Salmonella Infection in Herds of Swine

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Introduction

Salmonella spp. are ubiquitous in nature and they have been recovered from nearly all vertebrates including pigs, cattle, poultry (including eggs), turkeys, fin and shellfish.[1,2,3] In addition to the economic impact of salmonellosis on the human population, it also is a major economic disease of swine resulting in millions of dollars in lost income to the pork industry.[4] Although there have been over 50 serotypes of *Salmonella* isolated from swine carcasses at slaughter, little is known about their pathogenicity. Disease manifests itself in postweaning pigs of all ages and is most often attributed to *S. choleraesuis* var. *kunzendorf* and *S. typhimurium*. Infection in swine typically results in diarrhea and septicemia, with reduced feed efficiency and decreased weight gain.[3,5] *Salmonella choleraesuis* is the primary serotype isolated from swine and is associated with septicemia while *Salmonella typhimurium* (or *S. typhimurium* var. *copenhagen*) is associated with enterocolitis.[3,6,7] Both *S. choleraesuis* and *S. typhimurium* persistently infect swine[8-14] and both are known to infect humans. Pneumonia[15] and rectal strictures[16] also have been reported, but their occurrence varies according to the serotype of *Salmonella* involved. *Salmonella agona* has not been recognized as a significant pathogen of swine despite its importance in the human population.[5] Meningitis, encephalitis, or caseous lymphadenitis may be prevalent in some cases.

Salmonellosis is a worldwide problem and causes zoonotic disease. The potential to cause food-related problems increases as farms become larger and more contained, and the demand for meat and related products increases.[17] In a study of food-borne disease from 1977 to 1984, Bryan[18] observed that pork was responsible for 11% of the *Salmonella* outbreaks attributed to meat. Factors involved in *Salmonella* food-borne outbreaks are complex and multifactorial.

Ferris and Thomas[19] reported the top ten *Salmonella* serotypes recovered from swine in 1995 (Table 1). Although infection with *S. choleraesuis* in humans is rare, its importance as a food-borne pathogen lies not in the frequency of infection, but rather in the severity of disease.[20,21] Many other serotypes of *Salmonella* are associated with food-borne disease in humans and include *S. anatum, S. enteritidis, S. heidelberg, S. mbandaka, S. newport,* and *S. reading*.[22] The top ten serotypes recovered from humans as reported by the Centers for Disease Control (CDC) for 1994 are shown in Table 2.[23] Comparison of the swine and human serotypes indicate that three serotypes, *S. typhimurium*, *S. heidelberg*, and *S. agona* appear on both lists. This may be influenced by the fact that a majority of the isolates reported by Ferris and Thomas[19] were submitted as clinical cases, indicative of a primary or secondary associated infection. Serotypes from non-clinical isolates recovered from swine may or may not correlate with the CDC serotypes.

This paper describes the shedding of *Salmonella* in swine herds randomly selected for the NAHMS Swine >95 Grower/Finisher study as well as from on-farm surveys conducted in Iowa, Kentucky, Missouri, and Wisconsin.

Materials and Methods

Study Design-Swine: The USDA Animal Plant Health Inspection Service (APHIS) Veterinary Service (VS) conducted a study of the health and management of grower/finisher swine as part of the National Animal Health Monitoring System's (NAHMS) Swine '95 Survey.[24] A stratified random sample of producers with grower/finisher pigs from the major swine producing states (Georgia, Illinois, Indiana, Iowa, Kansas, Kentucky, Michigan, Minnesota, Missouri, Nebraska, North Carolina, Ohio, Pennsylvania, South Dakota, Tennessee, Wisconsin) was selected for the study. Of the 418 farms participating in the 1995 study, 152 farms participated in the fecal collection for *Salmonella*. Samples were collected either from July 1995 through

September 1995 or from November 1995 through January 1996 the following year. From each farm, a maximum of 50 fresh fecal samples were collected from the floor of pens containing late finisher pigs with a maximum number of 10 pens per farm sampled. Fecal samples per pen were adjusted according to the number of pens available per farm. All fecal samples (approximately 25 g./sample) were collected in sterile tubes and transported by mail overnight to the laboratory for bacteriologic culture. Samples were transported at room temperature.

Study Design-On-Farm: Approximately 50 fecal samples were collected from each stage of production from farms in Iowa. Additionally, 35 to 50 rectal swabs and 40 to 50 feed samples also were collected from each stage of production. From the other three farms, only fecal samples were collected. Farms were selected based on a history of salmonellosis, but without current clinical signs of disease.

