Objectives: To identify HLA alleles associated with susceptibility to develop an IMID in Paraguayan patients controlled in a reference centre. Methods: Paraguayan IMID patients were recruited from the Rheumatology Department of Hospital de Clínicas, Paraguay. IMID HLA II frequencies were compared with a control group of 50 unrelated individuals without disease and from the same geographic origin. Genotyping for HLA was performed using Luminex PCR technology. The association analysis with the IMID risks was performed using the chi-square allelic test.

Results: 249 IMID patients were included in the study. Patients with RA included 95 lupus, 104 rheumatoid arthritis and 50 systemic sclerosis. The study included 86 patients with psoriatic arthritis (PsA) and 162 healthy blood donors that served as a control group. The different associations between IMIDs and alleles were identified (table 1).

Abstract AB0005 – Table 1. List of associated alleles stratified by disease

<table>
<thead>
<tr>
<th>Allele (Systemic Lupus Erythematosus Cohort)</th>
<th>P-value</th>
<th>OR</th>
</tr>
</thead>
<tbody>
<tr>
<td>HLA-DQA1*02:01</td>
<td>0.0253</td>
<td>14</td>
</tr>
</tbody>
</table>


<table>
<thead>
<tr>
<th>Allele (Rheumatoid Arthritis Cohort)</th>
<th>P-value</th>
<th>OR</th>
</tr>
</thead>
<tbody>
<tr>
<td>HLA-DQB1*06:02</td>
<td>0.0367</td>
<td>0.11</td>
</tr>
<tr>
<td>HLA-DPB1*02:01</td>
<td>0.0003</td>
<td>54.62</td>
</tr>
<tr>
<td>HLA-DPB1*03:01</td>
<td>0.0010</td>
<td>7.92</td>
</tr>
<tr>
<td>HLA-DPB1*04:01</td>
<td>0.0001</td>
<td>29.69</td>
</tr>
<tr>
<td>HLA-DQA1*02:01</td>
<td>0.0467</td>
<td>0.24</td>
</tr>
<tr>
<td>HLA-DPB1*04:01</td>
<td>0.0022</td>
<td>0.07</td>
</tr>
<tr>
<td>HLA-DQA1*02:01</td>
<td>0.0022</td>
<td>0.029</td>
</tr>
</tbody>
</table>

Conclusions: In the genetic association analysis, already known associations have been replicated and new ones previously unpublished have been identified in Paraguayan IMID patients. This is the first genetic association study in IMID patients Paraguayan origin.

Disclosure of Interest: None declared


There was no significant difference in the miR-26a serum levels between patients and controls. Also miR-26a serum levels did not significantly differed between RA patients before, 3 and 6 months after the implementation of biological therapy with TNF-alpha inhibitors.

Conclusions: These results imply that miR-26a rs7372209 allelic variants differentially affect the risk of rheumatoid and psoriatic arthritis while anti-TNF biological treatment seems not to affect the miR-26a expression in RA patients.

Disclosure of Interest: None declared


AB0006

MIR-26A POLYMORPHISM IS ASSOCIATED WITH SUSCEPTIBILITY OF RHEUMATOID AND PSORIATIC ARTHRITIS

J. Swiertcek, R. Sokolik, M. Kozowski, L. Korman, P. Wiland, K. Bogunia-Kubicka. 1Department of Rheumatology and Internal Medicine, Medical University; 2Laboratory of Clinical Immunogenetics and Pharmacogenetics, Hirschfeld Institute of Immunology and Experimental Therapy, Polish Academy of Sciences, Wroclaw, Poland

Background: Serum levels of miR-26a has been reported to act as potential biomarker of rheumatic diseases.

Objectives: The aim of the study was to analyse the genetic variation and expression of miR-26a as potential diagnostic and/or prognostic markers of rheumatic diseases.

Methods: The miR-26a polymorphism was examined in 111 patients with rheumatoid arthritis (RA), 86 patients with psoriatic arthritis (PsA) and 162 healthy blood donors that served as a control group. Genotyping for miR-26a rs7372209 was performed using a LightSNiP assay. For analysis of the miR-26a expression, RNA was isolated from sera of 15 RA patients and controls. The similar tendency was observed in the expression of TNFA, which gene product was significantly decreased (4.28 ± 0.009). In addition, mRNA expression of FoxP3 in peripheral blood of RA patients.

Methods: Total RNA from peripheral blood was isolated from 32 patients matching the ACR/EULAR 2013 criteria for RA and 27 healthy controls. Quantitative real-time polymerase chain reaction was performed for the 8 genes of interests, using the TaqMan detection system. Relative quantitative evaluation of mRNAs was performed by the comparative ΔΔCt method and results were presented as n-fold mean difference (RO-relative quantity) of target genes relative to calibrator (healthy controls) after normalisation to the reference genes (GAPDH and 18srRNA). Serum quantities of cytokines were measured by ELISA.

