SAA1 A/A GENOTYPE IS A RISK FACTOR OF SECONDARY AMYLOIDOSIS IN BELORUSIAN PATIENS WITH RHEUMATOID ARTHITIS

N. Soroka[1], N. Danilenko[2], A. Chyzh[1], L. Sivitskaya[2]. [1]Internal Medicine, Belarusian State Medical University; [2]Institute of Genetics and Cytology, Belarusian NAS, Minsk, Belarus

Background: It is well known, that secondary (AA) amyloidosis development in rheumatoid arthritis (RA) mostly depends on genetic factors. In number of studies SAA γ/γgenotype as well as γhaplotype stimulate renal amyloidosis in Asian (including Japanese) RA patients. The *-13T* allele of *SAA1* gene (*-13T/C* polymorphism) was also performed as a risk factor of secondary amyloidosis.
Objectives: In presented study we compared the influence of the *SAA1* gene allele polymorphisms in AA-positive RA patients with those in AA-negative RA. All patients are Belarusian citizens.
Methods: Native DNA was extracted from leucocytes of blood samples obtained from 45 AA-positive RA patients (1st group) and 59 AA-negative RA patients (2nd group). Polymerase chain reaction (PCR) with subsequent restriction enzyme digest analysis was conducted to analyze *SAA1* gene polymorphisms. Statistical analyses of genotype and allele frequency comparisons between groups were performed using the chi-square test and odds ratio.
Results: Genetic polymorphism of the *SAA1* gene in Belarusian AA-positive RA patients (1st group) and AA-negative RA patients (2nd group) was determined. Comparison of groups on genotype and three allele frequencies showed statistically significant differences. The most notable differences were observed in α/α genotype - χ^2=31.1; P<0.001. 43 of 45 AA-positive RA patients had α/α genotype while only 32.2% AA-negative RA patients presented this genotype. The similar tendency was observed on allele α frequency: χ^2=47.01 (P<0,001). It's remarkable, that γ/γ genotype wasn't revealed in both groups. An odds-ratio (OR) calculatedfor the α/αgenotype was 45.26, and the 95% confidence interval was – 95%CI (9.9-206.8).
So, according to obtained data *SAA1* α/α (allele variants *2995T* and *3010C*) is the genetic risk factor of secondary amyloidosis in Belarusian patients with rheumatoid arthritis.
-13T allele of *SAA1* gene (*-13T/C* locus) presented in 10.2% AA-positive and in 11.1% in AA-negative RA patients (P=0.5). There were no homozygotic *-13T/T* patients in both groups. Thus, *-13T* allele has no influence on the manifestation of AA-amyloidosis in Belarusian patients with RA.
Conclusions: Relative risk of secondary amyloidosis in RA patients significantly increases in α/α genotype. In contrast to Japanese data, our results revealed that in Belarusian citizens (Caucasians) *SAA1* α/α isotype was the most amyloidogenic. Presence of the *-13T* allele in *SAA1* gene allele had no influence on the risk of AA-amyloidosis development in Belarusian patients with RA.
Disclosure of Interest: None Declared

Citation: Ann Rheum Dis 2011;70(Suppl3):217