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Background: Clinical joint count assessment is important for detecting synovitis but its reliability is controversial

Objectives: This study assessed the correlation between bone scintigraphy and positron emission tomography (PET)-derived parameters in 28 joints with disease activity and compared the reliability of joint counts between bone scintigraphy and clinical assessment in rheumatoid arthritis (RA).

Methods: We enrolled 86 patients with active RA who underwent bone scintigraphy, fluorine-18-fluorodeoxyglucose (FDG) PET/CT and disease activity evaluation at the same time. This two-step study involved a development (n=67) and validation (n=19) group. Bone scintigraphy-derived joint assessment were compared with PET/CT derived and clinical joint assessment. Subsequently, we developed a disease activity score (DAS) using bone scintigraphy-positive joints and validated it in an independent group.

Results: The number of bone scintigraphy-positive joints in 28 joints was significantly correlated with the swollen (SJC)/ tender (TJC) joint counts and PET/CT derived joint counts. Intra- and inter-observer reliabilities of bone scintigraphy for the affected joint counts were excellent. Inter-observer reliability between nuclear medicine physicians and rheumatologists was good for SJC/TJC and PET/CT derived joint counts in 28 joints except shoulders. After multivariate analyses including erythrocyte sediment rate (ESR) and patients global assessment (PGA) in addition to bone scintigraphy-derived parameters, bone scintigraphy/DAS was derived as $0.056 \times \text{number of bone scintigraphy-positive joints in 28 joints} + 0.012 \times \text{ESR} + 0.030 \times \text{PGA}$. A significant correlation between bone scintigraphy/DAS and DAS28-ESR was confirmed in the validation group ($p < 0.001$).

Conclusion: Bone scintigraphy-derived joint assessment significantly correlated with PET/CT derived joint counts. Bone scintigraphy could serve as a sensitive and reliable method for evaluating disease activity in RA patients.

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THU0104

THE GUT MICROBIOTA AND ITS RELEVANCE TO PERIPHERAL T REGULATORY CELLS AND T HELPER 17 IN PATIENTS WITH RHEUMATOID ARTHRITIS

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Background: Rheumatoid arthritis (RA) is a common autoimmune disorder with joint destruction and synovial inflammation characterized by abnormal immune responses to autoantigens. Our previous studies have demonstrated that impaired peripheral lymphocytes especially insufficiency of regulatory T cells (Tregs) played an important role in pathogenesis of RA^{1,2}. Interestingly, the dysbiosis of gut microbiota triggers several types of autoimmune diseases through the imbalance of T lymphocyte subsets³. However, the detailed gut microbiota of RA patients and its correlation with Tregs and helper T cells 17 (Th17) are unclear up until now.

Objectives: To compare the difference of gut microbiota between RA and healthy controls (HCs), and to investigate the relevance of gut microbiota with circulating Tregs and Th17 in patients with RA.

Methods: From December 2018 to August 2019, a total of 205 diagnosed patients with RA and 199 age and sex-matched HCs were enrolled in this study. Stool of Every participant was collected for bacterial DNA extraction and 16S ribosomal RNA (rRNA) gene sequencing. The absolute numbers of Tregs and Th17 in PB of these individuals were measured by Flow Cytometer (FCM) combined with standard absolute counting beads. Data were expressed as mean $\pm$ standard deviation to the distribution. Independent-samples T test and Spearman rank correlation test. P value < 0.05 were considered statistically significant.

Results: Patients with RA had a significantly difference of diversity and abundance of intestinal microbiota compared with those of HCs ($P < 0.05$). Detailedly, the abundance of Proteobacteria was significantly increased in RA patients ($P < 0.05$), and the abundance of Firmicutes, Fusobacteria and Verrucomicrobia were significantly reduced ($P < 0.05$) at the level of Phylum (Figure 1). At the genus level, in the RA group, the abundance of Escherichia, Ruminococcus2 and Clostridium_sensu_stricto were significantly increased ($P < 0.05$), but the abundance of Lachnospiraceae_incertae_sedis, Prevotella, Clostridium_XIVa, Roseburia, Dialister, Blautia, Megamonas and Gemmiger were significantly lower than

the healthy controls ($P < 0.05$) (Figure 2). Moreover, Blautia, Anaerostipes and Ruminococcus2 have negative correlation with the absolute number of Tregs, and Cloacibacillus and Streptophyta have positive correlation with the absolute number of Th17.

Conclusion: Patients with RA had a dysbiosis of the gut microbiota in both diversity and abundance, which is closely related to the impaired peripheral lymphocyte subsets, that may be related to the pathogenesis of RA, which might provide a new idea for RA treatment.

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Figure 1: The phylum-level profile for rheumatoid arthritis (RA) patients and healthy controls (HCs). Data were expressed as mean $\pm$ standard deviation to the distribution. Independent-samples T test was applied. (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$)

Figure 2: The genus-level profile for rheumatoid arthritis (RA) patients and healthy controls (HCs). Data were expressed as mean $\pm$ standard deviation to the distribution. Independent-samples T test was applied. (* $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$)

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THU0105

ISOTOPE-LABELING-LC-MS-BASED METABOLIC PROFILING OF MULTIPLE SERUM SAMPLE SETS FOR THE DISCOVERY OF HIGH-CONFIDENCE RHEUMATOID ARTHRITIS BIOMARKERS

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Background: Early diagnosis of rheumatoid arthritis (RA) is hampered by sub-optimal accuracy of currently available serological biomarkers. Metabolomics may reveal promising biomarker candidates associated with the biomolecular processes of RA. In this work, we applied a high-performance chemical isotope labeling (CIL) LC-MS technique for in-depth profiling of the amine/phenol-submetabolome in serum samples. To avoid false positives and obtain high-confidence biomarker candidates, we analyzed three independent sets of serum samples collected from RA patients and healthy controls to examine the common effects.

Objectives: We aimed to identify a metabolite signature with consistently high accuracy for RA.

Methods: Serum samples were taken from 3 RA cohorts, which comprised 50, 49, and 131 RA patients, respectively. Within each cohort, there were