Disclosure of Interests: Sinead Maguire: None declared, Gillian Fitzgerald Grant/research support from: Recipient of the Bresnihan-Molloy Scholarship funded by AbbVie, Claire Sheehy: None declared, Finbar Barry O'Shea: None declared

DOI: 10.1136/annrheumdis-2019-eular.2501

FRI0681

ASSOCIATION OF BODY COMPOSITION, PHYSICAL ACTIVITY AND PHYSICAL PERFORMANCE WITH KNEE CARTILAGE THICKNESS AND SUBCHONDRAL BONE AREA IN YOUNG ADULTS

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Background: Body composition, physical activity and physical performance may play roles in the incidence of knee osteoarthritis. However, the effects of body composition, physical activity and physical performance on knee cartilage thickness and subchondral bone area in young adults were unknown.

Objectives: To describe associations of body composition, physical activity and physical performance with knee cartilage thickness and subchondral bone area in young adults.

Methods: Body composition, physical activity and physical performance were measured 4-5 years prior to knee magnetic resonance imaging (MRI). Cartilage thickness and subchondral bone area of patella and lateral/medial femorotibial compartment were measured quantitatively from MRI. Total knee cartilage thickness was calculated as the weighted-average according to bone area of each compartment; total knee bone area was calculated as the sum of each compartment. Associations were assessed using linear regression analysis. Age, gender, height (if fat mass or lean mass was predictor) and BMI (if physical activity or physical performance measures were predictors) were examined as potential confounders and were included in the regressions. Mediator was identified using mediation analysis (Stata's medeff command).

Results: Participants were aged 31-40 years, 48% were female (n=186). Greater lean mass, but not fat mass, was positively associated with total knee cartilage thickness ($\beta=6.50 \mu\text{m/kg}$, 95% confidence interval (CI): 0.86 to 12.13) and subchondral bone area ($\beta=13.66 \text{ mm}^2/\text{kg}$, 95% CI: 5.73 to 21.59). Physical performance measures were positively associated with knee cartilage thickness (long jump: $\beta=2.36 \mu\text{m/cm}$, 95% CI 0.68 to 4.04; hand grip strength: $7.65 \mu\text{m/kg}$, 1.53 to 13.77; physical work capacity: $1.04 \mu\text{m/watt}$, 0.27 to 1.81) and subchondral bone area (long jump: $\beta=4.25 \text{ mm}^2/\text{cm}$, 95% CI 1.01 to 7.50; hand grip strength: $19.89 \text{ mm}^2/\text{kg}$, 8.23 to 31.55; leg strength: $3.32 \text{ mm}^2/\text{kg}$, 1.25 to 5.40; physical work capacity: $3.00 \text{ mm}^2/\text{watt}$, 1.54 to 4.45). Mediation analysis suggested these associations were mediated by lean mass (effect mediated: 29-95%). Questionnaire based activity measures (including walking, moderate activity, vigorous activity and total activity) were not associated with total knee cartilage thickness or subchondral bone area.

Conclusion: Greater lean mass and better physical performance measures were associated with greater knee cartilage thickness and subchondral bone area in young adults, and the associations of physical performance were largely mediated by lean mass. These findings suggest lean mass may play an important role in maintaining knee joint health in young adults.

Figure 1: Scatter plots and linear regression lines for associations between lean mass and knee cartilage thickness (A: MFTC; B: LFTC; C: Patella).

R and P values are from models adjusted for age, gender, knee injury and height.

MFTC, medial femorotibial compartment; LFTC, lateral femorotibial compartment.

