networks in different time scales and systemic roles can provide new insight of identifying risk of infectious disease transmission in each vehicle type. Furthermore, estimated values of risks will be used as parameters to establish better herd-level infectious disease transmission models.

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A Novel Unique Group of Torque teno Virus (TTV) in Aborted Fetuses in Korean Swine Farms

Hee-Chun Chung[1], Ga-Eun Lee[1], Hye-Jung Yang[1], Jung-Ah Kim[1], Bong-Kyun Park[*1]

[1]Department of Veterinary virology Lab, College of Veterinary Medicine and BK21 Program for Veterinary Science, Seoul National University, Seoul, Korea

Introduction: In 1997, Torque teno virus (TTV) was first discovered in the plasma of a Japanese patient with post-transfusion hepatitis of unknown etiology (1). The TTV of pig origin, Torque teno sus virus (TTSuV), was first reported in 1999 (1-2), and TTV infections were considered to be ubiquitous in both healthy and diseased pig herds and in pigs of all ages (2). Thus far, two distinct species, Torque teno sus virus 1 (TTSuV1, genus Iotatorquevirus) and Torque teno sus virus 2 (TTSuV2, genus Kappatorquevirus) have been identi fied from pigs. To get further insights on the vertical transmission of swine TTVs and the potential link of these viruses with reproductive disease, a prospective study was designed to assess the prevalence of both swine TTVs in cases of abortions (2). Moreover, swine TTVs have been detected in semen, colostrum, and sera from stillborns and gnotobiotic pigletsand reinforcing the idea that vertical transmission via transplacental/ intra-uterine, or lactation routes may play an important role in viral spread (2). At present, very little information is available about both incidence and genomic characterization of TTVs in fetuses in South Korea. In this study, genetic relationship of Korean TTV strains and TTV strains from other countries was analyzed.

Materials and Methods: During April to November 2013, we randomly collected fetus (n=112) from swine farms (n=46) in 9 provinces for detection viruses associated with abortion problems. The fetuses organs (kidney, liver, tonsil, heart and spleen) were pooled, homogenized. Viral DNA was extracted from 150 ml of the homogenized samples, using the Patho Gene-spin DNA/RNA Extraction Kit (iNtRON). Nested PCR performed using a Maxime PCR Pre Mix kit(iNtRON) was used to detect aborted fetuses DNA (3); the reaction and amplification conditions were slightly modified. Nested PCR was done with 1F (forward)/1R(reverse) primers (3), containing 1ul of 1F and 1R primers, respectively, 16 ul of i-Star Max, and 2 ul of sample DNA as follows: 95 °C for 5 min; 38cycles of 95 °C for 30 s, 54 °C for 30 s, 72 °C for 30 s. After then, at the second round, the products were 20-time diluted for the detection of the more partial specific sequences of TTV using 2F/2Rprimers, containing 1 ul of 2F and 2R primers, respectively, 17 ul of i-Star Max, and 1 ul of diluted products of first round as follows: 95 °C for 3min; 30 cycles of 95 °C for 20 s, 58 °C for 30 s, 72 °Cfor 1 min 30 s. Products from a nested PCR were visualized by electrophoresis on a 1.5 % agarose gel. PCR products of the expected size were 253 bases and directly asked for sequencing (Macrogen., South Korea).

Results: The screening results by Nest RT-PCR, 3 (2.68%) samples (CP13-346, M1531, PF2516) were positive for TTVs in Gyeongbuk and Geonbuk province from three each Korean swine farms. In 3 fetuses positive each samples, which were not diagnosed for viruses such as porcine respiratoryand abortion problems viruses (PRRS, PCV2, SIV, PPV, JEV, EMCV). For the genetic characterization, the maximum likelihood phylogenetic trees reconstructed from the 5'non-codingregion showed a clear separation among 1,2,3, Tux, and SANBAN in TTV groups. In this study, they located at different branches, were located another novel unique group. The unique groups closely related (93.3～ 96% similarity) to the Tux group rather than those in the other groups (77～ 89.7% similarity).

Conclusions: By screening the samples collected from April 2013 to November 2013, this study confirmed the presence TTV in Korean swine farms. In this study, the phylogenetic analyses suggested that the TTV fetuses isolated stains, which was shown different unique branch. The result is consistent with the report which TTV was detected from aborted fetus samples (2, 3).

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Genetic diversity of Porcine Reproductive and Respiratory Syndrome virus in Korea in 2015

Ji Eun Yu[1], In-Ohk Ouh[1], Hyeonjeong Kang[1], Seung-min Song[1], In-Soo Cho[1], Sang-Ho Cha[*1]

[1]Viral Disease Division, Animal and Plant Quarantine Agency, 177 Hyeoksin 8-ro, Gimcheon-si, Gyeongsangbuk-do, Republic of Korea

Introduction: Porcine reproductive and respiratory syndrome virus (PRRSV) is rapidly gaining importance as one of the most economically significant diseases in swine worldwide. PRRSV is an enveloped single-stranded positive RNA virus that can be divided into two different genotypes, the European genotype (type1) and the North American genotype (type 2). The genome of PRRSV is approximately 15 kb in length and contains at least 10 open reading frames (ORFs). ORF5, encoding GP5, is one of the most variable regions of the PRRSV genome, and often used to examine genetic diversity and monitor evolution of PRRSV. In this