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***CD55* genetic variations increase the disease severity of pandemic H1N1 (2009) influenza infection**

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Pandemic H1N1 2009 (H1N1pdm) influenza is commonly manifested as a mild infection but occasionally treated as a severe pneumonia. Unlike seasonal influenza, people under 65 years of age were infected preferentially, with high rate of severe infection and mortality in younger patients globally and in Hong Kong. Among these patients, about one third of the severe and fatal cases do not have co-morbid conditions, implicating that inter-individual genetic variation may account for the distinct disease severity of H1N1pdm infection. An initial small scale genome wide association study guided the selection of *CD55* single nucleotide polymorphisms in 425 Chinese patients with severe (n=177) and mild (n=248) disease. Carriers of rs2564978 genotype T/T were significantly associated with severe infection (OR 1.75, p=0.011) after adjusting the clinical confounders. Allele-specific effect on *CD55* expression was examined and ascribed to a promoter indel variation rs3841376, which was in perfect linkage disequilibrium with rs2564978. The promoter variant with deletion exhibited significantly lower transcriptional activity. We further demonstrated that *CD55* can protect respiratory epithelial cells from complement attack. We also demonstrated that *CD55* knockout mice are more susceptible to lethal infection of H1N1pdm. In conclusion, *CD55* gene polymorphisms are associated with severe H1N1pdm infection. *CD55* may exert a substantial impact on the disease severity of H1N1pdm infection.

Biography

Jie Zhou has completed her PhD from The University of Hong Kong. After her Postdoctoral studies in UCSF, USA she is now a Research Assistant Professor in Department of Microbiology at Hong Kong University.

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