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Swine dysentery is a highly contagious diarrheal disease of growing and finishing swine causing estimated losses of more than $2.4 million monthly to Iowa pork producers.

The spiral-shaped spirochete bacterium, *Serpulina hyodysenteriae*, is routinely identified by bacteriologic culture of intestinal specimens of swine affected with the disease. Specific differentiation of *S. hyodysenteriae* from other bacteria normally present in the intestines of swine is now possible with the use of a nucleic acid-based test developed by scientists in the Department of Veterinary & Biomedical Sciences at UN-L. The test can detect very low numbers of *S. hyodysenteriae* directly in the stools of swine by a process known as polymerase chain reaction (PCR).

We are investigating alternative ways to reduce the economic losses due to swine dysentery. *Serpulina hyodysenteriae* is known to occur outside the pig; however, it is not clear how this affects persistence of the disease on swine farms. Also, house mice (*Mus musculus*) have been shown to be involved in the spread of*S. hyodysenteriae* on farms with swine dysentery, but the spirochete bacterium of mice has not been conclusively identified as *S. hyodysenteriae*. Developing more effective control strategies for swine dysentery requires a more complete understanding of the factors involved in persistence of the spirochete bacterium in pigs and in habitats other than its natural host.

Serpulina hyodysenteriae strains belong to a species of bacteria with many shared characteristics; however, it is possible to distinguish variants within the species using specialized methods. One of these methods uses enzymatic digestion of deoxyribonucleic acid (DNA) obtained from closely related bacterial strains to compare them to each other. This method takes advantage of small differences in the DNA of individual strains to produce patterns of DNA banding or "DNA fingerprint" after separation of the DNA fragments by gel electrophoresis. DNA fingerprinting has become a method of choice for studies aimed at comparing organisms taken from different backgrounds and understanding the spread of disease-causing bacteria.

The objectives of this work were: (i) Determine the relationship between persistence of *S. hyodysenteriae* on farms with swine dysentery and the presence of *S. hyodysenteriae* in pigs, the environment, and house mice on the same farm; and (ii) confirm the presence of *S. hyodysenteriae* outside of its natural host using the PCR test.

Study Design

A cross-sectional study of four midwestern confinement-rearing swine operations with a history of swine dysentery was begun in 1991. The farms were identified on the basis of positive isolations of *S. hyodysenteriae* from the intestines of pigs submitted to the Veterinary Diagnostic Center-Lincoln for laboratory investigations. Each farm was visited and data pertinent to disease status, building design, management practices, and production records was collected. Stool samples from pigs with or without diarrhea at all stages of production, and manure samples from floors and gutters were collected. House mice were captured with multiple-catch mouse traps placed in and around farm buildings.

Each specimen was processed for bacteriologic culture and isolation of spirochetes by conventional methods. Cultures that were positive for the presence of spirochetes were subcultured to purity. Total DNA from representative strains of each source on each farm were examined using the *S. hyodysenteriae*-specific PCR test, and compared with each other by DNA fingerprinting. Recovery rates and DNA fingerprint patterns of *S. hyodysenteriae* were correlated with the source of isolation on each farm.

Results and Discussion

Pertinent management and medication practices for each farm are summarized in Table 1. Farm A was visited once in March, 1992 and again in July, 1992. Farm A and farm B were totally confined operations with ongoing swine dysentery in spite of continuous medication for the past 10 and 6 years, respectively. Farm C had lost a sow, 2 gilts, and approximately 30 piglets to swine dysentery in the month preceding our first visit in January, 1992.

The severity of the clinical problem was significantly reduced, 6 months later at our second visit, by cleaning and disinfecting the premises,

(Continued on next page)

Table 1. Management and medication practices on farms affected with swine dysentery.

Farm	Management	Number of animals	Stage of production	Medication		
				Feed†	Water‡	Parenteral§
A	Farrow/finish	330-sow	Grower	Carbadox	None	Tylosin
			Finishing	Lincomycin Tiamulin		
B	Farrow/finish	170-sow	Nursery	Carbadox Arsanilic acid	None	None
			Grow/finish	Tiamulin		
C	Farrow/feeder	60-sow	Grower	Carbadox	Tiamulin	Lincomycin
D	Finisher	350-pigs	Finish	Tiamulin	Gentamicin	None

† Inclusion rates as follows: carbadox = 50/t; lincomycin = 100 g/t; tiamulin = 35 g/t; arsanilic acid = 45 g/t.
‡ Tiamulin = 3.5 mg/lb/day for 5 days; gentamicin = 50 mg/gal for 5 days.
§ Tylosin = 4 mg/lb twice per day for 3 days; Lincomycin = 5 mg/kg for 3 days.

and medicating the pigs (Table 1). This farm consisted of a farrowing house with open dirt lots and sheds for breeding/gestation, and small sheds with outdoor solid concrete slabs for growing pigs. An outbreak of acute swine dysentery was brought under control with medication within a week from visiting farm D in October, 1991 (Table 1). The farm consisted of 11 outdoor pens with solid concrete slabs adjoining a shed. Each pen had groups of 20 to 50 pigs ranging in size from 50 to 200 lbs.

The cumulative results of spirochete isolations from specimens collected on each farm are presented in Table 2. *Serpulina hyodysenteriae* was isolated from swine on three farms, from the environment on all the farms, and from house mice on two farms. Except for a dramatic reduction in the prevalence of *S. hyodysenteriae* in swine at the second visit on farm C, the percentage of *S. hyodysenteriae* isolations were similar on two farms where sampling was repeated at several month intervals.

Table 2. Cumulative spirochete isolation results from specimens collected on farms with swine dysentery.

