

Isolation of *Clostridium perfringens* from equine feces in Jeju

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Introduction: *Clostridium perfringens* is everpresent in nature and can be found as a normal component of decaying vegetation, marine sediment, the intestinal tract of humans and other vertebrates, insects, and soil. *C. perfringens*, which causes various diseases in different animals, is differentiated into five subtypes (subtypes A to E) according to the major toxins produced by each subtype. Especially *C. perfringens* type A and C are important cause of Equine diarrhea. The purpose of this article is to know about *C. perfringens* distribution of equine in jeju and *C. perfringens* type of clinically normal equine feces in jeju.

Materials and Methods: Total 72 samples from 17 different horse farms were collected. Each sample was enriched in Brain heart infusion (BHI) broth and plated in *Clostridium perfringens* agars (CPA) containing 5% egg yolk, *C. perfringens* selective supplement (Oxoid). Isolates were tested by PCR for positive of *C. perfringens*. And isolates were tested by multiplex PCR for the presence of α , β , β_2 , ϵ , ι , and cpe genes

Results: Among 72 samples, 56 showed *C. perfringens* positive (77.8%) and 15 of 56 *C. perfringens* isolates were harboring α toxin (26.8%). Others toxin were not detected.

Conclusions: Isolation rate of *C. perfringens* is 77.8% from equine in jeju. Because many broodmares are in Jeju, continuous management and examination of *C. perfringens* are needed in future.

A/canine/Korea/BD-1/2013 and A/canine/Korea/DG1/2014, along with 57 worldwide CIVs, using comprehensive molecular analyses based on genomic genotyping.

Materials and Methods: Two Korean CIVs were isolated from nasal swabs of pet dogs in 2013 (A/canine/Korea/BD-1/2013) and in Daegu in 2014(A/canine/Korea/DG1/2014), respectively. The eight viral segments of the two Korean CIV isolates were amplified using RT-PCR and sequences were analyzed using CLC Main Workbench software. To infer phylogenetic relationships between the two Korean H3N2 CIV isolates and worldwide CIVs, the following phylogenetic methods were employed depending on different datasets: (a) RAxML 7.4.2 implemented in raxmlGUI, version 1.3 for a maximum likelihood (ML) method; (b) Garli 2.01 using genetic algorithm approaches for the ML search, allowing all possible submodels of the GTR (General Time Reversible) model; and (c) Mr Bayes, version 3.3.2, for Bayesian inference (BI) using the Markov chain-Monte Carlo (MCMC) method.

Results: Our results showed that the new two Korean CIV isolates are closely related to the predominantly circulating H3N2 CIVs with genotypes K, G, E, 3B, F, 2D, F, and 1E, carrying several mutations in antigenic and host determinant sites. Also, our findings show that the genome-wide genetic variations within the H3N2 CIVs are low.

Conclusions: The two newly isolated CIV isolates from Korea also possessed the same genotype combinations detected in Asian CIVs.

References

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Molecular analyses of H3N2 canine influenza viruses isolated from Korea during 2013–2014

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Introduction: Canine influenza A virus (CIV) causes a respiratory disease among dog populations and is prevalent in North America and Asia. Recently, Asian H3N2 CIV infection has been of particular concern, with recent reports related to reassortants with pandemic 2009 strains, direct transmission from a human H3N2, a possibility of H3N2 CIV transmission to other mammals, and even the first outbreak of H3N2 CIVs in North America in 2015. Here, we investigated the evolutionary history of the most recent two Korean CIV isolates,

Mathematical Modeling and Simulation of spread of FMD and HPAI in the Republic of Korea

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Introduction: Mathematical models describing outbreak pattern of major transboundary animal diseases, such as foot-and-mouth diseases(FMD) and highly pathogenic avian influenza(HPAI) were developed.

Materials and Methods: Within-farm spread models were developed for each diseases for the first step then they were