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Association of interferon-induced helicase C domain (*IFIH1*) gene polymorphisms with systemic lupus erythematosus and a relevant updated meta-analysis

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ABSTRACT. Systemic lupus erythematosus (SLE) is a complex autoimmune disorder presenting heterogeneous clinical manifestations. A number of genes involved in SLE susceptibility are related to the type

I interferon (IFN) pathway. IFN mediates innate immune responses and its increased levels contribute to the breakdown of peripheral tolerance. Interferon-induced helicase C domain 1 (IFIH1) activates and modulates IFN responses through its caspase recruitment domain. In this study, we analyzed four *IFIH1* single nucleotide polymorphisms (SNPs): rs6432714, rs10930046, rs1990760, and rs3747517, in 337 patients with SLE and 373 healthy individuals from southeast and northeast Brazil. Our results did not find an association between *IFIH1* SNPs and SLE (P value >0.025 after Bonferroni's adjustment). However, meta-analysis of peer-reviewed articles from 2008 to 2015 and data from this study indicated an association between rs1990760 and SLE onset ($P < 0.05$). This is the first association analysis on *IFIH1* polymorphisms and SLE susceptibility in Brazilian populations.

Key words: IFIH1; SLE; SNPs; SLE clinical manifestations; Meta-analysis