REFERENCES:
[1] Zhu et al. PLOSone 2016;
[2] Walsh et al. Genome Biology 2016;
[3] Muaaz Aslam et al. Disease Markers 2020;
[4] Acquati et al. Frontiers Immunol 2019
Acknowledgements: This work was supported by the Italian Ministry for University and Research (Prin 2017NTK4HY).
Disclosure of Interests: None Declared.
DOI: 10.1136/annrheumdis-2023-eular.1508

AB0060 ANALYSIS OF THE HUMAN GUT MICROBIOME AND NUTRITION PATTERNS IN RHEUMATOID ARTHRITIS

Keywords: Rheumatoid arthritis, Diet and nutrition, Gastrointestinal tract

J. Schirmer[1,2], K. Schlicht[2,3], C. Knappe[3], K. Türk[3,4], D. Schulte[2,3,4], K. Hartmann[3,4], U. Settgast[3,4], A. Franke[2,5], S. Schreiber[2,4,5], B. Hoyer[1,2], M. Laudes[2,3,4]. *[1]University Medical Center Schleswig-Holstein, Internal Medicine I, Rheumatology, Kiel, Germany*; *[2]Cluster of Excellence, Precision Medicine in Chronic Inflammation, Kiel, Germany*; *[3]University Medical Center Schleswig-Holstein, Institute of Diabetes and Clinical Metabolic Research, Kiel, Germany*; *[4]University Medical Center Schleswig-Holstein, Internal Medicine I, Kiel, Germany*; *[5]Christian-Albrechts-University, Institute for Clinical Molecular Biology, Kiel, Germany*

Background: The association of the gut microbiome with obesity and metabolic diseases as type 2 diabetes (T2D) as well as the influence of environmental factors like nutrition on its composition is well established. In addition, recent studies[1] described the composition of gut microbiota to be altered in inflammatory rheumatic diseases highlighting a pathogenetic link between the microbiome and autoimmune joint diseases.
Objectives: The aim of this study was to analyze food intake and the composition of the gut microbiota in rheumatoid arthritis (RA) in comparison to healthy controls (adjusted for metabolic conditions known to influence the gut microbiota composition).
Methods: A subset of the FoCus (Food chain plus) cohort (a cross-sectional survey of the general population in northern Germany) with RA and matched controls without RA (matched for age, gender, body mass index and diagnosis of Type 2 Diabetes mellitus [T2D]) was investigated regarding their nutrition patterns and gut microbiome in a case-control analysis. Nutrition patterns were derived from Food Frequency Questionaires (FFQ) and analyzed by hierarchical cluster analysis. The gut microbiota composition was analyzed by 16S rRNA gene sequence data clustered into operational taxonomic units (OTUs). Microbiome composition was analyzed by alpha- (phylodiversity, Shannon index, Chao index) and beta-diversity measures (Bray-Curtis distance, Jaccard index) and by hurdle-models.
Results: We identified n = 94 individuals with RA and n = 94 matched controls (mean age 57 years, SD 12.9; mean BMI 31.1, SD 8.9). Interleukin 6 was significantly higher in the RA group compared with controls (p=0.012), while no differences were observed between groups for HOMA-Index, CRP, lipoprotein (a) or triglycerides. Nutrition data from FFQs was used in a hierarchical cluster analysis, resulting in two main clusters (the second one defined by a significantly higher intake of vegetables, fruit and dairy products). Nutrition clusters did not differ significantly between RA cases and controls (p=0.228). When comparing the composition of the intestinal microbiota between RA patients and controls (adjusted for nutrition cluster and IL-6), significant differences in the beta-diversity were detected using Bray-Curtis distance (p=1.82e-9) and Jaccard index (p=1.82e-9). Hurdle model analysis of the core measurable microbiome identified three candidate species OTUs (Flavonifractor and 2x Blautia). No significant differences in alpha diversity was observed when analyzed by species richness (p=0.9), Shannon (p=0.3) and Chao index (p=0.6).
Conclusion: Participants suffering from RA had significant differences in the composition of the gut microbiome compared to controls matched for age, BMI, gender and T2D after adjusting for nutrition patterns and IL-6. Investigating differences in the functional capacity of the altered gut microbiome in RA may better characterize a possible link of gut microbes to the development of RA.
REFERENCE:
[1] Chu XJ, Cao NW, Zhou HY, Meng X, Guo B, Zhang HY, Li BZ. The oral and gut microbiome in rheumatoid arthritis patients: a systematic review. Rheumatology (Oxford). 2021 Mar 2;60(3):1054-1066. doi: 10.1093/rheumatology/keaa835. PMID: 33450018.
Acknowledgements: The project was supported by the German Society for Rheumatology (Deutsche Gesellschaft für Rheumatologie/ DGRh) and the Competence Network Rheumatology (Kompetenznetz Rheumatologie)/ DGRh Research Initiative 2020.
Disclosure of Interests: Jan Schirmer: None declared, Kristina Schlicht: None declared, Carina Knappe: None declared, Kathrin Türk: None declared, Dominik Schulte: None declared, Katharina Hartmann: None declared, Ute Settgast: None declared, Andre Franke: None declared, Stefan Schreiber: None declared, Bimba Hoyer: None declared, Matthias Laudes Speakers bureau: AstraZeneca, Lilly, Bayer, Consultant of: AstraZeneca, Lilly, Bayer.
DOI: 10.1136/annrheumdis-2023-eular.1998

