Absence of Swine Acute Diarrhea Syndrome Coronavirus (SADS-CoV) in Korean Domestic Swine Farms

Hee-Chun Chung[1]#, Van Giap Nguyen[2]#, Cheong Ung Kim[3], Yong-Ho Park[3]*, Bong-Kyun Park[1]*

[1]Department of Veterinary Medicine, Virology Laboratory, College of Veterinary Medicine and Research Institute for Veterinary Science, Seoul National University, Seoul 151-742, Korea
[2]Department of Veterinary Microbiology and Infectious Diseases, Faculty of Veterinary Medicine, Vietnam University of Agriculture, Hanoi, Vietnam
[3]Department of Veterinary Microbiology, College of Veterinary Medicine and Research Institute for Veterinary Science, Seoul National University, Seoul 151-742, Republic of Korea
#These authors have contributed equally to this study

*Correspondence: Yong Ho Park, D.V.M., MSc, PhD, Department of Veterinary Microbiology, College of Veterinary Medicine and Research Institute for Veterinary Science, Seoul National University, Seoul 151-742, Republic of Korea, Tel: +82-2-880-1255; Fax: +82-2-885-0263; E-mail: yhp@snu.ac.kr

Bong-Kyun Park, D.V.M., MSc, PhD, Department of Veterinary Medicine, Virology Laboratory, College of Veterinary Medicine and Research Institute for Veterinary Science, Seoul National University, Seoul 151-742, Korea, Tel: +82-2-880-1255; Fax: +82-2-885-0263, E-mail: parkx026@snu.ac.kr

Abstract

Swine acute diarrhea syndrome (SADS) is a newly discovered coronavirus, which was first identified in South China in January 2017. SADS-CoV is an enveloped, positive and single stranded sense RNA virus that belongs to genus

Alphacoronavirus within the subfamily Orthocoronavirinae of the family Coronaviridae swine acute diarrhea syndrome coronavirus (SADS-CoV) is considered to be the causative agent of the fatal swine acute diarrhea syndrome (SADS) with clinical signs of severe, acute diarrhea and rapid weight loss in piglets, which affects the development of the porcine industry seriously.

In this study, no evidence of SADS-CoV in any of the samples.

Keywords: SADS; Corona virus; Causative agent; RNA

INTRODUCTION

In January 2017, SADS-CoV was detected in a swine farm and subsequently spread rapidly to three other farms in Guangdong Province and caused the fatal swine acute diarrhoea syndrome (SADS) [1,2]. The clinical manifestations of SADS-CoV are similar to those that caused by other swine because it has led to the death of almost 25,000 piglets in a short time and resulted in more significant economic losses (Sun et al.) [3].

Not only Korean Peninsula, located in Northeast Asia, is bordered on the north by China, but also Korea and China have similar temporal, ecological environment, this study conducted investigation of 1,116 samples of domestic pigs in Korea through 2017-2020.

MATERIALS AND METHODS

The intestine sample of pigs showing signs of diarrhea (n=1,116) collected January 2017 to July 2020 were screened for the presence of swine acute diarrhea syndrome coronavirus from 125 commercial farms in 9 provinces. The numbers of samples are 431 samples in 2017, 183 samples in 2018, 213 samples in 2019 and 239 samples in 2020. All these samples were randomly collected from commercial swine farms in nine provinces of South Korea. Age groups ranged from suckling to sow pigs. Samples were eluted in PBS, pH 7.2, and stored at -20°C until use. This study employed reverse transcriptase-PCR to detect SADS-CoV in fecal samples.

Total RNA was extracted by using Trizol LS (Invitrogen, USA) following the manufacturer's instructions. The RNA was then converted into cDNA with the use of random hexamers and commercial RNA to cDNA EcoDry Premix kit (Clontech, Japan) following the manufacturer's protocol. Finally, PCR reactions were performed with pathogen-specific primers using AccuPower® ProFi Taq PCR PreMix (Bioneer Ltd., Korea).

The SADS-CoV-specific primers were designed as

SDCOVF-25661 [5'-GGTTGAACAAAAACGCTGGC-3'] and SDCOVR-26020 [5'-ATGTCAACAGACTGTGACGGC-3'], which references of GenBank MT199598, MT199601, and MT039231 strains nucleocapsid protein gene (N gene). The PCR thermal profile was initial denaturation at 50°C for 30 min, 95°C for 5 min, followed by 40 cycles of 94°C for 30s, 58°C for 30s, 72°C for 30s, and a final extension at 72°C for 7 min.

RESULTS AND DISCUSSION

A total of 1116 Korean domestic porcine samples were included in the study. The goals of this study were to perform a survey for detection of SADS-CoV in Korean domestic porcine, investigate possible positive results by more specific tests and also to implement diagnostic analysis for further SADS-CoV monitor (Tables 1-3).

Table 1: Number of samples according to the age.

Age	No. of samples			
	2017	2018	2019	2020
Gilt	22	16	0	0
Sow	96	41	84	40
Suckling	108	41	62	39
Weaned	38	17	67	133
Grower	59	42	23	27
Finisher	108	26	27	0
	431	183	263	239

Table 2: Number of samples according to the province.

Province	No. of samples			
	2017	2018	2019	2020
Gyeonggi	256	100	76	74
Gangwon	11	25	53	0
Chungbuk	9	10	19	1
Chungnam	61	32	80	16
Gyeongbuk	7	0	0	6
Gyeongnam	16	0	21	49
Jeonbuk	71	12	14	2
Jeonnam	0	4	0	0
Jeju	0	0	0	91
	431	183	263	239

Table 3: Number of samples according to the month.

Month	No. of samples			
	2017	2018	2019	2020
January	39	10	11	30
February	49	16	0	11
March	68	51	16	28
April	29	12	25	121
May	45	31	34	6
June	30	5	24	3
July	10	26	65	40
August	49	3	21	
September	38	13	9	
October	10	7	1	
November	52	9	41	
December	12	0	16	
	431	183	263	239

However, there is no evidence of swine acute diarrhea syndrome coronavirus (SADS-CoV) in any of the samples (data not shown) even the large number of samples since 2017. Several hypotheses could explain this result. At first, technical and experimental design limitations could lead to false-negative results. So real-time PCR could be considered as a further step, which may increase sensitivity and specificity.

CONCLUSION

The present data do not indicate the virus circulating in Korea though, considering the recurrence of SADS-CoV outbreak in South China, it is important to monitor Korean domestic pigs for the presence of the viruses. By careful observation, SADS-CoV's prompt recognition would allow the implementation of effective countermeasures to prevent rapid spreading.

COMPLIANCE WITH ETHICAL STANDARDS

This article does not contain any studies with live animals performed by any of the authors.

REFERENCES

1. Gong L, Li J, Zhou Q, Xu Z, Chen L, Zhang Y, et al. A new bat-HKU2 like coronavirus in swine, China, 2017. Emerg Infect Dis. 2017;23(9):1607.

2. Zhou P, Fan H, Lan T, Yang XL, Shi WF, Zhang W, et al. Fatal swine acute diarrhoea syndrome caused by an HKU2 related coronavirus of bat origin. Nature. 2018;556(7700):255-258.

3. Sun Y, Zhou L, Lan T, Wu R, Chen J, Wu Z, et al. Retrospective detection and phylogenetic analysis of swine acute diarrhoea syndrome coronavirus in pigs in southern China. Transbound Emerg Dis. 2019;66(2):687-695.