Occurrence of *Salmonella* serotype Typhimurium DT104 on a commercial swine farm before, during, and after depopulation and repopulation

Matthew M. Erdman, DVM, PhD; Isabel T. Harris, DVM, PhD; Montserrat Torremorell, DVM, PhD; Vincil M. Wilt, DVM; D. L. Hank Harris, DVM, PhD

Objective—To determine whether depopulation-repopulation could be used to eradicate *Salmonella* serotype Typhimurium DT104 from a commercial swine farm in the midwestern United States.

Design—Observational study.

Sample Population—A commercial swine farm undergoing depopulation-repopulation to eliminate porcine reproductive and respiratory syndrome virus and *Mycoplasma hyopneumoniae*.

Procedure—Pooled fecal samples, tissue samples, and serum samples were collected from pigs on the farm before and after depopulation-repopulation. When there were no pigs on the farm, environmental swab specimens were collected for bacterial culture. Serum was analyzed for anti-*Salmonella* antibodies with an indirect ELISA. *Salmonella* isolates obtained by bacterial culture of fecal, tissue, and environmental samples were characterized by means of serotyping, phage typing, pulsed-field gel electrophoresis (PFGE), and antimicrobial susceptibility testing.

Results—167 *Salmonella* isolates representing 9 serotypes were recovered from the farm. Results of PFGE and antimicrobial susceptibility testing suggested that *S* Typhimurium DT104 strain was not eradicated from the farm. However, seroprevalence of anti-*Salmonella* antibodies and the percentage of pooled fecal samples positive for *Salmonella* spp were significantly decreased following repopulation.

Conclusions and Clinical Relevance—Results suggested that depopulation-repopulation in conjunction with stringent cleaning and disinfection, attention to biosecurity procedures, control of other diseases, and changes in feed management may reduce the occurrence of, but likely will not eliminate, *Salmonella* spp in commercial swine herds. (*J Am Vet Med Assoc* 2005;227:460–466)

RUMINANTS/ SWINE

In food animals such as pigs, clinical infections with salmonellae have been associated with high morbidity and mortality rates. Subclinical infection may or may not lead to economic losses but poses a serious threat to food safety.[1] *Salmonella* infection has been estimated to cost pork producers $100 million annually,[2] and decreasing the prevalence of *Salmonella* organisms on pig farms has been shown to result in economic benefits.[3] In addition, studies[4-6] have identified the lairage period at the abattoir as an important time when pigs can become infected with *Salmonella* spp. Thus, decreasing the number of *Salmonella* carriers entering the abattoir may contribute to production of safer pork. Even if lairage operations are such that the prevalence of *Salmonella* infection does not increase during this period, shipping large numbers of *Salmonella*-infected pigs may still pose a food safety risk.[7]

Salmonella serotype Typhimurium DT104 has drawn considerable attention recently because the organism is widely distributed, can be isolated from humans as well as from food-producing animals, and typically is resistant to multiple antimicrobials. *Salmonella* Typhimurium DT104 isolates carry resistance genes on plasmids and the chromosome and are typically resistant to ampicillin, chloramphenicol, streptomycin, sulfonamides, and tetracylines (resistance type ACSSuT), although they may also be resistant to other antimicrobials.[8] Studies[9,10] suggesting that humans can acquire *S* Typhimurium DT104 from food animals have fueled efforts to control the organism at the preharvest level. In addition, *S* Typhimurium DT104 has been associated with diarrhea, septicemia, and meningitis in pigs,[11] making control of the organism important from a production standpoint as well.

It is not clear whether or how easily *S* Typhimurium DT104 can be eradicated from swine farms. Recently, we were involved with a swine farm located in the Midwest of the United States that was undergoing depopulation-repopulation in an effort to eliminate **porcine reproductive and respiratory syndrome virus (PRRSV)** and *Mycoplasma hyopneumoniae*, which provided an opportunity to determine whether *S* Typhimurium DT104 could also be eradicated from the farm. The purpose of the study reported here, therefore, was to determine whether depopulation-repopulation could be used to eradicate *S* Typhimurium DT104 from a commercial swine farm.

