A42 THE MAJOR RISK ALLELES OF AGE RELATED MACULAR DEGENERATION IN CFH, DO NOT PLAY A MAJOR ROLE IN RHEUMATOID ARTHRITIS

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Background and objectives Activation of the alternative pathway (AP) of complement plays an important role in the pathogenesis of age-related macular degeneration (AMD), an important eye disease in the older people. Next to histological data also genetic data support this contribution with especially genetic variants of the AP inhibitor complement factor H (CFH) contributing to this disease. Since activation of the AP of the complement system is an important aspect of AMD and has been implicated in rheumatoid arthritis (RA) the authors wished to address the question whether the genetic risk factors of the AP inhibitor CFH for AMD would also be risk factors for RA.

Materials and methods For this purpose the authors genotyped *CFH* single-nucleotide polymorphisms (SNPs) in a Dutch set of RA patients and controls. Likewise, a meta-analysis using a Spanish cohort of RA as well as six large genome-wide association studies was performed. For these SNPs the authors analysed over 6.000 patients and 20.000 controls.

Results The *CFH* variants; I62V, Y402H, IVS1 and IVS10, that represent the highest risk alleles for AMD, did not show a significant association with the risk to develop RA despite a strong statistical power to detect such differences.

Conclusions The major risk alleles of AMD in *CFH* do not have a similar effect on developing RA.