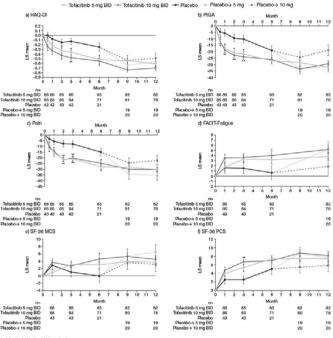
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10 mg BID). There were no major differences in demographics or baseline characteristics between treatment groups. At Month 3, tofacitinib resulted in significantly greater changes in HAQ-DI (5 mg BID, p<0.05; 10 mg BID, p<0.001), PtGA (5 mg BID, p<0.05; 10 mg BID, p<0.001), Pain (5 mg BID, p<0.001; 10 mg BID, p<0.001) and SF-36 Physical Component Summary (PCS) scores (5 mg BID, p<0.05; 10 mg BID, p<0.001) vs PBO (Figure). Numeric improvements in FACIT-Fatigue, SF-36 Mental Component Summary (MCS) [Figure] and EQ-5D health state profile (utility scores) were observed at Month 3 with tofacitinib vs PBO. There were no improvements in WLQ observed at Month 3 with tofacitinib vs PBO. Improvements were generally maintained at 6 and 12 months (Figure). The proportion of patients achieving HAQ-DI improvement ≥0.22 from baseline at Month 3 was significantly higher with tofacitinib vs PBO (5 mg BID, p<0.05; 10 mg BID, p<0.05).

Figure. LSM (±SE) ch



ronic lilinese Therapy; HAQ-OI, Health Assessment Questionnaire-Disability Index; LSM, least equares mean

Conclusions: Tofacitinib 5 and 10 mg BID administered with csDMARDs significantly improved PROs including SF-36 PCS, PtGA, physical function and pain vs PBO. These improvements were maintained for up to 12 months in Chinese patients with RA.

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THURSDAY, 15 JUNE 2017

SLE, Sjögren's and APS - etiology, pathogenesis and animal models -

THU0216 URINARY NEUROPILIN-1: A NEW BIOMARKER APPROACH IN THE PROGNOSIS OF LUPUS NEPHRITIS

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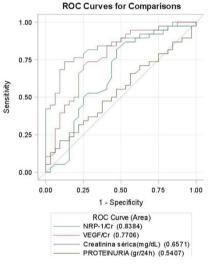
Background: Lupus nephritis (LN) affects up to 50% of patients with SLE and is a major cause of morbidity, despite modern therapeutic approaches [1,2]. To date, renal biopsy is still the gold standard for diagnosing and classifying the degree of renal inflammation and scarring, but its invasiveness makes it unsuitable for serial monitoring. A novel biomarker to predict the evolution of renal inflammatory injury is still needed. Neuropilin-1 (NRP-1) has important functions in adult tissues,

being involved in axonal guidance, vascular endothelial sprouting, regeneration and organ repair and immunosupression [3].

Objectives: Evaluate the protein and expression levels of NRP-1 at the time of the renal flare in patients with lupus nephritis and determine whether they could predict the disease progression.

Methods: Urine and serum of 70 patients with LN with nephrotic proteinuria, 25 patients with chronic non-lupus related nephopathy, and 25 healthy controls were analyzed by qPCR-RT and ELISA to determinate the levels of mRNA/protein of NRP-1. Immunohistochemistry of protein levels were done in renal biopsy (N=5). Urine and serum from 39 other patients with LN with nephrotic proteinuria were collected prospectively during two years.

Results: Increases in mRNA expression and protein concentration of NRP-1 were identified in urine samples of LN patients in flare compared with the different control groups. However, significant NRP-1 levels were found in LN patients that gone into remission compared with patients in non-remission after one year of treatment (p<0.0001). Urinary VEGFA, VEGFR1, VEGFR2 and SEMA3A mRNA and protein levels were also determinate. Results were confirmed with immunohistochemistry in renal biopsies (N=5). We observed a strong correlation with NRP-1 protein levels and VEGFA protein levels (r=0.466, p<0.0001). Areas under the receiver operating characteristic curve of urinary NRP-1 and VEGFA protein levels to distinguish between remission and non-remission patients were 0.8384 and 0.7706, respectively (Figure 1). In a prospective study (N=39), urinary protein NRP-1 and VEGFA levels decreased in LN patients going to complete remission; but no those with non-response that maintain their low levels during all the follow-up.



Conclusions: For first time, we demonstrate that urinary levels of NRP-1 might reflect the evolution of renal inflammatory injury and could be used as novel biomarker to predict the recovery of LN.

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Disclosure of Interest: None declared DOI: 10.1136/annrheumdis-2017-eular.5729

THU0217 | DNA METHYLATION ANALYSIS IN MULTIPLE CELLULAR **COMPARTMENTS DEMONSTRATES A UNIVERSAL DNA** METHYLATION INTERFERON SIGNATURE IN MULTIPLE CELLULAR COMPARTMENTS AND PREDOMINANT B-CELL HYPERMETHYLATION IN TWINS WITH SYSTEMIC LUPUS **ERYTHEMATOSUS**

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Background: Systemic lupus erythematosus (SLE) is a complex autoimmune