Materials and Methods

Herd history—The farm studied was a 1,300-sow, single-site, farrow-to-finish operation that used all-in–all-out procedures by room (nursery and finisher). The farm was being depopulated because of the adverse effects of PRRSV and *M hyopneumoniae* infection on herd health. Infection with PRRSV and *M hyopneumoniae* had been confirmed on the basis of consistent clinical signs and results of laboratory test-

From the Departments of Veterinary Microbiology (Erdman) and Veterinary Diagnostic and Production Animal Medicine (Harris D), College of Veterinary Medicine, and the Department of Animal Science, College of Agriculture (Erdman, Harris I, Harris D), Iowa State University, Ames, IA 50011; PIC USA, 3033 Nashville Rd, Franklin, KY 42134 (Torremorell); and the Paris Veterinary Clinic, 25010 Business Hwy 24, Paris, MO 65275 (Wilt).

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Address correspondence to Dr. Erdman.

ing, including an ELISA for *M hyopneumoniae* infection and an ELISA, polymerase chain reaction assay, indirect fluorescent antibody assay, and virus isolation for PRRSV infection. In addition, clinical salmonellosis was identified among the finishing pigs (3 to 6 months of age) and sudden death, diarrhea, and colonic ulcers seen at necropsy were all attributed to *S* Typhimurium infection. During the 12 months prior to depopulation, the mortality rate among finishing pigs ranged from 6% to 8%, with more than half of all deaths in this group attributed to clinical salmonellosis. Treatment generally consisted of administration of neomycin via the water.

Depopulation-repopulation procedure—The last mating of sows on the farm took place during mid-October 2001, and the farm was depopulated by mid-February 2002. Following depopulation, all buildings were extensively cleaned and disinfected. The cleaning protocol consisted of removal of all visible organic material followed by application of a disinfectant.[a] Emphasis was placed on cleaning feed lines, feeders, the ventilation system, water lines, ceilings, walls, and floors. Slats were not removed from the floors but were repeatedly chlorinated. The lagoon was pumped as low as possible, and the pits were drained. After being drained, the pits were thoroughly cleaned, and chlorine solution (0.45 kg/7,570 L of water) was added to the level of the bottom of the slats. Disposable materials, such as syringes, gloves, pharmaceuticals, vaccines, and other consumables, present on the farm prior to depopulation were discarded.

Offices, the shower area, and storage spaces were completely cleaned and remodeled as needed. Doors and windows were adjusted to ensure that they sealed tightly, and all holes around pipes and augers and at the ends of ribbed metal siding were sealed with mortar or metal. Rodent control was addressed first by sweeping and scraping all aisles and corners on a daily basis to remove foodstuffs, feces, and other debris. Rodent bait was placed inside cut polyvinyl chloride pipes that were placed approximately every 3.3 m for mice and every 12 m for rats inside and outside the buildings. A 15-cm-deep × 1-m-wide perimeter of 2.5-cm-diameter gravel was added to the outside of all buildings.

Various changes to farm management were implemented. Composting of waste material was discontinued in favor of burial. Incoming supplies were fogged with chlorine dioxide and held in isolation for at least 3 days. Changes in transport protocols were made so that cull animals were transported to a remote location and off-loaded to another vehicle before being transported to slaughter. Finally, a new feed mill was chosen and the ration changed from a pelleted ration to a meal.

An off-site location approximately 125 miles away was chosen for breeding replacement stock. This location had been thoroughly cleaned and disinfected prior to receiving replacement animals and had no history of clinical *Salmonella* infection. The breeding stock was acquired from a source known to be free from PRRSV and *M hyopneumoniae* infection, as determined by means of diagnostic testing, that did not have any detectable incidence of *Salmonella* infection, as determined by means of bacterial culture and serologic testing.

The entire farm was empty for at least 30 days after cleaning and disinfection before replacement gilts were transported to the farm, with some portions of the farm empty for > 30 days. Breeding of replacement gilts began in December 2001, and gilts were not transported to the depopulated farm until at least 40 days after they had been bred. For their first 2 weeks on the farm, incoming gilts were given feed to which tylosin had been added at a rate of 40 g/ton. Bred gilts began arriving on the farm in mid-March 2002, and the entire farm was repopulated by August 2002.

