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Association between rs12252 and influenza: An updated meta-Analysis

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To investigate the association between IFITM3 rs12252 and influenza and to identify differences with previous meta-analyses, PubMed, the Cochrane library, OVID, EBSCO and the Web of Science were searched for related studies published from the initial date to November 9, 2017. The Newcastle-Ottawa Scale (NOS) was used to assess the quality of included studies. Statistical analyses of data were performed using Revman 5.0 and Stata 12.0. Nine studies providing ten sets of data were included in this updated meta-analysis. These data represented 1365 patients with influenza and 5425 no-influenza controls from four different ethnicities. Significant association between rs12252 and influenza was found in all four genetic models (C vs T: OR=1.54, 95% CI: [1.34,1.77] ,P<0.00001; CC vs CT+TT: OR=2.80, 95% CI: [2.03,3.85], P<0.00001; CC vs TT: OR=2.39, 95% CI: [1.85,3.09], P<0.00001; CC + CT vs TT: OR=1.38, 95% CI: [1.14,1.67], P=0.001). The fixed-model was applied to all allelic models because no obvious heterogeneity was found. We also found significant results in the allelic model (C vs T: OR=1.35, 95% CI: [1.03,1.79], P=0.03) and homozygote model (CC vs TT: OR=2.74, 95% CI: [1.90, 3.94], P<0.00001) in the Asian subgroup, which were not found before. There were also significant differences in the allelic model (C vs T: OR=1.37, 95% CI: [1.08,1.73], P=0.009), dominant model (CC + CT vs TT: OR=1.48, 95% CI: [1.08,2.02], P=0.01), and homozygote model (CC vs TT: OR=2.84, 95% CI: [1.36,5.92], P=0.005) when patients with mild influenza were compared with healthy individuals, while previous meta-analyses only found association between rs12252 T>C and mild influenza. Our meta-analysis shows the IFITM3 rs12252 T>C polymorphism is associated with increased risk of not only severe but also mild influenza in both Asian and Caucasian populations.

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