AB0156 A NOVEL ASSOCIATION OF TLR-2 (23 BPINS/DEL: RS111200466) POLYMORPHISM WITH ANKYLOSING SPONDYLITIS – A POSSIBLE ROLE IN DISEASE SUSCEPTIBILITY: A HOSPITAL BASED CASE-CONTROL STUDY

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Background: Role of innate immunity in pathogenesis of ankylosing spondylitis (AS) has been well documented[1]. Higher expression of TLR2 has been reported in AS patients and associated with clinical severity[2]. Recently, a functional 23bp ins/del polymorphism at 5'UTR of TLR2 gene has been reported and association of variant with elevated TLR2 surface expression and proinflammatory molecules has been elegantly demonstrated[3]. This is associated with high TNF-alpha levels, one of the key molecules in the pathogenesis of AS [4]. In this preliminary study, we investigated the possible role of TLR2 (23bp ins/del) polymorphism with AS in a cohort from Odisha, India.
Objectives: To investigate the role of TLR-2 (23 bp ins/del: rs111200466) Polymorphism in Ankylosing Spondylitis
Methods: AS patients (n = 101), who fulfilled the ASAS classification criteria for axial spondyloarthritis or ASAS classification criteria for peripheral spondyloarthritis were enrolled along with 100 healthy age matched controls from similar geographical areas. Patients were examined in detail and BASDAI/BASFI recorded. TLR2 (23 bp ins/del) polymorphism was genotyped by polymerase chain reaction. Genotype and allele distribution among patients and controls were compared by Fisher's exact test.
Results: All patients enrolled in the present study were males. The mean age of AS patients and healthy controls was 31.21±11.43 and 28.28±9.62 years, respectively. At the time of enrolment, mean disease duration of patients was 2.07±1.13 years. BASDAI and BASFI scores were above 5. Distribution of TLR2 (23 bp ins/del) polymorphism was in accordance with Hardy-Weinberg Equilibrium. Prevalence of del/del genotype was significantly higher in AS patients compared to healthy controls (P=0.01, OR=5.65), indicating a possible contributory role of TLR2 on predisposition to AS. Distribution of heterozygous genotype (ins/del) and minor allele (del) were comparable among different clinical categories. Furthermore, no significant association of TLR-2 polymorphism was observed with disease severity.
Conclusion: TLR2 5'UTR homozygous mutants (23 bp deletion) were significantly associated with patients of AS in but not with disease severity. Larger sample size and levels of TNF alpha and IL17 in the mutants will further improve the understanding of its role in AS.

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Disclosure of Interests: None declared
DOI: 10.1136/annrheumdis-2019-eular.5566

AB0157 SYNOVIAL FLUID PROTEOMICS IN PATIENTS WITH ANKYLOSING SPONDYLITIS

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Background: Ankylosing Spondylitis (AS), affecting 0.5% of the population, is a chronic inflammatory rheumatic disease affecting the axial skeleton and peripheral joints. When peripheral arthritis in ankylosing spondylitis (AS) develops early in the disease course it is a predictor of more aggressive disease. SF is in contact with the primary tissues affected by arthritic diseases and has been implicated in disease pathophysiology. Therefore it is an excellent source for discovery of biomarkers.
Objectives: We used proteomic analysis using SFs from AS patients and other arthritis patients in order to discover novel diagnostic markers for AS. Our aim was to identify differentially expressed protein mediators in synovial fluid of ankylosing spondylitis.
Methods: A Total of 40 SF samples from 10 AS and each 10 controls [Osteoarthritis (OA), Rheumatoid Arthritis (RA), gouty arthritis (Gout)] were collected. Liquid chromatography and tandem mass spectrometry (LC-MS/MS), to identify differentially expressed proteins based on the ratios of the extracted ion current of each protein between the four groups. Among the 9 proteins showing 1.5 fold change, 8 were verified with the exception of the abundant protein Haptoglobin (HP). Matrix metalloproteinase-1(MMP1) and Matrix metalloproteinase-3(MMP3) were used as a positive control, and the remaining 6 proteins were subjected to western blot analysis.
Results: We identified 9 proteins that were found to be more than 1.5-fold differentially expressed in SF of AS patients compared to control groups. Proteins such as HP, MMP1, MMP3, Serum amyloid P-component(APCS), Complement factor H-related protein 5(CFHR5), Fumarylacetoacetase(FAH), Mannose-binding lectin2(MBL2), Complement component C9(C9) and Complement C4-A(C4A) were found to be upregulated in the SF of AS patients. CFHR5 and C9 were reported in previous studies with AS serum. APCS was reported in SF as well as serum. However, FAH, C4A and MBL2 were newly discovered through this analysis. We were able to verify the unique expression level of C9 and CFHR5 in AS sample using western blot analysis compared to the other three diseases.
Conclusion: We performed quantitatively proteomic profiling of the respective SF sample from 4 diseases, i.e., AS, OA, RA, and GOUT, by LC-MS/MS. The systematic comparative proteomic analysis of the four groups together was carried out for the first time, leading to several differentially expressed proteins in AS. Among them, we expect C9 and CFHR5, which expression levels were confirmed by western blot analysis, can be a potential biomarker for AS.

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Acknowledgement: This research was supported by the National Research Foundation of Korea (NRF) funded by the Ministry of Science, ICT & Future Planning (2017R1C1B5017278)
Disclosure of Interests: None declared
DOI: 10.1136/annrheumdis-2019-eular.2017

AB0157B FREQUENCY AND SPECTRUM OF ANEMIC SYNDROME IN PATIENTS WITH ANKYLOSING SPONDYLITIS, PECULIARITIES OF CYTOMETRIC CHARACTERISTICS AND HEMOPOIESIS

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Background: Anemia is one of the most common extraarticular manifestations in patients with ankylosing spondylitis (AS). According to various sources, from 18.5 to 45.8% of patients with AS have anemia. In the pathogenesis of anemic syndrome in the AS, a leading role is given to proinflammatory cytokines (IL-1, IL-6, and TNF-alpha), which is associated with the development of anemia of chronic disease (ACD) in this category of patients. Another type of anemia in patients with AS is iron deficiency anemia (IDA), and the relationship between the latter and the ACD varies significantly according to various literature data. As for other types of anemia in the AS, they are represented by anemia caused by drugs.
Objectives: The purpose of the work was to investigate the prevalence of anemia in the Ukrainian population of patients with AS and evaluate the hematopoiesis in patients with the main types of it.
Methods: The group with anemia included patients whose haemoglobin levels were below 120 g/l. The diagnosis of AS was determined according to the modified New York criteria (1984). Laboratory methods of research (general analysis of blood, erythrocytes, haemoglobin, color index, serum iron, total iron binding capacity (TIBC) included in the list of standard examinations of patients were performed according to standard methods. To verify the diagnosis of ACD, ferritin (FN) and levels of soluble transferrin receptor (sTfR) were determined.
Results: 118 patients with AS were included into the study, 11 (32.3%) females and 23 (67.7%) males. It was found that 34 patients (28.8%) had anemia. Anemia of mild degree was manifested in 27 (79.4%) patients and with moderate severity - 7 (20.6%) patients. Among 34 patients with anemia, patients with ACD - 15 (44.1%) predominated. In the second place, 10 (29.4%) showed a combination of ACD with functional deficiency of iron, and 8 (23.5%) patients had signs of IDA. Only one of the subjects had signs of scarce anemia. Consequently, anemic