Sample collection and processing—Three types of samples were collected during the study: individual blood samples, pooled fecal samples, and environmental swab specimens. Beginning in June 1998, jugular vein blood samples (10 mL) were collected from 10 to 40 pigs each month. Samples were shipped overnight on ice to Iowa State University, where serum was harvested by means of centrifugation and tested for anti-*Salmonella* antibody with an indirect ELISA.[12] Briefly, lipopolysaccharide in 0.1M sodium carbonate buffer (pH, 9.6) was added to wells in 96-well flat-bottom plates, and plates were incubated overnight at 4°C. Plates were emptied, and nonspecific binding was blocked by adding **phosphate-buffered saline (0.9% NaCl) solution (PBSS)** containing Tween 20 and 1% **bovine serum albumin (BSA)** for 15 minutes. Plates were then washed once with PBSS containing Tween 20, and test sera diluted 1:400 in PBSS containing Tween 20 and 1% BSA were added in duplicate to the plate. Control samples on each plate included PBSS containing Tween 20 and 1% BSA, a negative serum sample, serum samples from 4 pigs infected with *S* Typhimurium, and serum samples from 2 pigs infected with *Salmonella* serotype Choleraesuis. Plates were incubated for 1 hour at room temperature, then washed 3 times. Rabbit anti-swine IgG conjugated with horseradish peroxidase was added to each well, and plates were again incubated for 1 hour at room temperature. Plates were washed, and 100 mL of the enzyme substrate O-phenylenediamine dihydrochloride was added to each well. Plates were incubated for 10 minutes, and color development was stopped by addition of 0.5M sulfuric acid. **Optical density (OD)** of each well was read at 490 nm with an ELISA plate reader.[b] A regression line was created from the OD values for the negative serum sample and the 4 *S* Typhimurium-positive control samples, and OD percentage was calculated for test samples. Samples with OD percentage ≥ 30% were considered positive for exposure to *Salmonella* antigen. Seroprevalence was determined by dividing number of samples with positive results by total number of samples tested.

Pooled fecal samples were collected from pens in the finishing barn at various times starting in August 1999 and continuing through April 2003. A single pooled fecal sample was collected from a pen in the nursery barn prior to repopulation of the finishing barn. Fecal samples were collected and processed as described.[4] Briefly, 25 g of feces were collected in a sterile bag and shipped on ice overnight to the laboratory. Samples were processed immediately on arrival at the laboratory so that ≤ 24 hours had elapsed since collection. Fecal samples that arrived after 24 hours or were shipped without ice packs were discarded, and new samples were requested. Samples were pre-enriched in buffered peptone water,[c] then selectively enriched in Rappaport-Vassiladis broth[c] and plated on xylose-lysine-deoxycholate agar.[c] Up to 5 suspect colonies/plate were selected, and identification was confirmed by means of standard biochemical tests (Kligler agar, phenylalanine agar, lysine iron agar, and sulfide indole motility agar). *Salmonella* isolates were serogrouped with *Salmonella* O antiserum[c] and submitted to the National Veterinary Services Laboratory in Ames, Iowa, for serotyping and phage typing.

Starting in the winter of 2001 and continuing into the summer of 2002, environmental swab specimens were obtained to assess efficacy of cleaning and disinfection procedures. Areas from which specimens were obtained included feed bins, feeders, feed lines, nipple waterers, mist lines, floor drains, pits, pit plugs, and slats. Drag swab specimens were obtained by dipping a sterile 4 × 4-inch gauze pad in a 50-mL vial containing 40 mL of buffered peptone water and swabbing the area of interest. If the area was flat, a 10 × 10-inch area was swabbed with the moistened gauze. For other areas (eg, waterers, feeders, and drains), the entire area was swabbed. Following swabbing, the gauze was submerged in the vial containing buffered peptone water and transported to the laboratory. Bacterial culture procedures were as described

for fecal samples. If bacterial culture yielded *Salmonella* organisms, the area was again cleaned and disinfected and additional swab specimens were obtained within 1 to 2 days.

At various times during the study, tissue samples from clinically affected pigs were submitted to the University of Minnesota or University of Missouri veterinary diagnostic laboratory for testing. Tissue samples that were typically collected included portions of the lung and intestine and lymph node and blood samples. These samples were collected from ill pigs that had died or were euthanatized and were submitted for diagnosis of various diseases including, but not limited to, salmonellosis. Whenever *Salmonella* spp was cultured, isolates were forwarded to our laboratory for further analysis.

