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| Title: | Association between IFITM3 rs12252 polymorphism and influenza susceptibility and severity: A meta-analysis |
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| Abstract: | <p>Intrinsic host susceptibility to viral infections plays a major role in determining infection severity in different individuals. In human influenza virus infections, multiple genetic association studies have identified specific human gene variants that might contribute to enhanced susceptibility or resistance to influenza. Recent studies suggested, the rs12252 T > C polymorphism in the interferon-inducible transmembrane protein 3 (IFITM3) gene might be associated with susceptibility to severe influenza. However, the studies reported conflicting and inconclusive results. To resolve the controversy, we conducted a systematic meta-analysis to evaluate the role of the IFITM3 rs12252 polymorphism in influenza susceptibility and severity, including twelve studies published before February 19, 2018 with a total 16,263 subjects (1836 influenza cases and 14,427 controls). Odds ratios (OR) and 95% confidence intervals were used to assess the strength of the association. Our results indicated increased risk of both severe and mild influenza in subjects carrying the IFITM3 rs12252 polymorphism in the allele contrast C vs. T: OR (severe) = 1.69, 95% CI = 1.23–2.33, P = 0.001, and OR (mild) = 1.46, 95% CI = 1.13–1.87, P = 0.004. Similar results were obtained in the homozygote comparison and dominant model. Stratified analyses by ethnicity revealed increased risk of severe influenza in both the White and East Asian populations, but significant association with mild influenza was found only in the White population. Overall, our meta-analysis suggests a significant association between the IFITM3 rs12252 polymorphism and the risk of influenza in both the White and East Asian populations.</p> |
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