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Phylogenetic analysis of swine influenza viruses recently isolated from pigs in Korea

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Introduction

In a recent paper, Korean H1N2 and H1N1 swine influenza isolates were closely related to North American viruses [1, 2]. Virological and serological surveys have indicated that H1N1, H1N2 and H3N2 influenza viruses predominated in Korea. We describe the recently isolation of H3N2 and H1N2 influenza viruses from a pig in Korea and provide a phylogenetic analysis of Korean isolates and prove directly transmission of H1N2 virus from USA.

Material and methods

A total of 175 samples, including nasal swabs and lungs submitted to the Research Unit of Green Cross Veterinary Products and the Virology Laboratory, College of Veterinary Medicine, Seoul National University from swine farms in South Korea from 2005 to 2006. The sequences of the isolated virus were edited and analyzed using Bioedit software. The phylogenetic trees were generated with the MEGALIGN program (DNASTAR, Madison, WI) by using the Clustal alignment algorithm.

Results

Among 175 samples, one virus identified as H1N1 subtype, two viruses identified as H1N2 subtype and one virus identified as H3N2 subtype were isolated. Phylogenetic tree for the nucleotide sequences of recently Korean isolates HA genes of H1N1 and H1N2 viruses shows in Fig 1. Phylogenetic analysis of the HA genes were closely related to classical swine influenza viruses. Recent two H1N2 isolates clustered North American swine cluster

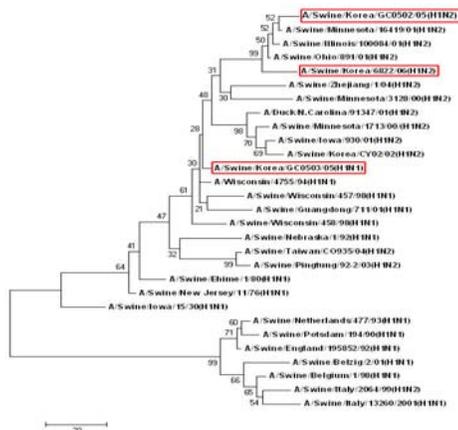


Fig 1. Phylogenetic trees of Korean isolates (H1 gene)

Phylogenetic analysis for the HA genes of H3N2

isolates (A/swine/Suwon/107/98, A/swine/Korea/GC0407/05) in Korea shows that different cluster each other. HA gene of A/Swine/Suwon/107/98 was closely related to human cluster. However, the HA gene of recent Korean isolate, A/Swine/Korea/GC0407/05, clustered North American swine cluster (Fig. 2).

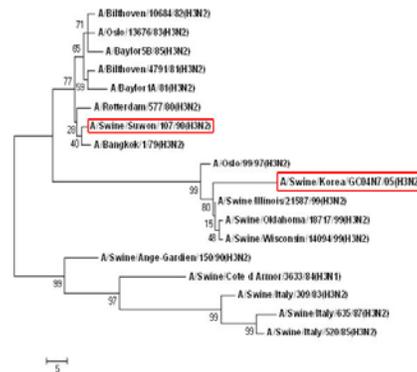


Fig 2. Phylogenetic trees of Korean isolates (H3 gene)

Discussion

All these subtypes of SIV isolates were very similar to North American SIV and these are dominantly circulating in Korean pig populations. Serologic and genetic analysis indicated that Korean H1N2 viruses were directly introduced from USA virus without recombination between Korean H1N1 and H3N2 viruses. In addition, all genes of these H1N2 isolates were also closely relates to Korean H1N2 influenza virus (A/Swine/Korea/CY02/02) transmitted from America. The Korean H3N2 isolate in 1998 are closely linked to human-like viruses in comparison of the all 8 segmented genes. However, recent H3N2 isolates were also closely related to the isolates from the United States influenza viruses in all eight gene segments. These results suggest that the H1N1, H1N2 and H3N2 viruses isolated in the Korean swine population are originated ones from North America.

References

1. D.S. Song, C.S. Lee et al, Virus Res. 125, 98-103 (2007)
2. K. Jung, C. Chae, Arch. Virol. 149, 1415-1422 (2004)