

Disease severity and genetic variation of glycoproteins in the respiratory syncytial virus-A ON1 genotype in Chongqing of China, from 2009 to 2016

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Respiratory syncytial virus (RSV) is a leading cause of acute respiratory tract diseases in younger children. ON1 is a new genotype of RSV-A found in 2010, which is characterised by a 72-nucleotide duplication in the G protein gene. To comprehensively understand the prevalence of the ON1 genotype in Chongqing, we monitored the circulation pattern of RSV-A over seven consecutive years (June 2009 to June 2016). We found that ON1 has become the predominant genotype in Chongqing. Compared with the NA1 genotype, children infected with ON1 genotype RSV-A tended to develop a more severe form of the disease. We searched for the reasons for this at the amino acid level and found that the ON1 genotype was subject to insertion of duplicate sequences, positive selection in G proteins, amino acid mutations in neutralising antigenic site Ø and HLA-restricted epitope HLA*B57 in F proteins. The evolutionary rate was 4.2×10^{-3} nucleotide substitutions/site/year for G proteins of the ON1 genotype and 8.6×10^{-4} nucleotide substitutions/site/year for F proteins. Surveillance of genotype ON1 and analysis of the molecular epidemiology of the G and F proteins may be helpful for the development of vaccines against RSV infection.

Key words: human respiratory syncytial virus, ON1 genotype, G protein, F protein, severe lower respiratory tract infections, child