Antimicrobial susceptibility testing—Antimicrobial susceptibility of *Salmonella* isolates was determined by use of the microdilution broth method for gram-negative organisms[13] with plates[d] designed for the National Antimicrobial Resistance Monitoring System.[14] Susceptibility to amikacin (breakpoint **minimum inhibitory concentration [MIC]**, 64 mg/mL), amoxicillin-clavulanic acid (breakpoint MIC, 32 mg/mL), ampicillin (breakpoint MIC, 32 mg/mL), ceftiofur (breakpoint MIC, 8 mg/mL), cefoxitin (breakpoint MIC, 32 mg/mL), ceftriaxone (breakpoint MIC, 64 mg/mL), cephalothin (breakpoint MIC, 32 mg/mL), chloramphenicol (breakpoint MIC, 32 mg/mL), ciprofloxacin (breakpoint MIC, 4 mg/mL), gentamicin (breakpoint MIC, 16 mg/mL), kanamycin (breakpoint MIC, 64 mg/mL), nalidixic acid (breakpoint MIC, 32 mg/mL), streptomycin (breakpoint MIC, 64 mg/mL), sulfamethoxazole (breakpoint MIC, 512 mg/mL), tetracycline (breakpoint MIC, 16 mg/mL), and trimethoprim-sulfamethoxazole (breakpoint MIC, 4 mg/mL for trimethoprim and 76 mg/mL for sulfamethoxazole) was determined. *Escherichia coli* ATCC 25922 was included in all runs as the quality control standard.

Genomic analysis—Pulsed-field gel electrophoresis (PFGE) following *Xba*1 digestion of genomic DNA was performed to compare *Salmonella* isolates as described.[15] Images were analyzed with standard software.[e] Cluster and dendrogram analyses were performed by use of the unweighted pair group method with arithmetic averages, Dice coefficient, and 0.8% optimization with 1.0% band position tolerances.

Table 1—Results of *Salmonella* culture of tissue, fecal, and environmental samples obtained from a commercial swine farm before, during, and after depopulation-repopulation.

Collection date	Sample type	Source	No. submitted	No. with positive result	Serotype (No.)
Before depopulation					
Oct 1997	TS	Finisher	1	1	Typhimurium cop (1)
Jan 1999	TS	Finisher	1	1	Typhimurium (1)
Mar 1999	TS	Finisher	1	1	Typhimurium cop (1)
Aug 1999	PF	Finisher	20	0	NA
Sep 1999	PF	Finisher	20	0	NA
Nov 1999	TS	Finisher	2	2	Typhimurium cop (2)
Feb 2000	PF	Finisher	20	3	Typhimurium cop (5)
Feb 2000	TS	Finisher	1	1	Infantis (1)
Apr 2000	PF	Finisher	20	6	Typhimurium cop (11) 6,7:nonmotile (3)
May 2000	PF	Finisher	11	1	Typhimurium cop (1)
Jun 2000	PF	Finisher	20	1	Typhimurium cop (1)
Jul 2000	PF	Finisher	8	0	NA
Dec 2000	PF	Finisher	20	0	Untypable (1)
Jan 2001	PF	Finisher	20	1	Putten (3)
Feb 2001	PF	Finisher	20	11	Typhimurium cop (24) Worthington (24)
Mar 2001	PF	Finisher	20	8	Typhimurium cop (35)
Apr 2001	PF	Finisher	20	0	NA
May 2001	PF	Finisher	20	2	Typhimurium cop (7)
During depopulation-repopulation					
Dec 2001	EV	Finisher	40	1	Worthington (5)
Jan 2002	EV	Finisher	40	0	NA
Feb 2002	EV	Finisher	120	1	Typhimurium cop (2)
Jul 2002	EV	Farrowing	23	0	NA
	EV	Nursery	50	3	Brandenburg (5) Worthington (8)
	EV	Finisher	47	3	Brandenburg (9) Heidelberg (5)
	PF	Farrowing	20	0	NA
	PF	Nursery	40	2	Brandenburg (10)
	PF	Finisher	40	0	NA
After repopulation					
Sep 2002	TS	Finisher	1	1	Typhimurium cop (1)
Feb 2003	PF	Finisher	20	0	NA
Mar 2003	PF	Finisher	20	0	NA
Apr 2003	PF	Finisher	20	0	NA
Sep 2003	TS	Finisher	1	1	Typhimurium cop (1)
Feb 2004	PF	Finisher	20	0	NA
Jun 2004	PF	Finisher	20	0	NA
Jul 2004	PF	Finisher	20	0	NA