AB0061 ENDOTHELIN-1 AS A POTENTIAL CANDIDATE TO SHED LIGHT ON THE CHALLENGE OF INTERSTITIAL LUNG DISEASE DIAGNOSIS IN PATIENTS WITH RHEUMATOID ARTHRITIS

Keywords: Lungs, Biomarkers, Rheumatoid arthritis

V. Pulito-Cueto[1], S. Remuzgo Martinez[1], B. Atienza-Mateo[1,2], F. Genre Romero[1], V. M. Mora-Cuesta[1,3], D. Iturbe Fernández[1,3], M. Sebastián Mora-Gil[1], V. Portilla[1,2], A. Corrales[1,2], I. Ferraz-Amaro[4], R. Blanco[1,2], J. M. Cifrián-Martínez[1,3,5], R. López-Mejías[1], M. A. González-Gay[6,7]. *[1]IDIVAL, HUMV, Research Group on Genetic Epidemiology and Atherosclerosis in Systemic Diseases and in Metabolic Bone Diseases of the Musculoskeletal System, Santander, Spain*; *[2]HUMV, Department of Rheumatology, Santander, Spain*; *[3]HUMV, Department of Pneumology, Santander, Spain*; *[4]Hospital Universitario de Canarias, Department of Rheumatology, Santa Cruz de Tenerife, Spain*; *[5]UC, Faculty of Medicine, Santander, Spain*; *[6]IDIVAL, UC, Department of Medicine and Psychiatry, School of Medicine, Santander, Spain*; *[7]IIS-Fundación Jiménez Díaz, Department of Rheumatology, Madrid, Spain*

Background: Interstitial lung disease (ILD) is one of the main causes of death in patients with rheumatoid arthritis (RA), constituting its **e**arly diagnosis in these patients a challenge for the clinicians [1]. In this sense, pulmonary endothelial activation is one of the essential steps to the development of lung lesions [2,3]. In this regard, endothelin-1 (ET-1), the most potent endogenous vasoconstrictor, has been described as a profibrotic molecule [3]. Accordingly, it is plausible to think that ET-1 is involved in the pathophysiology of RA-ILD$^+$.
Objectives: To explore the role of ET-1 as a biomarker of pulmonary fibrosis in RA-ILD$^+$.
Methods: Peripheral venous blood was collected from 21 RA-ILD$^+$ patients and two comparative groups: 25 RA-ILD$^-$ patients and 21 idiopathic pulmonary fibrosis (IPF) patients. All the subjects were recruited from the Rheumatology and Pneumology departments of Hospital Universitario Marqués de Valdecilla, Santander, Spain. Serum levels of ET-1 were determined by ELISA.
Results: RA-ILD$^+$ patients showed increased levels of ET-1 compared to those with RA-ILD$^-$ (p<0.01, **Figure 1A**). Interestingly, the ability of serum ET-1 levels to discriminate patients with RA-ILD$^+$ from those with RA-ILD$^-$ was further confirmed by receiver operating characteristic curves (area under the curve: 0.77, p<0.01, **Figure 1B**). The optimal cutoff value for ET-1 showing the best sensitivity and specificity was 1.02 pg/mL. Moreover, patients with RA-ILD$^+$ presented similar levels of ET-1 than those with IPF (p=0.50, **Figure 1A**). Additionally, a negative correlation between ET-1 serum levels and both forced vital capacity and forced expiratory volumen at first second was disclosed in patients with RA-ILD$^+$ (r=-0.56, p=0.04 and r=-0.65, p=0.01, respectively).
Conclusion: Our study suggests that ET-1 levels are linked to lung injury and worse lung function, supporting its role as a potential blood biomarker of ILD in RA patients.
REFERENCES:
[1] Expert Rev Clin Immunol. 2021;17(5):485-497;
[2] JCI Insight. 2021;6(22):e125635;
[3] Am J Respir Cell Mol Biol. 2010;42(1):16-20.
Acknowledgements: VP-C is supported by funds of PI18/00042 from Instituto de Salud Carlos III (ISCIII), co-funded by European Regional Development Fund; MSM-G is financed by funds of TRANS-VAL 22/01 from IDIVAL; RL-M is a recipient of a Miguel Servet type II Program fellowship from ISCIII, co-funded by the European Social Fund, `Investing in your future´ (CPII21/00004).
Disclosure of Interests: Verónica Pulito-Cueto: None declared, Sara Remuzgo Martinez: None declared, Belén Atienza-Mateo: None declared, Fernanda Genre Romero: None declared, Victor Manuel Mora-Cuesta: None declared, David Iturbe Fernández: None declared, María Sebastián Mora-Gil: None declared, Virginia Portilla: None declared, Alfonso Corrales: None declared, Iván Ferraz-Amaro: None declared, Ricardo Blanco Speakers bureau: Abbvie, Pfizer, Roche, Bristol-Myers, Janssen and MSD, Consultant of: Abbvie, Pfizer, Roche, Bristol-Myers, Janssen and MSD, Grant/research support from: Abbvie, MSD and Roche, Jose Manuel Cifrián-Martínez: None declared, Raquel López-Mejías: None declared, Miguel A González-Gay Speakers bureau: Abbvie, Pfizer, Roche, Sanofi, Lilly, Celgene, MSD and GSK, Grant/research support from: Abbvie, MSD, Jansen and Roche.
DOI: 10.1136/annrheumdis-2023-eular.2007