Disclosure of Interests: : Tao Meng: None declared, Benny Antony: None declared, Alison Venn: None declared, Felix Eckstein Shareholder of: Shareholder of Chondrometrics GmbH, Consultant for: Consulting fees from Merck KGaA, Samumed LLC, Abbvie, Bioclinica, TissueGene, Servier, and Roche, Employee of: Employee of Chondrometrics GmbH, Flavia Cicuttini: None declared, Lyn March: None declared, Marita Cross: None declared, Terence Dwyer: None declared, Graeme Jones: None declared, Laura Laslett: None declared, Changhai Ding: None declared

DOI: 10.1136/annrheumdis-2019-eular.1557

FRI0682

LEISHMANIASIS IN PATIENTSWITH CHRONIC INFLAMMATORY DISEASE TREATED WITH IMMUNOMODULATORS. MULTICENTER ANALYSIS

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Background: Patients with chronic inflammatory disease in treatment with immunosuppressants have an increased risk of opportunistic infections, including leishmaniasis.

Objectives: To describe a multicenter case series of leishmaniasis in patients with chronic inflammatory diseases treated with immunosuppressants. To analyze factors related to the infection.

Methods: Observational retrospective study. We reviewed the clinical history of patients with chronic inflammatory diseases treated with immunosuppressants, who were diagnosed with leishmaniasis between 2007 and 2018. Demographic (age, sex) and clinical (type and time of evolution of the inflammatory disease, comorbidities, current treatment, leishmaniasis form) variables were collected. Immunosuppressant withdrawal, subsequent reintroduction and recurrence were recorded. We analyzed differences in clinical presentation related to anti-TNF α treatment. Statistical analysis was performed using SPSS 22.0 program.

Results: 55 cases were collected. 58,2% were men and the average age was 57,2 (SD 1,9) years. Twenty-one patients had spondyloarthropathy, 17 rheumatoid arthritis, 14 inflammatory bowel disease, 1 systemic lupus erythematosus, 1 Behçet and 1 uveitis. The average duration of the disease was 11,4 (SD 1,4) years and 30,9% of patients had other causes of immunosuppression. Thirty-eight patients received treatment anti-TNF α (19 infliximab, 11 adalimumab, 5 golimumab, 2 certolizumab and 1 etanercept), 15 with DMARD (14 methotrexate, 1 leflunomide), 1 with tocilizumab and 1 with azathioprine. 27,3% patients received corticoids. 52,7% developed cutaneous form, 38,2% visceral form, 7,3% mucocutaneous form and 1 presented visceral and cutaneous involvement. Treatment was withdrawn in 37 cases and it was reintroduced in 23 cases (8 anti-TNF α). Four patients relapsed. More cases of visceral leishmaniasis were seen in patients treated with non-anti-TNF α drugs and in those treated with glucocorticoids. Most of the recurrences were associated with mucocutaneous form.

Conclusion: In our series, the majority of cases of leishmaniasis occurred in patients treated with anti-TNF α , but non-anti-TNF α patients developed more serious forms. It's important to keep in mind this infectious complication in daily clinical practice.

Disclosure of Interests: : L Montolio-Chiva: None declared, Elia Valls-Pascual: None declared, D Ybáñez-García: None declared, À Martínez-Ferrer: None declared, Marta Aguilar-Zamora: None declared, Ana V Orenes Vera: None declared, I Vázquez-Gómez: None declared, A Sendra-García: None declared, JM Paredes Arquíola: None declared, Meritxell Fernandez Matilla: None declared, L Gómez Escolar: None declared, José Miguel Senabre-Gallego: None declared, J Lluch Pons : None declared, C Campos Fernández: None declared, M Robustillo-Villarino : None declared, María Dolores García-Armario: None declared, S Antón-González: None declared, ANA URRUTICOECHEA-ARANA: None

declared, Isabel de la Morena Speakers bureau: Abbvie, Celgene, Pfizer, UCB, Ghebro, Roche, Sanofi, Janssen., J Fiter-Areste: None declared, Vega Jovani: None declared, A Martínez-Cristóbal : None declared, Lourdes Mateo: None declared, Sergi Ordoñez : None declared, D Reina-Sanz: None declared, C Vergara-Dangond: None declared, V Núñez-Monje: None declared, I Torner-Hernández: None declared, Juanjo J Alegre-Sancho: None declared

DOI: 10.1136/annrheumdis-2019-eular.5992

FRI0683

DEFINING THE GUT MICROBIOME IN PATIENTS WITH ANCA-ASSOCIATED VASCULITIS

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Background: Although a link between gut microbiome and autoimmune diseases has been suggested, there is a gap in the understanding of the gut microbiome in ANCA-associated vasculitis (AAV).

