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Background: Membrane-bound receptor for advanced glycation endproducts (mRAGE) expression increases in the presence of its ligands (e.g., High Mobility Group Box 1, HMGB1) and triggers an inflammatory immune response. In contrast, soluble RAGE (sRAGE) acts as a decoy receptor and downmodulates inflammation. Some studies have demonstrated that decreased sRAGE levels are negatively correlated with disease activity in juvenile idiopathic arthritis (JIA) but expression of mRAGE has not been studied.

Objectives: The aim of this study is to evaluate mRAGE and sRAGE on peripheral blood (PB) and synovial fluid (SF) mononuclear cells (MC) of patients with JIA and healthy controls and to assess whether there is an association with established inflammatory markers and clinical measures.

Methods: Matching samples of blood and synovial fluid were collected from patients with JIA (n=33) with active arthritis. RAGE expression on mononuclear cells was analyzed using flow cytometry. The intensity of RAGE expression was measured as mean fluorescence intensity (MFI). Levels of sRAGE and HMGB1 were determined with a specific ELISA kit in the serum and synovial fluid (SF) of patients with JIA. Relation between cellular RAGE and sRAGE with disease activity parameters [JADAS71, CHAQ, C reactive protein (CRP) and erythrocyte sedimentation rate (ESR)] and HMGB1 were described. We compare mRAGE expression in PBMC and serum sRAGE levels between JIA patients and age-matched healthy controls (n=43).

Results: 24 patients with oligoarticular JIA and 9 patients with polyarticular JIA were studied, 8/23 females with a mean age of 7.7 ± 3.6 . MFI of mRAGE in PBMC and SFMC of JIA patients were significantly decreased in comparison with MFI of mRAGE in PBMC of healthy controls. Although serum levels of sRAGE were not different between patients and controls, sRAGE levels were lower in SF (570.2 [458.5-773.0]) compared to PB (759.7 [628.6-890.3]) in JIA patients, especially in the polyarticular group. By contrast, HMGB1 levels in SF were significantly higher than in PB of JIA patients. MFI of mRAGE in PBMC was correlated with JADAS71 (p 0.01) and CHAQ (p 0.07). There were no significant correlations between serum sRAGE and HMGB1 with JADAS71, CHAQ, CRP and ESR.

Conclusion: The sRAGE/RAGE system may be a modulator of inflammation in JIA patients. Differences between levels of sRAGE and HMGB1 in synovial fluid versus peripheral blood in patients with JIA may suggest a local role in the pathogenesis of JIA.

	JIA patients (n=33)	Healthy controls (n=43)
Age (years)	7.7 ± 3.6	7.9 ± 4.7 SD
Sex (boys/girls)	9/24	30/13
JIA category		
Oligoarticular	24	
Polyarticular	9	
Treatment		
NSAIDs	20	
MTX	12	
ANTI-TNF α	1	
ESR (mm/h)	26.3 (4-78)	
CRP (mg/dL)	1.4 (0.5-6.5)	
CHAQ	0.375 (0.2-3.75)	
JADAS-71	8.1 (2.8-16.3)	

Disclosure of Interests: Daniel Clemente Paid instructor for: Novartis, Speakers bureau: Novartis, Abvie, Roche, Sobi, Alberto García-Salido: None declared, Gustavo Melen: None declared, Manuel Ramírez-Orellana: None declared, J.C. López Robledillo: None declared

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FRI0452

THE IMPACT OF SINGLE NUCLEOTIDE POLYMORPHISMS IN ADORA2A AND ADORA3 ON THE EARLY RESPONSE TO METHOTREXATE AND PRESENCE OF THERAPY SIDE EFFECTS IN CHILDREN WITH JUVENILE IDIOPATHIC ARTHRITIS

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Background: Juvenile idiopathic arthritis (JIA) is the most frequent rheumatic disease in children, with an estimated prevalence between 16 and

150 per 100 000 [1]. Methotrexate (MTX) administered at the dose 10-15mg/m² is currently recommended as the first-line treatment in most of JIA subtypes [2]. Despite its widespread use in rheumatology, the mechanism of MTX immunomodulatory action remains incompletely understood [3]. Free adenosine is one of the particles possibly associated with the action of MTX, acting via three types of adenosine receptor: ADORA2A, ADORA2B, and ADORA3 [4].

Objectives: The aim of our study was to determine the association between single nucleotide polymorphisms in ADORA2A (rs2236624, rs2298383) and ADORA3 (rs3393) receptors genes on the disease activity and presence of MTX therapy side effects in patients with JIA.

Methods: One hundred children with JIA of all subtypes treated with MTX were recruited to the study. Demographic and clinical parameters were collected at the baseline of MTX therapy and on a control visit 4-6 months (median 5.09 months) after starting MTX. The clinical parameters included inflammatory markers values, number of joints with active arthritis, number of joints with restricted range of movement, physician's global assessment of disease activity, parent/patient global assessment of overall well-being, functional ability (measured by the Childhood Health Assessment Questionnaire - CHAQ) and the value of Juvenile Idiopathic Arthritis Disease Activity Score 71 (JADAS 71). Presence of MTX side effects was evaluated on the control visit. SNP genotyping was performed using genomic DNA isolated from peripheral blood samples.

Results: Both polymorphic variants of ADORA2A (rs2236624, rs2298383 - CC/CT) were significantly associated with 3.5 times higher odds of gastrointestinal side effects occurrence (OR: 3.52, 95%CI: 1.12-11.03, p=0.03 and OR: 3.49, 95%CI: 0.89-13.66 p=0.07) after adjustment to age, sex, dose and route of MTX administration. In addition, children with the ADORA3 rs3393 polymorphic variant (CT/CC) after six months of MTX treatment had significantly lower number of joints with active arthritis (0.0 vs 1.0, p=0.04), lower JADAS 71 score (3.0 vs 5.1, p=0.16) and lower value of CRP (0.6 vs 2.4, p=0.02).

Conclusion: Although future studies are needed to verify our findings, polymorphisms in ADORA2A and ADORA3 genes may become the determinants of MTX treatment efficacy and gastrointestinal toxicity in children with JIA.

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FRI0453

COMPARATIVE GENE PROFILE IN MONOCYTES FROM CHILDHOOD- AND ADULT-ONSET SYSTEMIC LUPUS ERYTHEMATOSUS: CLUES TO DIFFERENT SYSTEMIC INVOLVEMENT

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Background:

Objectives: 1. This study, developed within the Innovative Medicines Initiative Joint Undertaking project PRECISESADS framework, aimed at identify specific inflammatory and oxidative stress determinants involved in the enhanced CV-risk present in SLE patients and to analyze the relevance of the sustained positivity for anti-dsDNA on the establishment of their atherothrombotic status.

Methods: One hundred and twenty-four SLE consecutive patients (not including patients with associated antiphospholipid syndrome), belonging to the PRECISESADS project, were evaluated for the presence of CVD and its association