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Prevalence of *Brachyspira hyodysenteriae* on selected swine farms in Gyeongbuk province by PCR

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Abstract

The purpose of this study is to determine the prevalence of *Brachyspira hyodysenteriae* from 43 swine farms with diarrhea or a history of diarrhea in Gyeongbuk province by PCR. The overall herd prevalence of *B hyodysenteriae* was 37.2%(16/43), and the average prevalence of *B hyodysenteriae* among all sampled pigs was 10.8%(50/462). Positive herds for *B hyodysenteriae* were distributed throughout Gyeongbuk province from 14.3~50%. Herd size had a effect on the frequency of *B hyodysenteriae*. The frequency of *B hyodysenteriae* in herds with less than 1,000 pigs was 47.4%, that of herds between 1,001 and 2,000 pigs was 41.7%. Also, the frequency of *B hyodysenteriae* in herds with more than 2,000 pigs was 16.7%.

Key words : Prevalence, *Brachyspira hyodysenteriae*, Swine dysentery, PCR

Introduction

Swine dysentery(SD) caused by *Brachyspira hyodysenteriae* is a severe mucohemorrhagic diarrheal disease that primarily affects pigs during the growing-finishing period. Six species of anaerobic intestinal spirochete are currently recognized in the genus *Brachyspira*[1]. Three of these are considered pathogenic in pigs : *B hyodysenteriae* is the agent of SD ; *B intermedia* has been implicated as a cause of typhlitis/colitis in both poultry and pigs ; and *B pilosicoli* is the agent of intestinal spirochetosis in pigs[2,3].

Diarrhea is the most consistent sign of SD. As the diarrhea progresses, watery stools containing blood, mucus and shreds of white mucofibrinous exudate are seen, with concurrent staining of rear quarters. Although the mechanism of tissue destruction

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has not been clearly elucidated, two toxins of *B hyodysenteriae*, lipopolysaccharide protein and hemolysin, have been described and characterized that may play a role in lesion development[4].

Diagnosis of SD should be made through the isolation of the causative agent. However, the isolation and culture of the organism require specialized anaerobic culture technique, which is not easy and time consuming. Use of polymerase chain reaction(PCR) has been accepted for the definitive identification of organism with high specificity and sensitivity. Accordingly, PCR methods have been developed for detection of pathogenic *B hyodysenteriae*[5~7].

In contrast to abundant epidemiological information on *B hyodysenteriae* overseas[8~10], there is relatively little published information on prevalence of *B hyodysenteriae* from clinical cases in Korea. We have already optimized an PCR assay for detection of *B hyodysenteriae* from diagnostic samples[11]. The purpose of this study is to determine the prevalence of *B hyodysenteriae* from swine farms with diarrhea or a history of diarrhea in Gyeongbuk province by previously developed PCR method.

Materials and Methods

Pig herds

A total of 43 farrow to finish herds with between 500 to 5,000 pigs per herd in Gyeongbuk province were selected on the basis of a history of diarrhea in a growing and finishing herd or presence of diarrhea at the time of the study.

Fecal samples and DNA extraction

A total of 462 fecal samples from 43 pig herds were collected between September 1999 and February 2000. Fecal specimens were randomly sampled from 4~16 growing/finishing period pigs of each herd. All specimens were taken from freshly deposited feces and were submitted to the laboratory. Total DNA was extracted from 0.2g of each fecal samples collected with sterile cotton swab, and processed by the methods as described[12].

PCR and oligonucleotides

The PCR was carried out as described by Suh *et al*[11]. The two primers for specific amplification of *B hyodysenteriae* defining a 421-bp DNA fragment by PCR were as following : forward primer 5'-GCTGGAGATGATGCTTCTGG-3' ; reverse primer 5'-GTCCAAGAGCTTGGCTGTTC-3'. The primer sets were designed using Primer 3 program(http://www.genome.wi.mit.edu) and synthesized from Bioneer Co (Cheongju, Korea).

Results and Discussion

The overall herd prevalence of *B hyodysenteriae* was 37.2%(16/43). Also, the average prevalence of *B hyodysenteriae* among all sampled pigs was 10.8%(50/462) (Table 1). Positive herds for *B hyodysenteriae* were distributed throughout Gyeongbuk province, but lowest in Youngchun(14.3%, 1/7) (Table 2). Herd size had a effect on the frequency of *B hyodysenteriae*. The frequency of *B hyodysenteriae* in herds with less than 1,000 pigs was 47.4%, that of herds between 1,001 and 2,000 pigs was 41.7%. Also, the frequency of *B hyodysenteriae* in herds with more than 2,000 pigs was 16.7%(Table 3). It was notable that only 2 of

Table 1. Prevalence of *B hyodysenteriae* in swine farms

No(%) of positive herds (n=43)	No(%) of positive pigs (n=462)
16(37.2)	50(10.8)

Table 2. Regional distribution of positive herds for *B hyodysenteriae*

Region	*B hyodysenteriae*	%
Andong(4)*	2	50
Koryung(5)	2	40
Kunwy(9)	4	44.4
Kyungju(4)	2	50
Pohang(6)	2	33.3
Youngchun(7)	1	14.3
Chungdo(2)	1	50
Sangju(4)	1	25
Sungju(2)	1	50
Total(43)	16	37.2

*( ) : No of herds selected.

Table 3. Effect of herd size on the frequence of *B hyodysenteriae*

Herd size	No of herds	*B hyodysenteriae*	%
< 1,000	19	9	47.4
1,001-2,000	12	5	41.7
> 2,000	12	2	16.7
Total	43	16	37.2

12 larger herds were affected with *B hyodysenteriae*.

Enteric diseases are acknowledged as important causes of performance and mortality in grower-finisher pigs. In addition, the treatment of these conditions has been reported to account for more than 50% of the antibiotics administered to this class of pig[13]. SD has been widely distributed throughout the world, about 18~36% of pig herds being infected overseas[8~10]. Since first outbreak report of SD at Kimhae in 1975 by Bak *et al*[14], It has been known that about 17~30% of pig herds in Korea were infected with *B hyodysenteriae*[15,16]. The herd prevalence of 37.2% and individual pig prevalence of 10.8% in this study were similar to those from the results by Jung *et al*[16], 30.7% and 10.6%, respectively.

It has been reported that outbreaks of and SD occur more often in the large production unit[17,18]. That is, the association between the herd size and disease outbreak. However, the results in this study showed the opposite result. ; only 2(16.7%) herds showed positive with *B hyodysenteriae*. Seasonality of the diseases has also been reported. Jackson and Baker[19] reported an increased incidence of SD during the winter. A sampling period throughout the year should be utilized to analyze association between seasonality and disease outbreak in this study.

Although the present study did not detect a relation between any of other pathogen such as viral, parasitic and/or metabolic disorders, it could be concluded that *B hyodysenteriae* was prevalent in grower-finisher pigs with clinical signs of diarrhea.

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