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AB0022 INTERRELATIONS OF INCREASED AXIAL SPONDYLOARTHRITIS ACTIVITY AND THE SERUM CONCENTRATION OF IMMUNOGLOBULIN A TO CD74 WITH GENETIC POLYMORPHISMS OF INTERLEUKIN 17 ALLELES

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Background: Genetic predisposition takes one of the main parts at pathogenesis of axial spondyloarthritis (axSpA). Currently, HLA-B27 is a single genetic marker that used in classification criteria of axSpA. However, the presence of HLA-B27 does not affect the activity of the disease. An alternative biomarker of axSpA activity could be an immunoglobulin (Ig) A antibody to an invariant chain peptide associated with class II human leukocyte antigen (HLA) (anti-CD74).

Objectives: The goal is to determine genetic polymorphisms of IL17 alleles prevalence in patients (pts) with axSpA and their interrelations with the disease activity and concentration of IgA to CD74.

Methods: In 48 patients with a reliable diagnosis of axSpA, aged 18 to 69 years ASDAS, BASDAI, BASFI were calculated. The polymorphisms of alleles of interleukin (IL)-17A197 a/g, IL-17F7 histidine (His)/arginine (Arg), IL-17F11139 c/g, HLA-B27 were evaluated. Serum concentration of IgA to CD74 was measured (the normal reference interval according to the instructions for the laboratory kit for serum IgA to CD74 is 0-12.0 U/L).

Results: The mean age of pts was 45.1±14.2 years, male 72.9%, BASDAI 2.99±0.28, ASDAS 2.29±0.16 (Cronbach's alpha for the scales – 0.830), IgA to CD74 16.9±11.0 mg/L. The most often found polymorphisms of interleukin-17 alleles demonstrated in **table 1**.

Table 1. Interleukin-17 alleles' polymorphisms in patients with axial spondyloarthritis, n=48

Indicator	Pts with presence of polymorphism, n	Indicator	Pts with presence of polymorphism, n
IL-17A-197 AA	14	IL-17F7 his/his	45
IL-17A-197 GG	18	IL-17F7 his/arg	2
IL-17A-197 GG	16	IL-17F7 arg/arg	1
IL-17F-11139 CG	26	IL-17F-11139 CC	22

Exceeded levels of IgA to CD74 were identified at 96 pts (70.1%). The factor analysis showed a relationship between ASDAS (R=0.857), BASDAI (R=0.842), BASFI (R=0.857) and level of IgA to CD74 (R=0.667**), (table 2).**

Table 2. Interrelations between serum concentration of IgA to CD74, the activity indices and genetic polymorphisms of interleukin-17 alleles in axSpA patients (factor loads), n=48

Indicator	Factor loading (R)		
Factor	Factor 1	Factor	Factor 1
IgA anti-CD74	0.525	0.925	0.667
BASDAI	0.734	0.816	0.842
ASDAS	0.657	0.576	0.857
BASFI	0.545		0.820
IL-17 F7 His/His	-0.421		
IL-17F7 His/Arg	0.631	0.544	

An increase in the factor load indices for IgA to CD74 (R=0.925) was established, provided that the IL-17F genotype is homozygous for the his / arg allele (R=0.544). The genotypes IL-17F his/his showed an inverse interrelation with the increase in serum IgA to CD74 level (R=-0.421).

Conclusion: Serum concentration of IgA to CD74 exceeded normal reference level in axSpA patients in 70.1% of cases that was associated with ASDAS and BASDAI levels. Presence of heterozygote IL-17F polymorphism in his/arg allele was associated with increasing serum concentration of IgA to CD74 and with increased disease activity (ASDAS and BASDAI). Decreasing of serum IgA to CD74 concentration, less axSpA activity (ASDAS and BASDAI) were found in patients with presence of heterozygote IL-17F polymorphism in his/his allele.

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AB0023 ASSOCIATION OF NCF2, NCF4 AND CYBA GENES POLYMORPHISMS WITH RHEUMATOID ARTHRITIS IN A CHINESE POPULATION

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Background: Recent studies have focused on the special roles of NADPH-oxidase, which is composed of gp91phox, p22phox, p47phox, p67phox, p40phox encoded by *CYBB*, *CYBA*, *NCF1*, *NCF2*, *NCF4* genes, in multiple autoimmune diseases. Nevertheless, the association of genetic variation in NADPH-oxidase genes with rheumatoid arthritis (RA) was not extensively studied in Chinese population.

Objectives: We performed this study to examine the association of *NCF2*, *NCF4*, *CYBA* genes polymorphisms with RA susceptibility in a Chinese population.

Methods: Six single nucleotide polymorphisms (SNPs) (*NCF2* rs10911363, *NCF4* rs1883112, rs4821544, rs729749, *CYBA* rs3794624, rs4673) were genotyped in a cohort composed of 593 RA patients and 596 normal controls. All patients were consecutively enrolled from the Department of Rheumatology at the First Affiliated Hospital of University of Science and Technology of China and the First Affiliated Hospital of Anhui Medical University, and the normal controls was enrolled from the same region. Improved multiple ligase detection reaction (iMLDR) was used for genotyping. Chi-square (χ^2) test was used to analyze the association of the genotype and allele frequencies of above SNPs and RA. Odds ratios (*OR*) and 95% confidence interval (*CI*) were also evaluated using Logistic regression analyses, and haplotype analysis was assessed using SHEsis software.

Results: There were 101 males and 492 females in RA group with a mean age of 51.59±6.68 years, and the normal control group included 97 males and 499 females with an average age of 52.32±12.63 years. We observed that *NCF4* rs4821544 CT genotype, C allele frequencies in RA patients were significantly decreased when compared to controls (CT vs. TT: $P = 0.043$; C vs. T: $P = 0.031$), and rs4821544 polymorphism was significantly associated with an increased RA risk under the dominant model (TT vs. CT+CC: $P = 0.031$). Moreover, our results also indicated that rs729749 CT genotype frequency was significantly lower in RA patients than that in controls (CT vs. CC: $P = 0.033$). No significant association between *NCF2*, *CYBA* genes polymorphisms and RA susceptibility was observed. There were no significant differences in allele, genotype frequencies of above SNPs between RA patients with RF-positive and with RF-negative, as well as anti-CCP-positive RA patients and anti-CCP-negative RA patients.

Conclusion: In summary, *NCF4* rs4821544, rs729749 polymorphisms might contribute to RA susceptibility, while *NCF2*, *CYBA* genes polymorphisms were not associated with RA susceptibility.

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