Prevalence of Salmonella in Swine and Pork: A Farm to Consumer Study

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Summary and Implications

Fecal, tissue, and environmental cultures and serological tests were performed on 100 swine on a multi–site farrow to finish production facility. *Salmonella* of 10 types were identified in the swine herd and environment but none were recovered from rodents or flies caught in the production units. At slaughter, 52% (24 of 46) of swine were serologically positive for *Salmonella* antibodies, while 9% (4 of 46) were positive by culture. Although clinical salmonellosis was not detected in the study herd, multiple serotypes of *Salmonella* were causing endemic infections in the study herd.

Introduction

The cost associated with foodborne-related illness in humans is estimated to be between $7.7 and $8.4 billion annually. For the period 1973–1987, *Salmonella* accounted for 42% of the outbreaks and 51% of the cases (1). Pork was implicated as the food vehicle for 25 outbreaks during this period. In other studies (2), pork was responsible for 11% of the *Salmonella* outbreaks attributed to meat. The presence of *Salmonella* spp. in meat animals has resulted in salmonellosis becoming the most important zoonosis in developed countries.

In addition to its impact on the human population, salmonellosis is also a major economic disease of swine. The septicemia or enterocolitis experienced by weaned to adult-aged pigs is reported to result in millions of dollars in lost income to the pork industry. Although there is a plethora of information regarding the pathogenesis and molecular biology of *Salmonella* spp., there is a paucity of information concerning the prevalence and incidence of those species (serotypes) associated with (or having the potential to contribute to) foodborne disease. Diagnostic centers provide clinical reports and the National Veterinary Services Laboratories publish an annual report on the recovery of *Salmonella* from swine and other animals (3). However, this information is usually obtained because clinical disease was present. Currently, there is no reliable information regarding the prevalence of *Salmonella* spp. in swine. Some information on *Salmonella* in grower/finisher swine will be available from the National Animal Health Monitoring System (NAHMS) Swine '95 study.

Although the carrier state has been defined for *S. typhimurium* and *S. choleraesuis* under experimental conditions (4,5,6,7,8), little is known about the exact modes of transmission and maintenance of the disease in swine herds. Transmission is thought to occur from introduction of carrier animals into the herd, through contaminated feed, or by exposure to infected rodents or farm personnel (9,10). However, most field studies have not examined a single population of pigs from farrow through finish when dealing with the epidemiology of *Salmonella* on the farm, choosing instead to sample pen fecal samples only (11,12). Even with the recent introduction of serologic testing of finisher swine for anti-salmonellae antibodies (13), information is lacking regarding the age of seroconversion on the farm.

The objectives of this work are to determine the prevalence of *Salmonella* in swine from farrow through finish. The goal is to be able to assess the level of *Salmonella* within a farm environment as well as to assess the serotypes most often recovered from swine and determine if these serotypes carry through in finished product.

Materials and Methods

We solicited cooperation from a swine producer from Iowa to determine the prevalence of *Salmonella* spp. in his multisite production facility. Surveillance began with the selection and tagging of 100 pigs at birth from multiple litters that were monitored through to slaughter weight. At select intervals (1,4,9,14, and 18 weeks of age, and at slaughter) swabs, fecal samples, and serum were collected from all of the tagged pigs. Additionally, 10 of the tagged pigs were necropsied at each sampling point weeks 1 through 18, 10 pigs were necropsied at slaughter weight but prior to removal from the farm, and 30 pigs were followed through slaughter at the processing plant. (Ten additional pigs were selected factoring in loss due to death or other means.) Tissues were collected for bacteriology and included tonsil, mandibular lymph nodes, lung, bronchiole lymph nodes, liver, spleen, middle ileum, ileocolic junction, ileocolic lymph nodes, cecum, cecal contents, colon, colonic lymph nodes, and stomach wall. Additionally, cheek meat also was collected for bacteriology. Bacteriologic protocols were followed as previously described (6,7,8). Blood was collected from pigs throughout the sampling times and sera was tested using ELISA technology developed in our laboratory (6,7).

To assess the impact of the farm environment on the tagged population of pigs, random pen fecal culture of age-matched litter mates on the farm that were not necropsied or followed through to commercial slaughter were collected. The farm environment was sampled throughout this period and included feed, rodents, flies, and water.

At slaughter weight, 10 pigs were slaughtered at the farm prior to shipping. Thirty remaining pigs were transported by conventional means to slaughter and samples were collected following transport, after lairage but before slaughter, and after slaughter.

Results and Discussion

Ten serotypes and one untypable isolate were recovered during the study. The farm environment was positive throughout the study but only 3 of 100 pigs were positive by fecal loop. Tissues were negative through 9 weeks. At 14 weeks, five serotypes were recovered from the tissues of seven pigs, two serotypes that had been previously identified on the farm and three serotypes that had never been recovered from the farm environment. At slaughter, only 5 of 40 pigs were tissue positive. Feed was positive at 4, 9, and 18 weeks and at slaughter. Serotypes found in the feed also were recovered from pigs and the environment. All rodents and flies were negative. Approximately 90% of the pigs were positive by serology at 1 week of age. This value decreased to 15% by week 9 but rose to 52% at slaughter. However, there did not appear to be a correlation between serology and culture as related to the carcass at slaughter. These data indicate that the life cycle of *Salmonella* on the farm will fluctuate over time and that seroconversion, as determined by our ELISA, does not predict the likelihood that *Salmonella* spp. will be present on the carcass.

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