TS = Tissue (ie, intestine, lung, and lymph node collected at necropsy). PF = Pooled fecal (ie, 25 g of feces from a pen containing approx 20 finishing pigs). EV = Environmental (ie, swab samples from feeders, feed lines, nipple waterers, mist lines, pits, pit plugs, and slats). NA = Not applicable. Typhimurium cop = Typhimurium var Copenhagen.

Statistical analyses—The χ^2 test was used to compare proportions of positive test results before and after depopulation-repopulation for serum and pooled fecal samples. Values of $P < 0.05$ were considered significant.

Results

Following repopulation, the farm was inspected monthly and samples were submitted for detection of PRRSV and *M hyopneumoniae* infection. During the first 24 months after repopulation, none of the pigs on the farm developed clinical signs of PRRSV or *M hyopneumoniae* infection and results of diagnostic testing (ELISA, polymerase chain reaction assay, indirect fluorescent antibody assay, and virus isolation for PRRSV infection and an ELISA for *M hyopneumoniae* infection) were negative. In addition, none of the finishing pigs developed signs of clinical salmonellosis (ie, diarrhea or typical postmortem abnormalities) during this period and mortality rate for growing and finishing pigs decreased by 40%, compared with the rate prior to depopulation.

A total of 167 *Salmonella* isolates representing 9 serotypes were recovered from the farm during the study period (**Table 1**). Of these, 115 were recovered from pooled fecal samples, 44 were recovered from environmental swab specimens, and 8 were recovered from tissue samples from clinically affected pigs. One hundred twenty-one *Salmonella* isolates were obtained prior to depopulation, including serotypes Typhimurium (n = 1), Typhimurium var Copenhagen (88), Worthington (24), Infantis (1), Putten (3), and 6,7:nonmotile (3) and an untypable isolate (1). Six of these isolates were recovered from pigs with clinical salmonellosis, and the remaining 115 were recovered from pooled fecal samples.

Environmental testing during depopulation indicated that *Salmonella* spp persisted on the farm, and 44 *Salmonella* isolates were recovered from environmental swab specimens or from pooled fecal samples collected following partial repopulation, including serotypes Worthington (n = 13), Typhimurium var Copenhagen (2), Brandenburg (24), and Heidelberg (5). Pooled fecal samples that yielded *Salmonella* isolates were collected from nursery pens prior to movement of pigs into the finishing barn. Environmental swab specimens that yielded *Salmonella* isolates were collected from slats, pit plugs, floor drains, nipple waterers, and feeders. On the basis of these results, cleaning and disinfection of the finishing barns was repeated with special attention given to those areas that had yielded positive results. Pigs were not moved into the finishing barns until results of bacterial culture of environmental swab specimens were negative.

During the 2 years following repopulation of the farm, 23 tissue samples from clinically ill pigs were submitted for *Salmonella* testing and *Salmonella* organisms were isolated from 2 (9%). Both isolates were identified as serotype Typhimurium var Copenhagen. *Salmonella* organisms were not isolated from any of the pooled fecal samples submitted during this period. The percentage of pooled fecal samples positive for *Salmonella* spp following repopulation (0%) was significantly lower than the percentage prior to depopulation (15.5%).

