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Urine metabolic profile in rheumatoid arthritis development

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1 Urine Metabolic Profiles in Rheumatoid Arthritis Development

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 Xavier

4 Abstract

Introduction: Rheumatoid arthritis (RA) is a chronic inflammatory disease characterized
by increased mortality <u>and</u> associated with metabolic disorders including dyslipidaemia,
insulin resistance and cachexia. Since <u>the</u> metabolomic profile is known to vary in
response to different inflammatory conditions, <u>those</u> <u>metabolite</u> analysis could
substantially improve diagnosis and prognosis.

10 Objective: To analyses the urine metabolic profile and assess to <u>its</u> correlation with 11 body composition parameters and disease activity of RA patients.

12 Methods: Seventy-nine RA patients, according to ACR/EULAR 2010 classification 13 criteria, aged between 40 and 70 years, were recruited and followed for 12 months. 14 Disease activity, body composition, fatigue and urine metabolome were measured. Body composition was assessed by total body dual-energy x-ray absorptiometry (DXA) 15 for measurement of appendicular lean mass index (ALMI). Disease activity was 16 assessed by Disease Activity Score-28 (DAS28) with erythrocyte sedimentation rate 17 (ESR). Fatigue as assessed by the Functional Assessment of Chronic Illness Therapy 18 19 (FACIT). Nuclear Magnetic Ressonance (NMR) spectroscopy measurements were 20 performed to evaluate the profile of metabolic changes during the disease 21 development, resulting in the identification of 48 metabolites in urine collected at the 22 baseline and after one year-after. Frequency analysis, Pearson Correlation and 23 Multivariate data analysis with orthogonal projections to latent structures (OPLS) 24 method were performed and a statistical significance was considered as p<0.05.

Results: The study population was characterized by the majority of women 25 (86.7%), mean age 56 years old, around 80% with anti-CPP and Rheumatoid 26 Factor reagent. During the one year of follow-up, there was no huge-substantial 27 variation in the DAS28 measurement (baseline: 3,8, after 12 months: 4,0). It is 28 By for this reason, we belive believe that we could not find any significant 29 correlation between the metabolome pattern and DAS28 score (p>0.05). 30 However, Tthere was a significant increase of methyl-histidine, creatinine, L-31 32 serine and urea by during the development of the disease, metabolites that are involved in the muscular muscle-related metabolismconstitutions pathways. 33 Fatigue was positively correlated with L-serine/creatinine (r: - 0,4, p<0.001). 34 Appendicular lean mass index (ALMI) also presented showed a difference when 35 which correlated to-with the increase of urea and creatinine (r: 0,3, p<0.019). 36

Conclusion: The potential biomarkers indicated that the RA metabolic disturbance might be associated with inflammation, injury, fatigue and amino acid metabolism. Those These findings suggest that urine metabolome analysis may be an interesting approach to monitoring rheumatological disease related

- 41 to <u>muscle changes and fatigue, which are of major concern to patients</u>, and this
- 42 that could be more <u>further</u> explored in future trials<u>studies</u>.