-F (fatigue), SF-36 (health-related quality of life) and patient global assessment (PtGA). Subjects with SLE were involved in the initial development and evaluation of the acceptability of the app. To test the utility of this app, a multi-center clinical study (VALUE, NCT03142711) was carried out in collaboration with subjects with SLE, in whom PRO information was collected with the app daily (PtGA) or weekly (FACIT-F and SF-36) in the subject's environment and also with the app and a standard paper form monthly at each clinical site. Demographic information, compliance and intra-class correlation coefficients between information collected with the app and using a paper form at the clinical site were assessed.

Results: Of the 80 subjects enrolled in this study, 91.3% were women; 57.5%, 16.3% and 17.5% identified themselves as of European, African or Asian ancestry, respectively. The mean age of the subjects was 42.6 years and the mean duration of education was 15.6 years. Overall compliance with completing the PRO instruments with the app at the scheduled time was 88%. To determine the consistency of information collected with the app, PRO instruments were completed on three occasions: a) in standard fashion using a paper form and b) using the app, separated by an interruption at the clinical site. The mean (SD) PtGA scores at baseline, month 1 and month 2 were 3.3(2.4), 3.5(2.4) and 3.5(2.5) using the app and 3.2(2.4), 3.5(2.3) and 3.3(2.4) using the paper form. The Intra-class Correlation Coefficient (ICC) and 90%CI were 0.97 (0.96-0.98), 0.96

(0.94-0.97) and 0.95(0.93-0.97) at the three time points, respectively. For the FACIT-F instrument, the mean (SD) score with the app was 33.2 (11.7), 31.0(12.6) and 32.3(12.7) and with the paper form was 34.1(11.6), 32.0(12.2) and 32.0(12.5) at the 3 time points with ICCs of 0.94(0.91-0.96), 0.96(0.95-0.98) and 0.96(0.94-0.97), respectively. For the SF-36 Physical Functioning score, the mean (SD) with the app was 66.3(26.1), 65.5(26.9) and 67.4(25.8) and with the paper form was 68.4(25.1), 66.1 (26.6) and 67.6(25.8) for the 3 time points, respectively. The ICCs were 0.96(0.94-0.97), 0.94(0.91-0.96) and 0.96 (0.94-0.97) for the 3 time points, respectively.

Conclusion: Compliance with completion of PRO instruments using a mobile app was excellent and the content collected with the app conformed with that collected using a standard paper form. Since patient compliance with the use of a mobile app to collect PRO information and the consistency of the information obtained compared to that obtained in standard fashion using a paper form were high, the app affords the potential opportunity to acquire frequent and highly reliable information about the impact of disease and response to medication in individual subjects with SLE.

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THU0249

URINARY NEUTROPHIL GELATINASE ASSOCIATED LIPOCALCIN AND PROSTAGLANDIN D-SYNTHETASE PREDICT DISEASE FLARES IN SYSTEMIC LUPUS ERYTHEMATOSUS

Serena Fasano, Luciana Pierro, Alessia Borgia, Melania Alessia Coscia, Ranieri Formica, Antonella Riccardi, Francesco Ciccia. *University of Campania "Luigi Vanvitelli", Rheumatology, Naples, Italy*

Background: Systemic Lupus Erythematosus (SLE) is a multisystem autoimmune disease commonly characterized by periods of flares and quiescence. Conventional markers of disease activity (serum complement and anti-dsDNA antibodies) have a limited predictive value of disease flares. Recent evidence suggests that urine biomarkers are able to discriminate between SLE patients with ongoing renal activity and those without nephritis (1-2).

Objectives: To investigate if urinary Neutrophil Gelatinase Associated Lipocalcin (NGAL) and Lipocalin-type Prostaglandin D-Synthetase (L-PGDS) are early biomarkers that could be used as flare predictors in SLE.

Methods: Patients prospectively followed at our clinic from March 2017 to September 2018, who fulfilled classification criteria for SLE (3), were considered for the study. Flares were identified by SELENA-SLEDAI Flare Index (SFI) after 3 months of urine collection (4). NGAL and L-PGDS levels were measured in the second void urinary sample by ELISA. Data were compared by the unpaired student's t test or the Mann-Whitney U test as appropriate. Logistic regression analysis was used to assess the independent baseline predictors of flares. Receiver operating characteristic (ROC) analysis was used to calculate the area under the curve (AUC) with associated 95% confidence interval (CI) to find the best cut-off values.

Results: Urine specimen was collected from 66 patients, including 64 females and 2 males with a median age at diagnosis of 27 years (IQR 21.5-38). During 3 months-follow-up, 18 (27%) out of the 66 patients experienced a single disease flare. Urinary levels of L-PGDS (Fig. 1) and NGAL (Fig. 2) significantly increased 12 weeks before a disease flare ($p = 0.0001$ and $p = 0.002$, respectively). Urinary NGAL levels correlated with anti-DNA antibody titre ($r = 0.254$, $p = 0.042$) and not with serum complement prior to the disease flare ($P > 0.05$). Moreover, urinary L-PGDS slightly correlated with anti-DNA antibody titre ($p = 0.08$), and was not associated with serum complement levels. Based on ROC analysis, urinary NGAL (AUC: 0.752) and L-PGDS (AUC: 0.811), outperformed conventional biomarkers (Table1). ROC analysis revealed that NGAL levels above 10.95ng/ml had a sensitivity of 84% and a specificity of 63% for flare prediction, while urine L-PGDS cut-off value in the ROC curve, 1500 ng/ml, predicted a flare with 78% sensitivity and 86% specificity. At multivariate analysis, NGAL and L-PGDS were independent predictors of flare with OR=10.34 (95% CI 1.46 – 73.05) and 24.85 (95% CI 4.32-