Results: No statistically significant differences between patients with IgAV and healthy controls were observed when each IL17A genetic variant was analyzed independently. Similarly, no statistically significant differences between patients with IgAV and healthy controls were found when the five IL17A polymorphisms were evaluated combined conforming haplotypes. In addition, there were no statistically significant differences in genotype, allele and haplotype frequencies of IL17A when patients with IgAV were stratified according to the age at disease onset or to the presence/absence of gastrointestinal or renal manifestations.

Conclusion: Our results do not support an influence of IL17A on the pathogenesis of IgAV.

References:

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AB0011 INFLUENCE OF IL17A GENE ON THE PATHOGENESIS OF IMMUNOGLOBULIN-A VASCULITIS


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Background: Cytokines signaling pathway genes represent a key component of the genetic network implicated in the pathogenesis of Immunoglobulin-A vasculitis (IgAV) [1], an inflammatory vascular pathology. Interleukin (IL)17A is a genetic risk locus for autoimmune diseases, such as giant cell arteritis [2] and spondyloarthrits [3].

Objectives: To determine the potential influence of IL17A on IgAV.

Methods: Five IL17A tag polymorphisms (rs4711998, rs8193036, rs819024, rs2775913 and rs7747909) were genotyped in 360 Caucasian patients with IgAV and 1,003 sex and ethnically matched healthy controls.

No statistically significant differences between patients with IgAV and healthy controls were observed when each IL17A genetic variant was analyzed independently.