

Phylogenetic analysis of swine influenza viruses isolated in Poland

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Abstract

Swine influenza virus (SIV) of H1N1 and H3N2 subtypes are dominated in European pigs population. “Classical swine” H1N1 subtype was replaced by “avian-like” H1N1 subtype. It co-circulates with H3N2 reassortant possessing “avian” genes. In the present study, 41 SIV strains isolated from pigs with pneumonia, raised in 20 Polish farms, were identified and characterised. Since it was evidenced that isolates from the same geographic district and the same year of isolation are in 100% similar, 15 strains representing different district and different year of isolation were chosen to construct phylogenetic trees. Two genes, conservative matrix 1 (M1) and the most variable, haemagglutinin (HA), were sequenced and subjected into phylogenetic analysis. The results of the analysis confirmed that “avian-like” swine H1N1 strains evolved faster than classical SIV strains. HA gene of these isolates have been derived from contemporary strains of “avian-like” SIV. In contrast, the M1 gene segment may have originated from avian influenza viruses. H3N2 strain is located in swine cluster, in the main prevalent European group of H3N2 isolates called A/Port Chalmers/1/73-like Eurasian swine H3N2 lineage, which has evolved separately from the human H3N2 virus lineage around 1973.

Key words: swine influenza virus, M1, HA, phylogenetic analysis