

Conclusions Our data indicate that serum sphingolipids can be a good candidate for SLE diagnostic markers. In particular, we identified that Cer16 to S1P could be useful for diagnosing lupus nephritis.

LSO-045 MULTIPLE MOLECULAR BIOMARKERS THAT PREDICT RESPONSE TO TREATMENT IN LUPUS NEPHRITIS

¹Dae Jin Park*, ^{2,3}Young-Bin Joo, ³Eunwoo Nam, ³Jiyoung Lee, ^{2,3}So-Young Bang, ^{2,3}Hye-Soon Lee, ^{2,3}Sang-Cheol Bae. ¹Rheumatology, Yonsei University Wonju College of Medicine, Wonju, Republic of Korea; ²Rheumatology, Hanyang University Hospital for Rheumatic Diseases, Republic of Korea; ³Hanyang University Institute for Rheumatology Research, Seoul, Republic of Korea

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Background Little has been known regarding the biomarker to predict the treatment response in lupus nephritis. This study aimed to identify potential biomarkers that predict treatment response in lupus nephritis (LN).

Methods In this prospective longitudinal study, 66 active LN patients were included and underwent renal biopsy at the time of enrollment. Patients were divided into two groups according to one-year response: 50 responders and 16 non-responders. Serum and urine samples were collected at 0, 12, 24, and 48 weeks after induction therapy. Twelve serum and urine biomarkers were measured by the multiplex immunofluorescence assay.

Results Urine (VDBP, MCP-1, IL-6, and IP-10) and serum (IP-10 and IL-23) levels of 12 biomarkers sampled one year after treatment differed significantly between responders and non-responders. Compared with the baseline, their levels in one year were significantly higher in non-responders than in responders. Urine VDBP was significantly correlated with proteinuria ($\rho=0.62$, $p < 0.0001$), creatinine ($\rho=0.37$, $p=0.0025$), and renal activity index ($\rho=0.35$, $p=0.0042$).

The change in urine IL-6 and IL-23 levels during three months after induction treatment could predict the treatment response in lupus nephritis with an AUC of 0.70 ($p=0.025$) and 0.71 ($p=0.018$), respectively. A model incorporating these two predictors into complement C3 and C4, which are significant clinical factors for treatment response, showed increased predictive value with an AUC of 0.78.

Conclusions Urine VDBP, MCP-1, IL-6, IP-10, and serum IP-10 and IL-23 after one year of treatment differed significantly between responders and non-responders. Moreover, our predictive model composed of urine IL-6, 23, and complement showed increased discriminative ability between responders and non-responders in patients with LN.

LSO-046 METABOLOMIC ANALYSIS FOR THE UNIQUE PROFILE AND NOVEL BIOMARKERS OF NEUROPSYCHIATRIC SYSTEMIC LUPUS ERYTHEMATOSUS

¹Xue Li, ¹Yixue Guo, ²Huaqing Lu, ¹Wenwen Pei, ¹Yifan Wang, ¹Jing He, ¹Xiaolin Sun*. ¹Department of Rheumatology and Immunology, Peking University People's Hospital, China; ²Department of Rheumatology and Immunology, Zhengzhou University, Fifth Affiliated Hospital, China

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Background Neuropsychiatric systemic lupus erythematosus (NPSLE) is a common manifestation of systemic lupus

erythematosus (SLE), with high mortality and disability rate. The lack of effective diagnostic methods, such as biomarkers, makes it difficult to diagnose and treat NPSLE. Metabolomics studies in autoimmune diseases shed new light on the identification of biomarkers beyond autoantibodies and cytokine profiling. This research aimed to explore the unique metabolomic profile, and discover novel molecular biomarkers and pathways for NPSLE.

Methods Cerebrospinal fluid samples from 26 NPSLE patients, 9 SLE controls, 7 connective tissue disease (CTD) controls and 9 nervous system disorder (NSD) controls were analysed to identify metabolomic signatures, significant pathways and biomarkers in the discovery cohort, using ultra performance liquid chromatography-tandem mass spectrometry (UPLC-MS). Next, the potential biomarkers were verified in an independent validation cohort including 22 NPSLE patients, 11 SLE controls and 4 NSD controls.

Results The metabolite profiles of cerebrospinal fluid (CSF) samples allowed significant differentiation of NPSLE patients from other disease controls. β -alanine metabolism and inositol phosphate metabolism pathways were significantly perturbed in NPSLE group. In the discovery cohort, 44 CSF metabolites with variable importance in projection (VIP) scores >1.5 and $p < 0.05$ were considered as the most differential metabolic biomarkers, including β -alanine amino acid and inositol. The diagnostic value of inositol was verified in the validation cohort, with the greatest specificity of 95.45% and the sensitivity of 60.00% for NPSLE. The CSF inositol level was higher in NPSLE patients with neuropsychiatric damage, cranial neuropathy and cerebrovascular disease.

Conclusions CSF metabolomic profile of NPSLE patients is unique from other disease controls. The pathway perturbations are involved in β -alanine metabolism and inositol phosphate metabolism. Inositol is a promising biomarker for the diagnosis and neuropsychiatric damage evaluation of NPSLE, and has potential relationships with specific NPSLE manifestations.

LSO-047 UTILITY OF AUTOANTIBODY AGAINST AN UCH-L1 EPI TOPE AS A SERUM DIAGNOSTIC MARKER FOR NEUROPSYCHIATRIC SYSTEMIC LUPUS ERYTHEMATOSUS

Yixue Guo, Xue Li, Xiaolin Sun*. Department of Rheumatology and Immunology, Peking University People's Hospital, China

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Background Neuropsychiatric systemic lupus erythematosus (NPSLE) is one of the most serious complications of systemic lupus erythematosus (SLE), lacking efficient diagnostic biomarkers. Previous studies have shown that anti-ubiquitin carboxyl hydrolase L1 (UCH-L1) autoantibody is a promising cerebrospinal fluid (CSF) biomarker for NPSLE diagnosis. The purpose of this study is to explore the serum autoantibodies against different UCH-L1 epitopes and investigate the potential diagnostic value of serum autoantibodies against different UCH-L1 epitopes in NPSLE.

Methods The epitopes of UCH-L1 protein were predicted in DNASTar software. The serum levels of different UCH-L1 epitope autoantibodies in 40 NPSLE patients, 32 SLE patients without neuropsychiatric symptoms and 21 healthy controls