Genotyping Assay in blood samples obtained from 47 patients BD diagnosed according to 1990 international criteria for behcet disease and 50 matched healthy controls. Disease activity was done using BD current activity form (BDCAF).
Results: Study of miRNA-499 polymorphism, showed that the genotype frequencies of TT, CT, and CC were 21.3%, 63.8%, and 14.9% in BD patients and 18.0%, 52.0%, and 30.0% in the control group respectively. A significant increase in the relative expression of miRNA-499 was found in BD patients compared to control ($P<0.05$). There was no significant relation between relative expression of miRNA-499 and activity of BD patients assessed by BDCAF ($P>0.05$). In addition there was association between genotypes of miRNA-499 and posterior uveitis ($P<0.05$). There was association of the relative expression of miRNA-499 with miRNA-499 (rs3746444) polymorphism and vascular manifestations ($P<0.05$).
Conclusions: Genotyping of miRNA-499 showed higher percentage of TT genotype in BD patients than control and also miRNA relative expession, they may be implicated in pathogenesis of the disease. Genotype TT for miRNA-499 is associated with posterior uveitis. miRNA relative expression is associated with vascular manifestations and aneurysm.
Disclosure of Interest: None declared
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AB0007 SHARED GENETIC PREDISPOSITION IN RHEUMATOID ARTHRITIS–INTERSTITIAL LUNG DISEASE AND FAMILIAL PULMONARY FIBROSIS

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Background: Despite its high prevalence and mortality, little is known about the pathogenesis of RA–associated interstitial lung disease (RA-ILD). Given that familial pulmonary fibrosis (FPF) and RA–ILD frequently share the usual interstitial pneumonia pattern and common environmental risk factors, we hypothesized that the two diseases may share additional risk factors including FPF-linked genes.
Objectives: Our aim was to identify coding mutations of FPF-risk genes associated with RA-ILD.
Methods: We used whole-exome sequencing (WES) followed by restricted analysis of a discrete number of FPF-linked genes and performed a Burden test to assess the excess number of mutations in RA–ILD patients compared to controls.
Results: Among the 101 RA–ILD patients included, 12 (11.9%) had 13 WES-identified heterozygous mutations in the *TERT*, *RTEL1*, *PARN* or *SFTPC* coding regions. The burden test, based on 81 RA–ILD patients and 1010 controls of European ancestry, revealed an excess of *TERT*, *RTEL1*, *PARN* or *SFTPC* mutations for RA–ILD patients ($p=9.45'10^{-4}$, odds ratio [OR] 3.17 95% CI 1.53–6.12). Telomeres were shorter for RA-ILD patients with a *TERT*, *RTEL1* or *PARN* mutation than controls ($p=2.87x10^{-2}$).
Conclusions: Our results support the contribution of FPF-linked genes to RA–ILD susceptibility.
Disclosure of Interest: None declared
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AB0008 THE ASSOCIATION OF THE PTPN22 RS2476601 GENE POLYMORPHISM WITH JUVENILE IDIOPATHIC ARTHRITIS IN CHILDREN FROM RUSSIA

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Background: Juvenile idiopathic arthritis (JIA) is the most common chronic rheumatic disease in children. The exact cause of the disease is still unknown, but seems to be related to both genetic and environmental factors [1]. The protein tyrosine phosphatase non-receptor type 22 (*PTPN22*) gene single-nucleotide polymorphism (SNP) rs2476601 was shown to be associated with JIA in different populations, but according to resent reports this association is restricted only to females [2,3].
Objectives: The aim of the study was to determine whether the *PTPN22* rs2476601 SNP is associated with the development of JIA and its subtypes in children from Russia.
Methods: The study included 330 patients with JIA and 346 healthy controls from Russia. Genotyping was performed using real-time PCR method and statistical analysis - using two-tailed Fisher's exact test (p), odds ratio (OR), 95% confidence interval (95% CI).
Results: The frequencies of the genotype AG and the allele A were significantly higher and the frequencies of the genotype GG and the allele G were significantly lower in patients with JIA than in controls (p=0.016, OR=1.65, 95% CI 1.10–2.48; p=0.028, OR=1.48, 95% CI 1.05–2.08; p=0.016, OR=0.62, 95% CI 0.43–0.91; p=0.028, OR=0.68, 95% CI 0.48–0.95, correspondingly). The same analysis was then performed separately for patients with two the most frequent ILAR subtypes: persistent oligoarthritis (n=106) and RF-negative polyarthritis (n=85). Significant associations similar to those in the whole JIA group were found only for persistent oligoarthritis (p=0.018 for the genotype AG; p=0.037 for the allele A; p=0.022 for the genotype GG; p=0.037 for the allele G). No significant differences were found for patients with RF-negative polyarthritis ($p>0.6$). Sex-stratified analysis showed that for the whole JIA group and for persistent oligoarthritis the association with the *PTPN22* rs2476601 SNP is restricted only for girls (for girls with the genotype AG: p=0.024 and p=0.0098; with the allele A: p=0.016 and p=0.0061; with the genotype GG: p=0.015 and p=0.0047; with the allele G: p=0.016 and p=0.0061, correspondingly; for boys: $p>0.2$ for all comparisons).
Conclusions: In this study we revealed the association of the *PTPN22* rs2476601 SNP with the development of JIA and its persistent oligoarticular subtype in girls from Russia.
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AB0009 GENOMIC SIGNATURES MAY BE ASSOCIATED WITH VASCULAR PATHOLOGY ASSOCIATED WITH RHEUMATOID ARTHRITIS

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Background: Accelerated atherosclerosis and cardiovascular (CV) disease have been associated with rheumatoid arthritis (RA). Many genes have been implicated in atherosclerosis, RA or both. However, most of these studies described SNPs in *CD40, SMAD3, HLADR, CTLA4* and other alleles. Very few studies on genetic signatures have been performed that would link RA and CV pathology. We have previously associated some genomic profiles with pathological carotid atherosclerosis (ccIMT), arterial stiffness (PWV) and brachial artery flow-mediated vasodilation (FMD). In other studies we have also found 165 genes that separated anti-TNF responder patients from non-responders.
Objectives: Here we looked for associations between clinical and "vascular" response to biologics and vascular pathology in RA patients.
Methods: In this study, 19 RA patients were treated with either etanercept (ETN) or certolizumab pegol (CZP) for one year. We separated responders (R) and non-responders (NR) according to EULAR response criteria. Microarray gene expression study was performed (Affymetrix) followed by analysis using the GeneSpring software, hierarchy clustering and principal component analysis (PCA). "Vascular response" (VR) to biologics was defined as an at least 20% improvement in FMD, ccIMT or PWV. Good Vascular Response (GVR) was defined as an at least 20% improvement in two or three of these variables.
Results: Among the 19 patients, 13 were R and 6 were NR. With respect to VR, FMD, ccIMT and PWV responded to anti-TNF treatment in 10, 9 and 8 patients, respectively. GVR was observed in 8 patients and 5 patients had VR in all 3 parameters. When comparing clinical response and VR, 7 out of 8 patients showing GVR also had good clinical response to biologics. Up-regulation of 99 and down-regulation of 67 genes separated clinical R and NR patients. Significant correlation was found between ccIMT improvement upon biological therapy and clinical response (R=0.418, p=0.04).
Conclusions: Genomic signature analysis may be able to separate clinical responders and non-responders to biologics, as well as patients that show or do not show imporvement of vascular pathology.
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