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Identification of *TMPRSS2* as a susceptibility gene for severe 2009 pandemic A (H1N1) influenza and A (H7N9) influenza

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The genetic predisposition to severe A (H1N1) pdm09 influenza was evaluated in 409 patients including 162 severe cases and 247 mild controls. We prioritized candidate variants based on the result of a pilot GWAS and a lung eQTL dataset. The GG genotype of rs2070788, a higher-expression variant of *TMPRSS2*, was a risk variant (OR 2.11, 95% CI 1.18~3.77, P=0.0113) to severe A (H1N1) pdm09 influenza. A potentially functional SNP, rs383510, accommodated in a putative regulatory region was identified to tag rs2070788. Luciferase assay results showed the putative regulatory region was a functional element, in which rs383510 regulated *TMPRSS2* expression in a genotype-specific manner. Notably, rs2070788 and rs383510 were significantly associated with the susceptibility to A (H7N9) influenza in 102 A (H7N9) patients and 106 healthy controls. Therefore, we demonstrate that genetic variants with higher *TMPRSS2* expression confer higher risk to severe A (H1N1) pdm09 influenza. The same variants also increase the susceptibility to human A (H7N9) influenza.

Biography

Zhou Jie Jane is the Research Assistant Professor from the Department of Microbiology at the University of Hong Kong. Her major research interests include host genetics of infectious diseases, pathogenesis of respiratory viral infection. She has published papers in reputed journals.

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