Background: Immune-mediated diseases such as spondyloarthritides (SpA) consistently coincide with dysbiosis of the gut microbiota and frequently present with additional inflammatory pathologies such as Crohn’s disease (CD) and acute anterior uveitis (AAU). Deep profiling of gut microbiota may reveal new pathways of how SpA and its related diseases are initiated and perpetuated.

Objectives: To identify the presence of shared and specific gut microbiota signatures for SpA and its related diseases as a whole, as well as for the individual diseases, relative to healthy controls.

Methods: Patients were recruited with a definite diagnosis of axial SpA, AAU, or CD and were compared to controls (patients with back pain and previously ruled out SpA/CD-AAU diagnosis). All patients were naïve to or did not receive treatment with biological disease-modifying antirheumatic drugs for at least 3 months before enrollment of the study. Fecal samples were collected and microbiota composition was determined by 16S rRNA gene sequencing, followed by computational analysis referencing the SILVA138 database. Nonparametric Wilcoxon tests were used to calculate differential abundances between binary groups, and the Spearman correlation was used with continuous covariates. Nested linear models and likelihood ratio tests were used to assess confounding with respect to patient characteristics, HLA-B27 expression, inflammatory markers, and the presence of other immune-mediated diseases.

Results: A total of 300 patients were recruited for the study: 111 axial SpA, 110 AAU, and 79 CD patients and were compared to 63 control individuals. Fifty-three of patients were males with an age (mean±SD) of 39.1±12.3 years. The prevalence of HLA-B27 was 63.0% by patients compared to 7.9% by controls. Fifty-three of patients were males with an age (mean±SD) of 39.1±12.3 years.

Conclusion: There is a robust shared taxonomic signature among related immune-mediated diseases, in addition to individual disease phenotype signatures. Patients frequently exhibited a strong depletion in Blautia and an enrichment in Lactobacillus as well as pathogen-harboring genera such as Escherichia-Shigella and Fusobacterium.

Disclosure of Interests: None declared

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