Bacteriology - Swine '95: Approximately 1 g. of feces from each sample was placed into each of two culture media; tetrathionate broth (Tet; Accumedia, Baltimore, MD) or GN Hajna broth (GN; Accumedia). All cultures were incubated overnight at 37°C. At 24 hour, approximately 100 ul. from the GN culture was transferred into Rappaport R-10[25] medium (R-10) (GN-R). At 48 hour, 100 ul. was also transferred from the Tet culture into R-10 (T48-R). All GN-R and T48-R media were incubated overnight at 37°C, then the GN-R was struck onto brilliant green agar with sulfadiazine (BGS; Accumedia) plates. The T-48R culture was struck onto xylose-lysine-Tergitol 4 (XLT4; Difco, Detroit, MI) and brilliant green agar with novobiocin (BGN; Difco). All plates were incubated overnight at 37°C. Colonies having the typical appearance of *Salmonella* were picked to triple sugar iron and lysine iron agar slants. All slants were incubated overnight at 37°C. Presumptive positive isolates were serogrouped using serogroup specific typing sera (Difco) and subsequently serotyped at the National Veterinary Services Laboratories.

Bacteriology - On-Farm: Feces (1g.) and rectal swabs were processed as described above except that the agar plates were BGS alone or BGS and XLT-4 for both GN-R and T48-R. Feed (approximately 10 g.) was placed into 100 ml. of buffered peptone water for 24 hour at 37°C, then 100 ul. was transferred into GN and Tet and processed as described above.

Results and Discussion

Swine '95: A total of 6,655 samples were cultured for *Salmonella*. The sample and herd prevalence rates were 6.2% (414/6,655 positive) and 38.2% (58/152 positive), respectively. The number of serotypes recovered from the positive farms ranged from one to six (one serotype per farm was recovered from 35 farms). The ten most common serotypes recovered were *S. derby* (32.3%), *S. agona* (13.0%), *S. typhimurium* (*copenhagen*) (11.3%), *S. brandenburg* (7.7%), *S. mbandaka* (7.7%), S. typhimurium (3.6%), *S. heidelberg* (3.6%), *S. anatum* (1.9%), *S. enteritidis* PT13A (1.7%) and *S. worthington* (1.7%). Among the positive farms (n=58), 15.8% were positive for *S. derby* while 6.6% of the farms were positive for *S. agona*.

Only one serogroup was recovered from 39 (67.2%) of the farms. The most common serogroup recovered was B (72.7%) followed by C1 (11.1%). Recovery from all other serogroups was less than 5%. The frequency of any farm positive for a specific serogroup indicated that the likelihood of recovering an isolate belonging to serogroup B was the greatest (81.0%) followed by C1 (17.2%), G2 (12.1%), and D1 (6.9%). Untypable, O group 16, or nonmotile isolates were recovered from 22.4% of the herds.

On-farm: Fifteen farms have been visited to date. Twelve have been positive for *Salmonella* and three have been negative. Ten of the 12 positive farms yielded multiple serotypes (2 to 6). A total of 16 different serotypes have been recovered from all the farms surveyed, 5 of which have appeared on the list of the top 20 isolates recovered from human sources.[23] *Salmonella derby* was recovered from 8 farms followed by *S. anatum* (6 farms), *S. brandenburg* (4 farms), *S. agona, S. choleraesuis (kunzendorf)*, and *S. heidelberg* (3 farms each). All other serotypes were only recovered from one farm with the exception of *S. untypable* which was recovered from two farms.

From an animal and public health perspective, serotype information is critical to determining prevention and control strategies and for identifying new serotypes that are emerging as disease-producing agents.

Acknowledgments

Further information regarding the Swine '95 study, including NAHMS factsheets, serotypes of isolates, and risk management factors, are available by contacting Dr. Eric Bush at USDA-APHIS-VS, Centers for Epidemiology and Animal Health, 555 South Howes, Fort Collins, CO 80521. Other collaborators on the Swine '95 study included the National Agricultural Statistics Service (NASS) and State and Federal Veterinary Medical Officers.

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Table 1. The ten most frequently identified *Salmonella* serotypes from swine compiled by NVSL from 7/94 through 6/95

Rank	Serotype	Serogroup
1	S. derby	B
2	S. choleraesuis (kunzendorf)	C1
3	S. typhimurium (copenhagen)	B
4	S. agona	B
5	S. typhimurium	B
6	S. heidelberg	B
7	S. choleraesuis	C1
8	S. anatum	E1
9	S. mbandaka	C1
10	S. schwarzengrund	B

Table 2. Ten most frequently reported *Salmonella* serotypes from human sources compiled by CDC for 1994

Serotype	Serogroup
Enteritidis	D1
Typhimurium[a]	B
Heidelberg	B
Newport	C2
Hadar	C2
Agona	B
Montevideo	C1
Oranienburg	C1
Thompson	C1
Muenchen	C2

[a]includes var. copenhagen