

# Reassortant Eurasian Avian-like H1N1 Influenza Viruses from Diseased Swines, Southern China

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## Abstract

958 lung tissue samples of swine influenza were collected in Guangxi from 2013 to 2014 to further study the pathogenic mechanism and prevention and control technology of influenza virus, and influenza virus isolation and biological characteristics analysis of Eurasian avian influenza (ER-H1N1) were performed. The positive rate of the 14 strains of ER-H1N1 swine influenza virus isolated was 1.46%, with 8 gene pieces all from avian sublineages, followed by recombinant Pdm/09 H1N1 fragments. Although their HA cleavage site is PSIQSR—GLF or GIF, which has typical low-pathogenicity characteristics, the isolated virus strain grows well on the cell, and after the BALB/c mouse challenge experiment, the evidence of the isolated strain multiplying in the respiratory tract of mice is obvious, and the mice lose weight quickly, all die within a week and are accompanied by severe systemic infection. Based on changes in the amino acid residues of the A/swine/Guangxi/6/2013 (No.6) strain, it is thought that the NA protein E119G mutation is the main site where highly dangerous changes happen. D<sup>701</sup>N mutations in the PB2 strains G2, g14, g21, g30, S2, 32, 7, and 8 show that these strains are gradually adapting to human sources. According to the traits of strains 30, G2, G14, and G21, NP develops D<sup>375</sup>E, which boosts pathogenicity. In summary, the ER-H1N1 subtype influenza virus is widespread in the Guangxi swine herd, and it is pathogenic to mice, with the trend of genomes derived from Pdm/09 H1N1 fragments increasing.

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