Ten PFGE band patterns were obtained for the 167 *Salmonella* isolates (**Table 2**). Considering all of the isolates, resistance to tetracycline and resistance to streptomycin were most common, whereas all isolates tested were susceptible to amikacin, ceftiofur, ciprofloxacin, amoxicillin-clavulanic acid, ceftriaxone, cefoxitin, gentamicin, kanamycin, and trimethoprim-sulfamethoxazole. Only 1 serotype, Typhimurium var Copenhagen, was isolated during all 3 stages of the study, and PFGE revealed that all isolates of this serotype were of subtype ST18 (**Figure 1**). Further analysis revealed that all were phage-type *S* Typhimurium DT104. Antimicrobial susceptibility profiling of these ST18 isolates revealed 2 resistance patterns: resistance type ACSSuT and resis-

Table 2—Genotypic and phenotypic comparisons of *Salmonella* isolates obtained from a commercial swine farm before, during, and after depopulation-repopulation.

Collection time	Serotype	No. of isolates	PFGE type	Phage type	Antimicrobial resistance
Before depopulation					
	Typhimurium cop	87	ST18	DT104	ACSSuT
	Typhimurium	1	ST6	ND	None
	Typhimurium	1	ST8	ND	Na
	Infantis	1	SI2	ND	None
	Putten	3	SP1	ND	None
	Worthington	24	SW1	ND	T
	6,7:nonmotile	3	SN1	ND	None
During depopulation-repopulation					
	Typhimurium cop	1	ST18	DT104	ACSSuT
	Typhimurium cop	1	ST18	DT104	ACCeSuT
	Brandenburg	19	SBG2	ND	None
	Brandenburg	5	SBG2	ND	Ce
	Worthington	6	SW1	ND	T
	Worthington	7	SW4	ND	T
	Heidelberg	5	SH13	ND	ST
After repopulation					
	Typhimurium cop	2	ST18	DT104	ACSSuT

PFGE = Pulsed-field gel electrophoresis. ND = Not determined. A = Ampicillin. C = Chloramphenicol. S = Streptomycin. Su = Sulfamethoxazole. T = Tetracycline. Na = Nalidixic acid. Ce = Cephalothin.
See Table 1 for remainder of key.

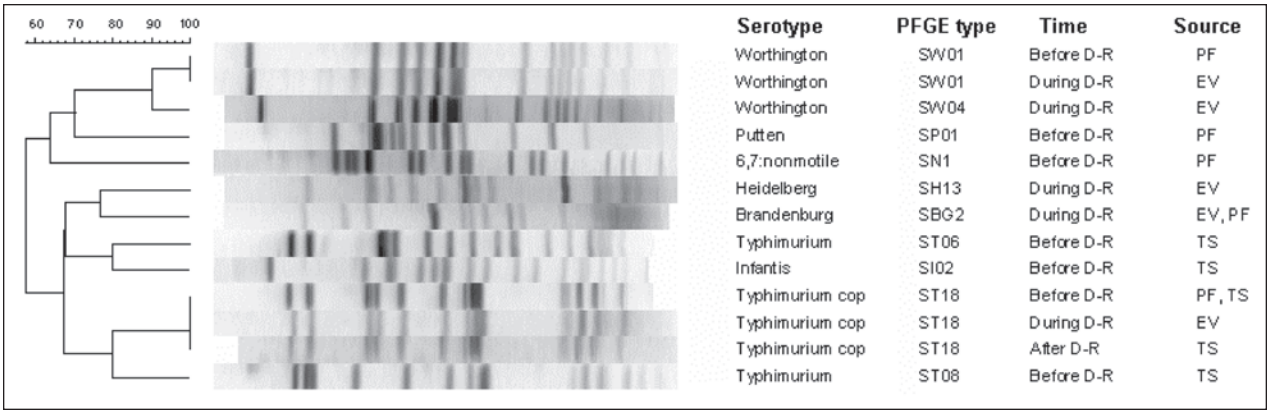

Figure 1—Results of pulsed-field gel electrophoresis of *Salmonella* isolates obtained from a commercial swine farm before, during, and after depopulation-repopulation (D-R). Bars on the left indicate percentage homology between isolates. PF = Pooled feces. EV = Environmental. TS = Tissue. Typhimurium cop = Typhimurium var Copenhagen.