Results: From studied pro-inflammatory cytokine genes, we found down-regulation in the following order: IL6 + TNFA=IL12B; up regulation of IL23A and no change in IL18 gene expression in RA patients group compared to healthy controls. For anti-inflammatory genes we detected significantly increased quantity for IL10 mRNA and no change for TGFbeta1 mRNA. The most profound down-regulation (more than 7-fold) was observed for IL6 gene (p<0.001), while the serum level of the same cytokine was significantly increased as compared to the same controls. The similar tendency was observed in the expression of TNFA, which gene expression was approximately 2-fold down-regulated, whereas serum levels were increased. IL23B mRNA were slightly but not significantly decreased (RO=0.709; p=0.169) in RA patients. An upregulation of IL-23 was detected for IL23A gene (RO=2.422; p=0.002) and serum level of IL-23 as well. TGFbeta1 mRNA levels were approximately equal in patients and controls in contrast to IL-10, which was upregulated in both mRNA (RO=1.5; p=0.034) and serum levels (over 6.6 fold; p<0.05). In addition, mRNA expression of FoxP3, a master transcription factor for Treg subset was also down-regulated over 4-fold in RA patients (p<0.001). A positive correlation was found between gene expression of IL6 with FoxP3, TNFA and TGFbeta1 in RA (r=0.744, p=0.004; r=0.6, p=0.03; r=0.556, p=0.048, respectively).

Conclusions: Our results demonstrated significant differences in the expression of mRNA encoded cytokines and their protein quantities at systemic level of RA patients, mostly on IL-23, IL-6 and TNF-alpha.

Disclosure of Interest: None declared


AB0007

ASSOCIATION AT SYSTEMIC LEVELS OF CYTOKINE MRNAS AND PROTEIN QUANTITIES IN RHEUMATOID ARTHRITIS

I. Manolova, M.G. Ivanova, G. Vasilev, R. Stoilov, L. Mitева, S. Stanilova. 1Department of Molecular Biology, Immunology and Medical Genetics, Medical Faculty, Traika University, Stara Zagora; 2Clinic of Rheumatology, University Hospital “St. Iv. Rilski”, Medical Faculty, Medical University; 3Laboratory of Clinical Immunogenetics, University Hospital “St. Ivan Rilski”, Medical Faculty, Medical University, Sofia, Bulgaria

Background: Rheumatoid arthritis (RA) is an autoimmune inflammatory disease, characterised by chronic synovitis, bone and cartilage destruction, as well as systemic manifestation. In accordance with the pivotal role of cytokines in autoimmunity and their impact as biomarkers, we analysed gene expression at both mRNA and protein levels of several cytokines in peripheral blood of RA patients.

Objectives: The aim of the present study was to investigate the gene expressions at mRNA and protein levels of main pro-inflammatory (TNF-α, IL-18, IL-12p40; IL-23, IL-6) and immunosuppressive (TGF-β1 and IL10) cytokines and transcription factor Foxp3 in peripheral blood of RA patients.

Methods: Total RNA from peripheral blood was isolated from 32 patients matching the ACR/EULAR 2013 criteria for RA and 27 healthy controls. Quantitative real-time polymerase chain reaction was performed for the 8 genes of interests, using the TaqMan detection system. Relative quantitative evaluation of mRNAs was performed by the comparative ΔΔCt method and results were presented as n-fold mean difference (RO-relative quantity) of target genes relative to calibrator (healthy controls) after normalisation to the reference genes (GAPDH and 18srRNA). Serum quantities of cytokines were measured by ELISA.

Results: From studied pro-inflammatory cytokine genes, we found down-regulation in the following order: IL6 + TNFA=IL12B; up regulation of IL23A and no change in IL18 gene expression in RA patients group compared to healthy controls. For anti-inflammatory genes we detected significantly increased quantity for IL10 mRNA and no change for TGFbeta1 mRNA. The most profound down-regulation (more than 7-fold) was observed for IL6 gene (p<0.001), while the serum level of the same cytokine was significantly increased as compared to the same controls. The similar tendency was observed in the expression of TNFA, which gene expression was approximately 2-fold down-regulated, whereas serum levels were increased. IL23B mRNA were slightly but not significantly decreased (RO=0.709; p=0.169) in RA patients. An upregulation of IL-23 was detected for IL23A gene (RO=2.422; p=0.002) and serum level of IL-23 as well. TGFbeta1 mRNA levels were approximately equal in patients and controls in contrast to IL-10, which was upregulated in both mRNA (RO=1.5; p=0.034) and serum levels (over 6.6 fold; p<0.05). In addition, mRNA expression of FoxP3, a master transcription factor for Treg subset was also down-regulated over 4-fold in RA patients (p<0.001). A positive correlation was found between gene expression of IL6 with FoxP3, TNFA and TGFbeta1 in RA (r=0.744, p=0.004; r=0.6, p=0.03; r=0.556, p=0.048, respectively).

Conclusions: Our results demonstrated significant differences in the expression of mRNA encoded cytokines and their protein quantities at systemic level of RA patients, mostly on IL-23, IL-6 and TNF-alpha.

Disclosure of Interest: None declared


AB0008

CROSS-TALK BETWEEN BONE TurnOVER AND CARDIOVASCULAR DISEASE: ASSOCIATION OF MICRORNAs EXPRESSION, FRACTURE AND ABDOMINAL AORTIC CALCIFICATIONS

M.-E. Pickering, M. Crosse, M. Millier, E. Somay-Rendu, J.-C. Rousseau, O. Bové, P. Szulc, R. Chapurlat, Hospices Civils de Lyon, INSERM U1033, Lyon, France

Background: MicroRNAs (miRs) have emerged as pivotal epigenetic key actors of gene regulation and several miRs have been shown to be at the crossroads of angiogenesis and of bone turnover, taking part in the calcification process by acting on osteoblasts and osteoclasts. 1 Calcification of the aortic media is highly