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P-020

Identification of canine parvovirus type 2a and 2c in faeces of korean dogs

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Introduction: Canine parvovirus (CPV) is a major pathogen of diarrhea disease in dogs. CPV type 2 have three of antigenic variants such as 2a, 2b and 2c. New type antigenic CPV have been identified in many countries such as Germany, Italy, Spain, Belgium, France, Greece, China and Japan. In this study, we extracted DNA from faeces of two dogs would determine of infection by CPV and confirmed as CPV strain, based on PCR and nucleotide sequence analysing and compared with *VP2* gene sequence through NCBI blast system.

Materials and Methods: The DNA extraction with QIAamp DNA mini kit (QIAGEN, Germany) from faeces of dogs from Gun-san city of Jeonrabookdo province, South korea. The primer were tested with PCR of determined CPV infection, according to D. K. Yang et al (2015). The PCR was carried out in Hot start PCR premix (Bioneer, Korea) containing 1 μL denatured DNA, 1 μL each primer (10 pmol), and 27 μL distilled water in a 30 μL final volume. The cycling profile was denaturation at 95℃ for 5 min, followed by 35 cycles of denaturation at 95℃ for 30 sec, annealing at 55℃ for 30 sec, extension at 72℃ for 1 min, and a final extension at 72℃ for 5 min. The PCR products were visualized after 1.0% agarose gel electrophoresis containing the Red safe Nucleic acid staining solution (iNtRON Korea). All PCR product purified was QIAquick PCR purification kit (QIAGEN, Germany). The sequences of the purified PCR products were determined using primers tree partial *VP2* genes from D. K. Yang et al (2015) (Apply to MACROGEN korea). The nucleotide sequences, accession numbers, and names of the strains used for the phylogenetic analysis were obtained from the GenBank database (National Center for Biotechnology Information, USA). Genetic distances were calculated using the BioEdit correction parameter and a phylogenetic tree was constructed using the neighbor-joining method in MEGA7

Results: We detected that CPV 2a and 2c from faeces of each two dogs via PCR analysis and sequence analysis results. Phylogenetic analysis results proved that CPV 2c K01708-1 was genetically similar within the VP2 gene to CPV 2c strain BJ14-9 isolated from China and CPV 2a K01708-2 was genetically similar within the VP2 gene to CPV 2a strain BJ1 isolated from China.

Conclusions: The present study identified CPV 2a and 2c variant infection from faeces of each two dogs and provides evidence for the existence of a novel CPV 2c variant in South Korea. CPV 2c K01708-1 is the first report to identify a novel CPV 2c variant in South korea. In addition CPV 2a K01708-2 have different genetic species with other CPV 2a from South korea.

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P-021

Behavioral observations of swine exposed to nitrogen gasfoam as euthanasia

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Introduction: Foot and mouth disease is a great concern for the swine industry and depopulation of the infected pig inaccordance to animal welfare is important to prevent the disease transmission. Nitrogen-gas foam euthanasia method was developed as an alternative way of mass emergency swine depopulation.

Materials and Methods: New type of gas foam containing nitrogen (N_2) and carbon dioxide (CO_2) was applied for euthanasia swine.

Results: The loss of consciousness of swine was induced shortly after headshaking as a result of anoxic anoxia in both N_2 and CO_2 gas foam. For N_2 gas foam, the loss of consciousness was taken at 85±10 seconds in swine, while in CO_2 gas foam, it was taken at 73±10 seconds in swine. Unlike with N_2 gas foam, gasping was observed in CO_2 gas foam. In the postmortem examination, small mass of feed stuff was detected in entering area of trachea in CO_2 gas foam, however, there was no observation in N_2 gas foam.

Conclusions: N_2 gas foam was proven alternative method of swine euthanasia.