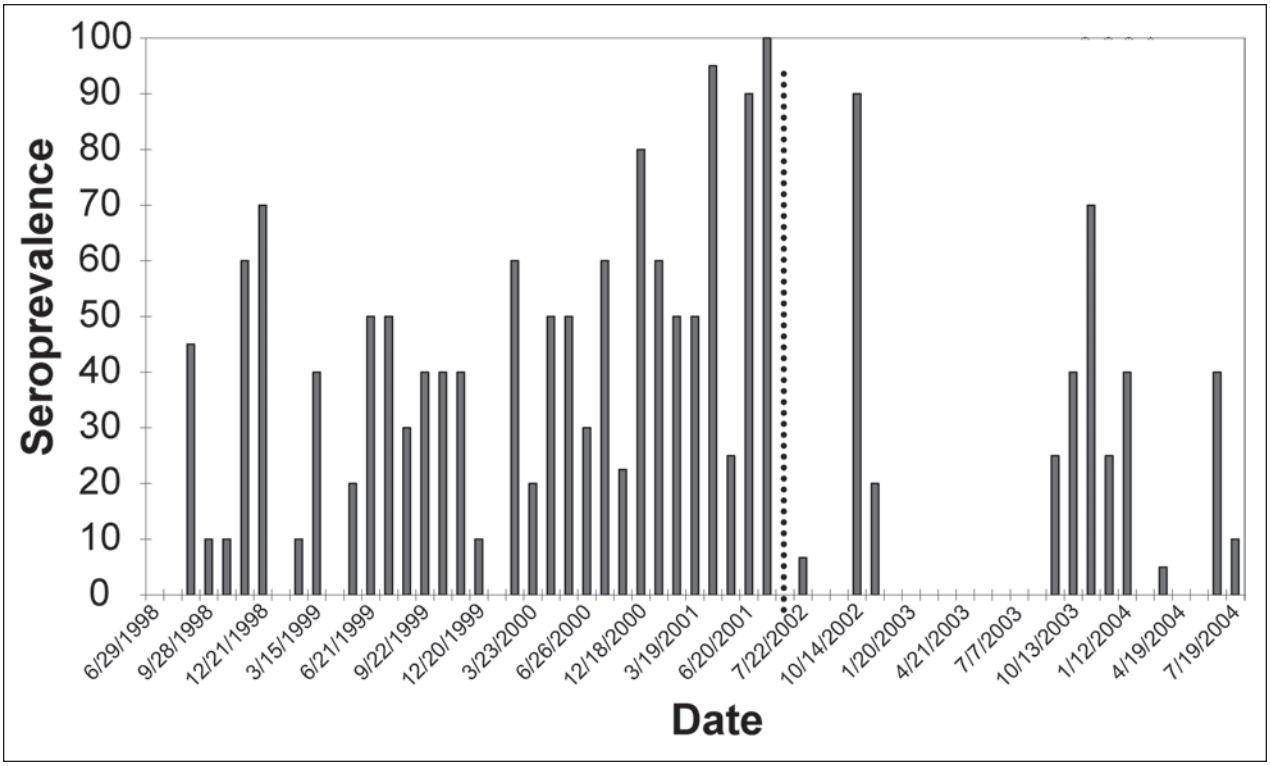

Figure 2—Results of serologic testing of pigs on a commercial swine farm for anti-*Salmonella* antibodies; samples were collected on a monthly basis before and after D-R (dashed line).

tance type ACCeSuT (ie, resistance to ampicillin, chloramphenicol, cephalothin, sulfonamides, and tetracyclines). Isolates with the ACSSuT resistance pattern were obtained during all 3 stages of the study.

Salmonella serotype Worthington was the only other serotype isolated during > 1 stage of the study. For this serotype, PFGE revealed > 1 subtype and indicated that isolates obtained before and during depopulation were different (Figure 1). Two subtypes of *S* Typhimurium were identified, but neither was isolated after depopulation. All other serotypes represented only a single subtype, as determined by PFGE.

A total of 890 serum samples were collected during the study, and results of the indirect ELISA were positive for 250 (**Figure 2**). Monthly seroprevalence for the entire study ranged from 0% to 100%. Results of serologic testing following repopulation agreed with results of bacterial culture, in that both indicated that *Salmonella* organisms were still present on the farm. However, seroprevalence prior to depopulation (186/480 [39%]) was significantly ($P < 0.001$) higher than seroprevalence following repopulation (64/410 [16%]).

