



Meta-analysis demonstrates association between *TLR* polymorphisms and rheumatoid arthritis

Y.H. Lee¹, S.-C. Bae² and G.G. Song¹

¹Division of Rheumatology, Department of Internal Medicine, College of Medicine, Korea University, Seoul, Korea

²Division of Rheumatology, Department of Internal Medicine, Medical Center, Hanyang University, Seoul, Korea

Corresponding author: Y.H. Lee

E-mail: lyhcggh@korea.ac.kr

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ABSTRACT. We investigated whether Toll-like receptor (*TLR*) polymorphisms confer susceptibility to rheumatoid arthritis and whether they influence clinical characteristics of rheumatoid arthritis. Studies were considered relevant for our meta-analysis if at least two comparisons of an issue were available. Eleven studies with 2078 patients with rheumatoid arthritis and 2581 controls were included, encompassing European and Asian studies. Meta-analysis of three European studies showed no significant association between the *TLR4* Asp299Gly (rs4986790) polymorphism and rheumatoid arthritis (odds ratio = 0.897, 95% confidence interval = 0.734-1.096, P = 0.289). One Turkish study showed a significant difference between *TLR9* rs187084 allele frequencies and rheumatoid arthritis patients and controls, while another study revealed a significant association between rheumatoid factor and *TLR8* rs5741883. A Korean study on the numbers of guanine-thymine [(GT)_n] repeats in intron II of the *TLR2* gene found a significantly higher S-allele frequency in rheumatoid arthritis patients than in controls (30.3 vs 23.0%). Overall findings for the meta-analysis

including all the studies conclude that *TLR* polymorphism is associated with development and clinical characteristics of rheumatoid arthritis in Asian and Middle East populations.

Key words: Toll-like receptor; Polymorphism; Rheumatoid arthritis