PRRSVs antigen, the typing for NA and EU was implemented. We also analyzed HP- PRRSV based on investigating the positive samples of PRRSV (n=728).
For RNA extraction, Patho -RNA viral Gene-spin (TM) Viral DNA/RNA Extraction Kit (Intron/ Korea) was used according to the manufacturer's recommendation.
The N26, N21, ERT primers were used for PRRSVs detection (1). PRRSVs typing was performed using specific primer sets EU type (N23, N25), and NA type (N22, N24) (1). For detect of HP-PRRSVs, the conventional RT-PCR was performed by using the NSP2-F and NSP2-R primers (2). The reaction mixtures were performed at the amplification condition: 95°C for 5 min, followed by 38 cycles of 95°C for 30 s, 58°C for 30 s, and 72°C for 40 s, and a final extension step of 7 min at 72°C. The PCR products were detected by 1.5% agarose gel electrophoresis in 1 × TAE.

Results: The PRRSVs screening results by RT-PCR from January to December2015, showed 501/7,045 (7.11%). For 501(sera and organs pooling) which were positive for PRRSVs antigen, the typing for EU and NA was implemented. There were 114(22.75%) EU, 273 (54.49%),8 (1.59%) EU + NA, and unknown type 106 (21.15%), respectively. January to August 2016, showed 227/6997 (3.24%). For 227 (sera and organs pooling) which were positive for PRRSVs antigen. There were17 (7.48%) EU, 62 (27.31%), 5 (2.20%) NA +EU, and unknown type 143 (62.99%), respectively. From January 2015 to August 2016, 728PRRSV positive samples, which were all negative of HP-PRRSV.

Conclusions: We found EU and NA types of PRSVs are prevalent in South Korea, and even co-infection of both types of PRRSVs occurred. Both 2015 and 2016 typing results, NA type showed the more positive rate than EU type. In this study, HP-PRRSV, were not detected from 9 provinces domestic Korean swine farms. However, as potential risk that the monitoring against HP-PRRSV is important for effective prevention and control of swine respiratory disease in swine industry in South Korea.

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P-061

Comparison of the accuracy of serological tests with microbial culture for the diagnosis of canine brucellosis

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Introduction: Canine brucellosis is a major worldwide zoonosis, caused by *Brucella canis*, and main clinical signs of this infection are abortion in pregnant bitches and orchitis, epididymides and prostatitis in males. As canine brucellosis is a great cause of economic losses in breeding kennels as well as there is risk to human infection in public health, diagnosis for brucellosis should be conducted quickly and correctly. Several different serologic tests have been developed for diagnosis of *B. canis* infection, but the present screening diagnosis method still has problem of non-specific reaction. Thus, this study is to compare conventional serological tests with microbial culture which is considered as a golden standard for the diagnosis of canine brucellosis, ultimately to find out improvement of the diagnostic tests.

Materials and Methods: A total of 347 whole blood samples were collected from kennel dogs in south Korea in January to June 2016. The serologic tests analyzed in this study were rapid slide agglutination test (RSAT), RSAT with 2-mercaptoethanol (2-ME RSAT), and immunochromatographic assay (ICT). In comparative study, bacterial isolation was attempted by direct microbiological culture from whole blood of dogs which were interpreted as positive in serologic tests (2-ME RSAT and/or ICT). All *Brucella*-suspected cultures were confirmed as *B. canis* by differential multiplex PCR.

Results: Of the 347 dogs that were examined, the following tests were positive: RSAT, 101 (29.1%); 2-ME RSAT, 43 (12.4%); ICT, 36 (10.4%). Of the 45 dogs which were positive in serological tests (2-ME RSAT and/or ICT), *B. canis* were isolated from 11 dogs (24.4%). Correlation between bacterial isolation and serological test, 2-ME RSAT and ICT, were 25.6% and 30.6%, respectively. As a result, the RSAT showed a positive rate value greater than that observed in the 2-ME RSAT and ICT. But, correlation with bacterial isolation was the highest in ICT.

Conclusions: We compared the accuracy of serological tests, RSAT, 2-ME RSAT, and ICT, with microbial culture for improvement of the diagnostic tests. Although we couldn't find out significance among serological tests in this study due to small amounts of samples and seropositive individuals, in the further study, we will reach the dependable results with more samples to confirm the ways that can supplement discordance among serological tests.

