study. The same is true for the effect of functional impairment – it would be interesting to know whether this was due to inflammation or structural damage.

REFERENCES:

- [1] Neovius M et al. *Ann Rheum Dis* 2015; 74:354-360
- [2] The study was funded by Hexal Germany.

Figure 1. Treatment trajectories of ADA therapy in patients with CIRD during two years ADA: adalimumab; bDMARD: biological disease modifying anti-rheumatic drug.

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AB0824

ANALYSIS OF GUT MICROBIOTA IN RHEUMATOID ARTHRITIS PATIENTS

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Background: Gastrointestinal microbiota, particularly gut microbiota is an indispensable environmental factor in the progression of Rheumatoid Arthritis (RA). Understanding the diversity and function of the intestinal flora in patients with RA is part and parcel to understand the relationship between microbiota and human health.

Objectives: This study aimed to identify the diversity and function of the intestinal flora in patients with RA.

Methods: A total of 166 participants were recruited in this study, comprising 93 RA patients and 73 age and sex-matched healthy controls (HCs). Microbial genome was extracted from approximately 250mg fresh fecal samples from all participants using QIAamp PowerFecal DNA Kit (Qiagen). The V3-V4 variable regions of bacterial 16S rRNA genes were sequenced with the Illumina Miseq PE300 system. Sequence data were compiled and processed using Qiime2. Sequences were grouped into operational taxonomic units (ASVs)¹. Microbial diversity was estimated by the Simpson index. PICRUST2 was used to predict KEGG functional pathway differences between RA and HC intestinal flora functions based on ASV Tables². Linear Discriminant Analysis (LDA) Effect Size (LEfSe) analysis was performed using LEfSe software to discover the different intestinal flora and functions between RA and healthy.

Results: The alpha-diversity index of Simpson the microbiome in RA patients was lower than that of HCs (Figure 1a, $P < 0.05$). Compared with HCs, bacterial Bacilli and Lactobacillales were more abundant in patients with RA (Figure 1b, $P < 0.05$). In contrast, Marinifilaceae, Peptococcaceae, Peptococcales and Phascolarcto bacterium were less abundant in the RA group (Figure 1b, $P < 0.05$). As shown in Figure 1c, propanoate metabolism, taurine and hypotaurine metabolism, ascorbate and aldarate metabolism, biosynthesis of siderophore group nonribosomal peptides and glutathione metabolism were the most significantly altered pathways in RA ($P < 0.05$). Epithelial cell signaling in *Helicobacter pylori* infection, RNA transport, RNA degradation and plant-pathogen interaction were the most significantly altered pathways in HC ($P < 0.05$). The different KEGG

metabolic pathways were mainly concentrated in carbohydrate and amino acid metabolism.

Conclusion: Gut dysbiosis in RA patients mainly characterized by reduced the diversity and impaired abundance of the intestinal flora, which severely influence the metabolism of gastrointestinal microbiota. The discovery of the associated intestinal microbiota of RA may provide a new idea for RA treatment.

REFERENCES:

- [1] Han L, Zhao K, Li Y, et al. A gut microbiota score predicting acute graft-versus-host disease following myeloablative allogeneic hematopoietic stem cell transplantation. *Am J Transplant* 2020;20(4):1014-27. doi: 10.1111/ajt.15654 [published Online First: 2019/10/13]
- [2] Liss MA, White JR, Goros M, et al. Metabolic Biosynthesis Pathways Identified from Fecal Microbiome Associated with Prostate Cancer. *Eur Urol* 2018;74(5):575-82. doi: 10.1016/j.eururo.2018.06.033 [published Online First: 2018/07/17]

Figure 1 (a) Comparison of Simpson index between HC and RA groups was shown using boxplot. (b) LEfSe was used to detect difference in Flora functions according to RA and HC. Pathway differences plot as LDA score (log 10). Bars to the right of zero represent bacterial functions enriched in the RA, and bars to the left of zero represent bacterial functions in HC. * $P < 0.05$.

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AB0825

JAK2 (V617F) MUTATION AND ASSOCIATION TO IMMUNE MEDIATED DISEASES. STUDY OF 130 PATIENTS FROM A SINGLE UNIVERSITY HOSPITAL

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Background: Janus Kinases (JAK) are tyrosin-kinases that can promote cytokine production in immune and hematopoietic cells. The JAK-2 (V617F) mutation is the most frequently detected mutation in myeloproliferative neoplasms (MPN) which include essential thrombocythemia (ET), polycythemia vera (PV), primary myelofibrosis (PMF) and undifferentiated MPN. JAK-2 (V617F) mutation displays a pro-inflammatory phenotype that may be associated to a higher risk of immune mediated diseases (IMD), thromboembolic complications or other cancers (1-3).

Objectives: To evaluate the presence of a) IMD (rheumatic and non-rheumatic), b) cancer and, c) Deep vein thrombosis/ Venous thromboembolism (DVT/VTE) events in a cohort of patients with a positive JAK-2 (V617F) mutation.

Methods: We studied all the patients diagnosed with a positive JAK-2 (V617F) mutation in a single University Hospital between January, 2004 and December, 2019.

Results: The study included 130 patients (73 men/57 women; mean age, 70.1±14.5 years). They were diagnosed of ET (n=64, 49.2%), PV 46 (35.4%), undifferentiated MPN (n=12, 9.2%) and PMF (n=8, 6.1%). Of these patients, 54 (41.5 %) (44 non rheumatic and 10 rheumatic) were diagnosed with at least one IMD, 46 (35.4%) with other cancer different of MPN and 36 (27.7%) with DVT/VTE events. (Table 1/Figure 1).

Conclusion: Due to its prevalence and potential complications, IMD should be taken into consideration when a patient is diagnosed with a positive JAK-2 (V617F) mutation.

REFERENCES:

- [1] Perner F, et al. *Cells*. 2019;8:854.
- [2] Xu Q, et al. *Clin Rheumatol*. 2020 Jul 16.