Objectives: This study evaluated the gut microbiome in AAV (granulomatosis with polyangiitis (GPA), microscopic polyangiitis, and eosinophilic granulomatosis with polyangiitis) compared to healthy controls.

Methods: Using cross-sectional and longitudinal designs, the gut microbiome was compared among patients with i) newly-diagnosed AAV (active and remission); ii) chronic AAV (active and remission), and iii) healthy controls. Fecal samples were collected using standardized methods and analyzed by sequencing the bacterial 16S rRNA gene (V1-V2 region). Taxa with mean abundance >1% were compared using Wilcoxon rank sum test, correcting for multiple comparisons. Disease severity was assessed with the Birmingham Vasculitis Activity Score for Wegener's Granulomatosis (BVAS/WG). Effects of medications were studied using mixed effects models.

Results: 63 fecal samples were studied: 29 active AAV (15 new diagnosis/14 chronic), 20 in remission, and 14 healthy controls. Compared to controls, patients with active AAV had a different microbial composition ($p=0.01$). There was no statistical difference between the gut microbial composition of controls and patients in remission ($p=0.16$). The relative abundance of the taxa *Dialister* and *Prevotella* were different between active and remission AAV. The relative abundance of the genera *Faecalibacterium* and *Sutterella* were different between active and remission newly-diagnosed AAV (**Figure 1A**). The relative abundance of *Dialister* was significant in patients with high BVAS/WG compared to patients with low BVAS/WG ($p<0.01$) (**Figure 1B**). High BVAS/WG was associated with greater dysbiosis (**Figure 2**); similar results were found in a multivariate linear model ($p=0.02$). The gut microbiome in patients with GPA on immunosuppressive agents was similar to controls ($p=0.54$), whereas the gut microbiome of patients with GPA not on these therapies was significantly different from controls; similar results were found with glucocorticoids and antibiotics use.

Conclusion: Active AAV is associated with an altered gut microbial composition. Patients in clinical remission have microbial composition similar to healthy controls. Immunosuppressive agents, glucocorticoids, and antibiotics may re-establish a healthy gut microbiome. Severe disease activity is associated with worsening gut dysbiosis suggesting a potential role of gut bacteria in the pathogenesis of AAV.

Figure 1. Bacteria with Differential Abundance Between Various Subgroups of Patients with ANCA-Associated Vasculitis (AAV). (A) Compared to patients with AAV in remission, patients with active AAV had a lower proportion of the taxa *Dialister* and *Prevotella* ($p=0.02$ and $p=0.03$, respectively, corrected for false discovery rate). Compared to patients with a new diagnosis of AAV in clinical remission, patients with a new diagnosis of active AAV had a lower proportion of the genera *Faecalibacterium* and *Sutterella* ($p=0.02$ and $p=0.05$, respectively, corrected for false discovery rate). (B) Compared to patients with less disease activity, patients with severe disease had a lower proportion of *Dialister* ($p<0.01$, corrected for false discovery rate).

Figure 2. Scatter Plot of BVAS/WG by Shannon Diversity Index in Patients with Active AAV. High BVAS/WG correlated with a greater gut microbiome dysbiosis (lower Shannon diversity index) in patients with active AAV (Pearson coefficient = -0.35; $p<0.01$).

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Disclosure of Interests: None declared

DOI: 10.1136/annrheumdis-2019-eular.8322

FRI0684

NOVEL MAPPING FUNCTION ILLUSTRATES NONLINEARITY BETWEEN TRIAL ACR RESPONSE, DAS28 CHANGE AND EULAR RESPONSE CRITERIA

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Background: The American College of Rheumatology (ACR) definition of improvement is a standardised, widely used outcome measure for clinical trials in rheumatoid arthritis. In routine clinical practice (and registries),