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P-062

Phylogenetic Analysis of Bovine Norovirus from Korean calves with diarrhea, 2015~2016

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Introduction: Noroviruses are small non-enveloped, positive-sense single-stranded RNA viruses belonging to the family *Caliciviridae*. Noroviruses have five genogroups, GI, GII and GIV, are isolated in humans (GII-11, GII-19 are porcine), and genogroup GIII and GV strains are found in cows and mice. Bovine norovirus (BNoV) has two prototype strains, Jena virus and Newbury agent-2, belonging to genotype 1 and 2 within GIII, respectively. The aims of this study were to investigate for the presence of norovirus in Korean calves by reverse transcription-polymerase chain reaction (RT-PCR) and real time-PCR to determine the phylogeny of strains.

Materials and Methods: Of the 872 bovine fecal samples were collected from January 2015 to August 2016. RT-PCR and real time-PCR using the primers for norovirus were performed by method described previously (H.Yilmaz et al., 2011). The 515-bp PCR products were amplified and directly sequenced by Macrogen (Seoul, Korea). Phylogenetic trees were constructed using Mega 6.0 with the maximum likelihood method.

Results: Amongst the 872 diarrheic calves, 16 (1.8%) were found to be positive for norovirus genogroup III. The age of these calves was between 3 days and 1 year. A phylogenetic tree was generated form the nucleotide sequence using the data from sequence analysis. The alignment indicated that the sixteen Korean BNoVs clustered with the GIII-2 prototype, the Bo/Newbury2/UK strain.

Conclusions: In this study, norovirus (GIII-2) was detected in sixteen diarrheic calves. The alignment indicated that the sixteen BNoVs clustered with the GIII-2 prototype. Further investigations are needed to determine the clinical symptoms and epidemiology of norovirus infections in calves in Korea.

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P-063

Infection of *Clostridium* and *Salmonellain* Diarrhea Fecal Samples from Korean Swine Farms, 2015~2016

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Introduction: In many countries, contamination of meat and poultry products with bacteria potentially pathogenic to humans has become a major public health and trade concern. Specially, domestic pigs have been recognized as the source of many food poisoning microorganisms (1, 2), and in many cases, strategies to eliminate the food pathogens must be implemented on the farm; when an infected pigs enters the food-chain it is often more difficult to control growth, cross-contamination, and recontamination with the microbes *Clostridium. perfringens* and *salmonella spp.* are an important cause of foodborne illness. In this study, we identified incidence rate of *Clostridium. perfringens* and *salmonella spp.* intestinal diseases by different age groups, using porcine fecal swabs collected from domestic swine farm in Korea in 2015, 2016.

Materials and Methods: Molecularanalysis of *Clostridium* and *salmonella* pathogens was performed using fecal (n=1,583) samples from Korean swine farms collected between January, 2015 and August, 2016. DNA was extractedusing phenol: chloroform: isoamyl alcohol (25:24:1) (1). We have developed polymerase chain reaction (PCR) assay for the alpha toxin gene (cpa), allowing detection of entero toxigenic strains of *Clostridium. perfringens*. Primers were those designed by others (1) (F: 5'-GTTGATAGCGCAGGACAT GTTAAG-3', R: 5'-CATGTAGTCATCTGTTCCAGCATC-3'). For detect of *salmonella* designed specific primer sets (SAF:5'-TTGGTG TTTATGGGGTCGTT-3', SAR 5'-GGGCATACCATCCA GAGAAA-3'). For molecular typing analysis, PCR products directly asked for sequencing (Macrogen., South Korea).

Results: This study describes the monitoring of *Clostridium* and *salmonella* from diarrhea pigs samples in South Korea during a 2-year period. The *Clostridium* and *salmonella* screening results by RT-PCR from January to December 2015, showed positive rates 41/77 (53.25%), and 55/472 (11.65%) respectively. January to August 2016, showed 101/292 (34.59%), and 17/742 (2.29%) respectively.
In molecular typing analysis, *Salmonella* was the identified serotype I; *Typhimurium* from 9 positive samples, which were showed 98~99% similarity in South Korea. In *Clostridium*, 34 positive of *Clostridium. perfringens* showed the alpha toxin and were confirmed to be *Clostridium. perfringens*type A. (96~99% similiarity).

Conclusions: Theresults of this study illustrate the diversity of *Clostridium. perfringens* and *salmonella* isolates and the prevalence of these pathogens in Korean domestic swine farms. Our system of monitoring is effective in identifying most points of contamination in the production chain and will be useful in ongoing efforts to develop a *Salmonella and Clostridium* - free production system.

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