Association of IL-18 polymorphisms with rheumatoid arthritis: a meta-analysis

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ABSTRACT. Interleukin-18 (IL-18), an important proinflammatory cytokine, has been reported to play a potential pathological role in rheumatoid arthritis (RA). Results from previous studies on the association between IL-18 polymorphisms and RA are conflicting. To clarify this, an updated meta-analysis of all available studies on IL-18 polymorphisms and RA was conducted. Eligible articles were identified by searching databases, including PubMed, Ovid, Cochrane Library, EMBASE, and China Knowledge Resource Integrated Database, for the period up to May 1, 2015. The pooled odds ratios (ORs) with 95% confidence intervals (95%CIs) were used to assess the strength of association in the homozygote, heterozygote, dominant, recessive, and additive models. The software STATA (Version 13.0) was used for statistical analysis. Finally, 14 articles were included in the present meta-analysis. The IL-18 -607C/A polymorphism showed pooled ORs and 95%CIs for the homozygote model (AA vs CC: OR = 0.598; 95%CI = 0.395-0.907), and the association between
the IL-18 -137G/C polymorphism and RA showed pooled ORs and 95%CIs for the homozygote (CC vs GG: OR = 0.699; 95%CI = 0.364-1.342) and heterozygote (CG vs GG: OR = 0.924; 95%CI = 0.803-1.064) models. In summary, the current meta-analysis, which was based on the most current studies, showed that the -607A/C, -920C/T, and -105A/C polymorphisms in IL-18 were significantly associated with increased RA risk. However, the -137C/G polymorphism was not associated with RA risk under any genetic model. More evidence is needed to support or deny such a conclusion.

**Key words:** IL-18; Polymorphism; Rheumatoid arthritis; Meta-analysis