Discussion

In the present study, *S* Typhimurium DT104 was not eradicated from a commercial swine farm following depopulation-repopulation. However, results of serologic testing and bacterial culture suggested that the prevalence of *Salmonella* organisms on this farm was

greatly diminished following repopulation. This may be important for 2 reasons. First, a reduction in *Salmonella* load on the farm may decrease the chance of pigs developing clinical salmonellosis. Prior to depopulation-repopulation, the mortality rate among finishing pigs ranged from 6% to 8%, with more than half of all deaths in this group attributed to clinical salmonellosis. In contrast, the farm owner reported minimal problems with clinical salmonellosis following repopulation of the farm. Second, a reduction in *Salmonella* load on the farm may reduce carriage of *Salmonella* organisms when pigs are sent to slaughter.

Eradication of PRRSV and *M hyopneumoniae* from this farm was apparently successful, in that no pigs developed clinical signs of disease following repopulation and results of diagnostic testing for infection with these organisms were negative. Production losses prior to depopulation were likely attributable to the combination of PRRSV, *M hyopneumoniae*, and *S* Typhimurium DT104 infection in the herd. A synergism has been previously shown between *Salmonella* spp and PRRSV, whereby pigs that were coinfected were more likely to develop disease and shed *Salmonella* organisms in higher numbers and for a longer time.[16] Thus, eliminating these other pathogens may have been partially responsible for the lack of shedding and clinical salmonellosis following repopulation of the farm.

Changes in biosecurity procedures likely contributed to the reduction in *Salmonella* prevalence on the farm, as did the change from a pelleted feed to a meal. It has been demonstrated that pigs fed a coarse, nonpelleted feed had lower stomach pH, higher concentration of organic acids, and higher numbers of anaerobic bacteria, compared with pigs fed a pelleted diet.[17] A study[18] in Denmark showed that better hygiene and a change to a meal feed may reduce the prevalence of *Salmonella* spp, specifically *S* Typhimurium DT104, in pig herds. A significant difference in *Salmonella* seroprevalence was also shown between herds feeding pelleted versus nonpelleted feed.[19] One of the authors of the present study (ITH) has found similar results on 2 farms in the United States that changed to a meal feed.

Serotyping, PFGE, phage typing, and antimicrobial susceptibility profiling were valuable epidemiologic tools for comparing isolates obtained during the various stages of the present study. Our results suggest either that the *S* Typhimurium DT104 strain was never eliminated from the farm or that the same strain was reintroduced after depopulation-repopulation. Because the origin of the first isolates is unknown, it is possible that the repopulated herd became infected from a common source. In contrast, new serotypes and subtypes that had not previously been isolated from the pigs were isolated from the environment during depopulation. These new strains of *Salmonella* have not been identified in the herd since its repopulation.

Depopulation of farms to eliminate infection with *S* Typhimurium DT104 has been attempted previously in Denmark.[20] That study concluded that it was not possible to eradicate *S* Typhimurium DT104 from all pig farms studied. Our work indicates that even though pooled fecal samples were negative for *Salmonella* spp following repopulation, *S* Typhimurium DT104 was still present on the farm, as evidenced by its subsequent isolation from tissue specimens. However, this *S* Typhimurium DT104 strain was apparently not causing substantial production losses, given the lack of clinical signs of salmonellosis and deaths attributable to salmonellosis following repopulation. The organism was isolated from only 2 pigs, neither of which had salmonellosis, indicating that the *S* Typhimurium DT104 strain may have been infecting only immunocompromised pigs.

Results of the present study suggest that depopulation-repopulation in conjunction with stringent cleaning and disinfection, attention to biosecurity procedures, control of other diseases, and changes in feed management may reduce the occurrence of *Salmonella* spp in a commercial swine herd. Although it is unlikely that a producer would choose depopulation-repopulation solely to eliminate *Salmonella* infection, we have shown that it is possible to address *Salmonella* concerns while aiming to eradicate other diseases, such as PRRSV and *M hyopneumoniae*. Although eliminating *Salmonella* spp from a pig farm may be difficult, decreasing the *Salmonella* load could lead to fewer problems with clinical salmonellosis and possibly decrease contamination of pork products by reducing the amount of *Salmonella* spp entering the abattoir.

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d. Sensititre, Trek Diagnostics, Westlake, Ohio.
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