

bacteria flora in swine feces was different in the microbial community between associated with *Salmonella* and *Salmonella*-specific bacteriophage. Specific changes in the family levels associated with bacteriophage treatment showed decreases in the percentages of total sequence of Enterobacteriaceae which includes *Salmonella* spp.

References

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First report of bovine viral diarrhea infection in goats from the Republic of Korea

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Introduction: The genus *Pestivirus* includes four species, namely bovine viral diarrhoeavirus (BVDV), border disease virus (BDV), classical swine fever virus and atypical pestivirus of giraffe. BVDV is an economically important viral pathogen in the livestock industry worldwide. BVDV infection causes acute hemorrhagic syndrome, persistent infection, mucosal disease, as well as diseases of the respiratory tract and/or reproductive systems. BVDV can be divided into two major genotypes: BVDV1 and BVDV2. Both BVDV1 and BVDV2 may also infect sheep, goats, wild ruminants and pigs. The objective of this study was to investigate the presence of BVDV infection in goat from the Republic of Korea (ROK).

Materials and Methods: Whole blood samples from 10 goats on Namwon city, Jeonbuk province in the ROK were collected in April, 2015. This herd usually grazed in the pasture for at least one season every year. Total RNA was extracted from whole blood samples by using the RNAiso Plus (Takara, Japan) according to the manufacturer instructions. RT-PCR was performed with a Maxim RT-PCR

PreMix (Intron, Korea). Amplification and sequencing of 5'-UTR was performed using 324 (5'-ATGCC WTA GTA GGA CTA GCA-3' (W = A or T)) and 326 (5'-TCA ACT CCA TGT GCC ATG TAC-3') primers. The predicted size of the amplified PCR product was 288 bp. The PCR products were purified with a AccuPrep® PCR purification kit (Bioneer, Korea). The sequence data were aligned initially using the Clustal X (version 1.8). Phylogenetic tree based on the nucleotide alignments was constructed using the neighbor-joining (NJ) method [26]. Bootstrap analysis was carried out using 1,000 replications and the tree was visualized using Treeview.

Results: None of all animals exhibited any clinical sign of illness. BVDV infection was performed on ten blood samples by RT-PCR and two samples were identified as positive for BVDV. Two different BVDV sequences were identified. On one farm, even two different subtypes occurred that one case belonged to BVDV-1b and the other isolate classified as BVDV-2a. Phylogenetic analysis revealed that our BVDV-1a isolate (sanyang 7) was closely related to previously isolated from Korean goat and our BVDV2 isolate (sanyang 9) had the highest sequence homology against Sweden and USA strains, respectively.

Conclusions: Although it is known that BVDV infects goat, this is the first report of the identification of BVDV in the ROK. Therefore, further study should be described the genetic characterization whether different regions in the ROK belong to another genetic group, and focus on BVDV control procedures.

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Characterization of Potentially Probiotic *Bacillus subtilis* KBNP-BS3 as Livestock-environment Improving Agent

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Introduction: In recent years livestock operations units have grown in both number and size. Control of odor-causing compounds such as ammonia, hydrogen sulfide, or trimethylamine is a significant environmental issue regarding air quality. In this study, we present the characterization of *B. subtilis* strain KBNP-BS3 isolated from Cheonggukjang, with a view to selecting potential probiotics.

Materials and Methods: Cheonggukjang samples, produced in Yesan-gun of Chungcheongnam-do, Korea, were collected. After sampling, 3 g of Cheonggukjang was ground in a mortar and inoculated into 30 ml of autoclaved nutrient broth in a 100 ml Erlenmeyer flask immediately. After incubation at 37°C for 24 hours on an orbital shaker, 200 µl culture broth was spread onto plates of nutrient agar (NA). Then the plates were incubated at 37°C for 24 hours. Individual colonies were isolated from NA plates. This process was