

The PCR products were cloned into a pGEM-T easy vector (Promega, Madison, WI, USA) prior to sequencing. Six specific primers were designed from the complete sequences of the TGEV purdue strain (GenBank Accession No. DQ811789).

**Results:** The nucleotide sequence of the S glycoprotein gene for three TGEV strains was determined and compared to published sequence of TGEV Purdue strain. The S glycoprotein genes of TGEV Pyeongtaek, 175L and 175LK strain consist of 4344, 4334 and 4347 nucleotides (nt), respectively. Three Korean TGEV S glycoprotein genes have 99% nucleotide sequence identities with each other. The TGEV 175LK strain was 3-nt and 10-nt longer than the homologous gene in the Pyeongtaek strain and in 175L strain, respectively. As compared to TGEV Purdue strain, three Korea TGEV strains showed significant differences that involve 6-nt deletion located between at position 1123 and 1128. The TGEV 175LK strain only had a 9-nt insertion located at position 1151. In addition, both TGEV 175L and 175LK strain had a 3-nt deletion located between at position 4229 and 4231.

**Conclusions:** As compared to virulent TGEV purdue strain, three Korean TGEV strains showed distinct genetic signatures, insertion and deletion in the S glycoprotein gene that involved notable two deletions and one insertion. Therefore, it could be carefully suggest that the unique S-indel sequences in three Korean TGEV strains might be related to the pathogenicity of TGEV.

#### References:

- [1] Rasschaert D, Duarte M, Laude H. (1990) Porcine respiratory coronavirus differs from transmissible gastroenteritis virus by a few genomic deletions. *J Gen Virol.* 71. 2599-607.

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### Seroepidemiological Survey of porcine epidemic diarrhea virus in wild boar in habited in South of Korea

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**Introduction:** Wild boars (*Sus scrofa*) are regarded as a source for infectious disease in domestic livestock. Outbreaks of porcine reproductive failure caused by infection of viral pathogens, such as Aujeszky's disease virus, encephalomyocarditis virus, and porcine parvovirus have been well identified that associated with indirect or direct contact with infected wild boars. In addition, the existence of those viral agents in the wild boar populations was indirectly confirmed by sero-epidemiological survey. Porcine epidemic diarrhea (PED) virus causes acute diarrhea and dehydration in swine. The disease caused by PED virus (PEDV) is concerned about significant economic losses in the swine industry. Outbreaks of PED have been reported frequently on pig farms in Republic of Korea, since the first the beginning of 1992. In the present study, we analyzed the presence of antibodies against PEDV in serum samples obtained from wild boar hunted in South of Korea.

**Materials and Methods:** Collection of serum samples: Wild boars were hunted for a classical swine fever eradication campaign undertaken in Republic of Korea. A total of 184 serum samples were randomly collected from wild boars hunted between December 2014 and November 2015.

**ELISA test:** The serum samples were tested by using the commercial ELISA kit for PEDV antibody detection according to the manufacturer's instructions. The results were expressed as the absorbance at 405 nm after subtracting the background value of the blank. Serum samples were evaluated as positive if the specific absorbance was higher than the cut-off absorbance value.

**Results:** Of the 184 serum samples tested, the overall seroprevalence rates were 22.3% (41/184) for PEDV. PEDV antibody prevalences were high in all areas except for Jeonnam province (0%, 0/3). The highest seroprevalence rate was recorded in Kangwon province (30%, 3/10).

**Conclusions:** Our results indicated that PEDV-positive wild boars were distributed throughout the mainland of South Korea that particularly clustered at the Gyeongnam province and in mountainous regions. While the commercial ELISA test kit used in this study was useful for detecting PEDV antibodies in serum samples, doubtful or positive results determined by ELISA will need to be validated by VN test in future studies.

#### References:

- [1] Dong-Kun Yang, Jin-Ju Nah, Ha-Hyun Kim et al. (2014) Seroepidemiological Survey of Aujeszky's Disease Virus in Wild Boar (*Sus scrofa*) and Raccoon Dogs (*Nyctereutes procyonoides koreensis*) in Korea. *J Bacteriol Virol*, 44(4) p.336 - 341

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### Sero-surveillance against rabies virus in wild boars in Korea, 2014-2015

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**Introduction:** Rabies is one of the most fatal zoonotic diseases and causes 70,000 human deaths worldwide each year, mainly in Asia and Africa. In Korea, rabies outbreaks have occurred in Gangwon and Gyeonggi province since 1993. In order to prevent and control rabies, Korean veterinary authority has implemented massive vaccinations program to domestic animals and distribution of bait vaccine to wild animals in Gangwon and Gyeonggi province. Among wildlife, the raccoon dogs (*Nyctereutes Procyonoides*) is the reservoir species transmitting to other animals such as cattle, dogs, and cats and main target of bait vaccine in Korea. As previous study described, other wildlife and domestic animals also intake bait vaccines and show the presence of antibodies against rabies virus (RABV) (1). Presence of anti-rabies antibodies definitely indicates bait consumption of wild animals. Wild boars is one of the most numerous and edacious wild animal