Farm	Visit	Hemolytic Pattern†	No. Isolations (% Recovery)		
			Pigs	Environment	Mice
A	1	Strong	16 (50.0)	9 (45.0)	0 (0.0)
		Weak	3 (9.4)	1 (5.0)	0 (0.0)
	Total no. specimens examined:		32	20	3
	2	Strong	1 (50.0)	7 (46.7)	0 (0.0)
		Weak	0 (0.0)	0 (0.0)	0 (0.0)
	Total no. specimens examined:		2	15	0
B	1	Strong	0 (0.0)	6 (17.1)	3 (9.7)
		Weak	0 (0.0)	0 (0.0)	0 (0.0)
	Total no. specimens examined:		27	35	31
C	1	Strong	15 (28.8)	5 (41.7)	1 (16.7)
		Weak	1 (1.9)	1 (8.3)	0 (0.0)
	Total no. specimens examined:		52	12	6
	2	Strong	1 (9.1)	7 (53.8)	0 (0.0)
		Weak	0 (0.0)	1 (7.7)	0 (0.0)
	Total no. specimens examined:		11	13	3
D	1	Strong	5 (15.6)	1 (5.0)	0 (0.0)
		Weak	1 (3.1)	0 (0.0)	0 (0.0)
	Total no. specimens examined:		32	20	3

†A strong hemolytic pattern suggests *Serpulina hyodysenteriae* whereas a weak hemolytic pattern suggests spirochetes distinct from *S. hyodysenteriae*.

The prevalence of *S. hyodysenteriae*-shedding in pigs ranged from 0% on farm B to 50% on farm A. Because pigs on each farm were medicated for swine dysentery, factors other than medication appeared to affect the pattern of *S. hyodysenteriae* shedding by the pigs. Low *S. hyodysenteriae* shedding in swine from farm B and farm D together with low environmental contamination suggested that the environment may be a major contributor to reinfection of medicated pigs. Scraping of floors together with sunlight and dryness appeared to be effective in reducing environmental contamination on farm D.

Although house mice were caught on all the farms, *S. hyodysenteriae* was isolated from house mice only on two farms; one mouse each in the farrowing houses on farm B and farm C, and two mice in a finishing building on farm B (Table 2 and Table 3). Considering the prevalence of *S. hyodysenteriae*-positive mice on farms B and C, sampling of mice on farms A and D might have been insufficient to demonstrate *S. hyodysenteriae* in the mouse populations on those farms. Mice infected with *S. hyodysenteriae* are known to transmit the disease to pigs by contaminating feedstuffs with their stools. Although, the prevalence of mice carrying *S. hyodysenteriae* was small, rodent control should continue to be an essential part of swine dysentery control and eradication.

Spirochetes that are weakly hemolytic by culture are known to be different from *S. hyodysenteriae*, and some of these spirochetes are associated with a diarrheal disease of swine different from swine dysentery and designated porcine colonic spirochetosis. The weakly hemolytic spirochetes isolated from pigs on farm D and from pigs and the environment on farm A and farm C were not characterized further (Table 2). The widespread distribution of weakly hemolytic spirochetes, which can be difficult to differentiate from *S. hyodysenteriae* by conventional culture, emphasizes the usefulness of the PCR test for laboratory confirmation of swine dysentery; none of the weakly

hemolytic strains tested gave positive results in the *S. hyodysenteriae*-specific PCR test (Table 3). Weakly hemolytic spirochetes were not isolated from house mice, suggesting that mice might not be an important source for persistence of these organisms on swine farms.

Geographic variations in the prevalence of different strains of *S. hyodysenteriae*, as well as the presence of different strains of *S. hyodysenteriae* on the same farm can affect the interpretation of antibiotic sensitivity testing and the efficacy of preventative strategies including vaccination with defined antigen preparations. DNA fingerprint analyses indicated only one pattern (pattern A) in all the samples examined (Table 3). This suggested that *S. hyodysenteriae* strains present in different sources on each farm and also between farms in the midwest were highly conserved.

Table 3. Cumulative results of *Serpulina hyodysenteriae*-specific PCR and DNA fingerprint analyses of representative spirochete strains isolated from specimens obtained from farms with swine dysentery.

Farm	Hemolytic Pattern	No. PCR Positive/No. Tested			DNA Fingerprint Pattern/No. Tested		
		Pigs	Environment	Mice	Pigs	Environment	Mice
A	Strong	5/5	1/1	NA†	A/1	A/6	NA
	Weak	0/1	0/0	NA	ND‡/0	ND/0	NA
B	Strong	NA	2/2	1/1	NA	A/6	A/3
	Weak	NA	NA	NA	NA	NA	NA
C	Strong	0/0	1/1	1/1	A/2	A/5	A/1
	Weak	0/1	0/1	NA	ND/0	ND/0	NA
D	Strong	3/3	1/1	NA	A/1	A/1	NA
	Weak	0/0	NA	NA	ND/0	NA	NA

†NA = Not applicable.
‡ND = Not determined.

Conclusions

Results from this investigation provide information on the distribution of *S. hyodysenteriae* on farms with swine dysentery. Environmental contamination appears to be a major contributor to persistence of *S. hyodysenteriae* on swine farms affected with swine dysentery.

Medication of pigs can reduce the prevalence of *S. hyodysenteriae* in the pigs, but successful control and/or eradication of the disease requires cleaning and disinfection of premises and control of rodents. Environmental sampling rather than sampling of medicated pigs may be more accurate for *S. hyodysenteriae* detection when monitoring progress of eradication efforts.

Absence of regional variation in the distribution of *S. hyodysenteriae* strains from different sources on each farm and also between farms suggested that broad control strategies such as strain specific vaccines may be successful in controlling swine dysentery in the midwest.

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