Prevalence of *Salmonella* spp on conventional and organic dairy farms

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Objective—To describe the occurrence of fecal shedding, persistence of shedding over time, and serogroup classification of *Salmonella* spp on a large number of dairy farms of various sizes.

Design—Longitudinal study.

Sample Population—22,417 fecal samples from cattle and 4,570 samples from the farm environment on 110 organic and conventional dairy farms in Minnesota, Wisconsin, Michigan, and New York.

Procedure—5 visits were made to each farm at 2-month intervals from August 2000 to October 2001. Fecal samples from healthy cows, calves, and other targeted cattle groups and samples from bulk tank milk, milk line filters, water, feed sources, and pen floors were collected at each visit. Bacterial culture was performed at 1 laboratory.

Results—*Salmonella* spp were isolated from 4.8% of fecal samples and 5.9% of environmental samples; 92.7% of farms had at least 1 *Salmonella*-positive sample. The 75th percentile for median within-herd prevalence of *Salmonella* spp in cattle for 5 sampling visits to a given farm was 2.0% and for maximum within-herd prevalence of *Salmonella* spp was 13.6%. Farms with a median within-herd prevalence of *Salmonella* spp of ≥ 2.0% accounted for 76.3% of *Salmonella*-positive samples. There was no significant difference in the prevalence of *Salmonella* spp between conventional and organic farms. Seasonal differences in *Salmonella* shedding were observed. More farms had at least 1 serogroup B isolate than any other serogroup, whereas serogroup E1 was the most common among all *Salmonella*-positive samples. More than 1 serogroup was isolated on 76.4% of *Salmonella*-positive farms.

Conclusions and Clinical Relevance—*Salmonella* spp were isolated from > 90% of dairy farms; however, 25% of farms accounted for > 75% of *Salmonella*-positive samples. This information is critical for the direction of intervention strategies to decrease the prevalence of *Salmonella* spp on dairy farms. (*J Am Vet Med Assoc* 2004;225:567–573)

Salmonella spp are among the most common and costly causes of foodborne illness in humans[1,2] and can also cause disease, occasionally leading to death, in cattle.[3] Shedding of *Salmonella* organisms can occur subsequent to illness or in the absence of clinical signs, occasionally for extended periods. Under the Hazard Analysis and Critical Control Points regulations of the USDA Food Safety and Inspection Service, a system is in place that monitors contamination of meat with *Salmonella* spp. This system, coupled with greater public interest in food safety, has stimulated interest in identifying means to decrease *Salmonella* shedding in cattle on the farm.

Salmonella organisms are widespread in the environment and can be introduced onto a farm in many ways, including via feed, purchased cattle, rodents or other wild animals, birds, humans, insects, or water.[4-6] Because of the multitude of opportunities for introduction of salmonellae onto a farm and the nature of cattle production, eradication of salmonellae is unlikely[5,7]; most herds would not be expected to remain *Salmonella*-free over time.[8] However, some farms have a higher prevalence of *Salmonella* spp than others. Approximately 5% of cattle were shedding *Salmonella* organisms at 1 point in time in 2 studies involving 91[9] and 105[10] farms; however, there was wide variation in herd prevalences. Results of the National Animal Health Monitoring System Dairy '96 study, in which 91 herds were enrolled without regard to a previous history of clinical *Salmonella* infections, revealed that the top quartile of *Salmonella* culture-positive dairy farms had within-herd prevalences that ranged from 40% to 90% for a single sampling.[9] It is not known whether these high prevalences of *Salmonella* spp on the farm are transient phenomena or whether they persist over time. Herds with high prevalences, especially those in which high prevalences persist over time, could be regarded as a greater concern from a public health standpoint than herds in which the prevalence of *Salmonella* spp is low. Only a few *Salmonella* serogroups and serotypes are responsible for causing most of the clinical illness in humans and livestock[11-13]; the herds with those *Salmonella* serogroups or serotypes could also be considered a greater concern from a human or veterinary health standpoint. Longitudinal studies evaluating *Salmonella* shedding in

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a large number of dairy herds are lacking; therefore, *Salmonella* persistence on dairy farms is not well-described. The purpose of the study reported here was to describe the occurrence of fecal shedding, persistence of shedding over time, and serogroup classification of *Salmonella* spp on a large number of dairy farms of various sizes.

Materials and Methods

Herd selection—One hundred thirty-one dairy farms were enrolled in 4 states (Michigan, Minnesota, New York, and Wisconsin). One producer sold all cows between the time of farm enrollment and scheduling of the first sampling visit; therefore, biological samples were collected from 130 farms. Data are reported only for 110 farms to which 5 sampling visits were made. Five visits were not made to all farms for the following reasons: the producer left the dairy business, logistic conflicts with scheduling of farm visits and laboratory availability, and the producer's decision not to continue participating in the study. Dairy herds were enrolled in the study on the basis of farm type (organic vs conventional) and farm size (number of cows, both lactating and nonlactating). For inclusion in the study, a herd had to consist of at least 30 milking cows, with at least 90% of those cows of Holstein breed, and farms had to raise their own calves as replacement cattle and ship milk year-round. Organic farms had to be certified as organic by a recognized organic certification agency. Lists of conventional farms were obtained from respective state departments of agriculture, and dairy farmers located within an approximately 100-mile radius of the respective university (University of Minnesota, Michigan State University, University of Wisconsin, and Cornell University) were randomly selected to receive, via mail, information describing the research project (500 to 571 herds/state; total, 2,102 letters). Farmers were requested to indicate their interest in participating in the study by returning a postcard. The final list of farms was obtained via random selection of 100 farms from among the 295 respondents that indicated a willingness to participate in the study. Contact information for organic farms was obtained from independent organic certifying agencies, organic milk cooperatives, and personal contacts. In Minnesota and Wisconsin, all known organic farmers located within a 150-mile radius of the respective university were contacted to determine eligibility on the basis of selection criteria and their desire to participate in the study. Predetermined numbers of farms in 4 size categories (30 to 49, 50 to 99, 100 to 199, and ≥ 200 cows [both lactating and nonlactating]) were enrolled on the basis of ability to evaluate potential risk factors. This study was part of a larger investigation that examined risk factors for *Campylobacter* and *Salmonella* infections and antimicrobial drug resistance on dairy farms. Therefore, calculation of numbers of farms for enrollment was not directed toward detection of a single pathogen. Calculations indicated that 31 herds/category would provide adequate power (0.8) for the detection of major risk factors (25% difference in proportions at $\alpha = 0.1$, assuming 30% of herds are infected and a 2:1 ratio of unexposed to exposed); therefore, 31 herds were the minimum goal for enrollment within categories of predominant interest (herd sizes of 50 to 99, 100 to 199, and ≥ 200 cows; organic vs conventional herds; and numbers of herds within each state).

Sample collection—Samples were collected from participating farms at 5 time points from August 2000 to October 2001. The first farm visits took place between October 2000 and January 2001 for 98% of farms. Subsequent visits to each farm were made at approximately 2-month intervals. The mean ± SD (range) interval between sampling visits was 68.1 ± 19.6 (28 to 140) days.

Samples from cattle—Fecal samples were collected via rectal retrieval; approximately 10 g of fecal material was placed into a commercially available bag[a] and sealed. A new glove was used to collect each sample. The number of fecal samples collected per visit from each herd and from specific cattle groups was calculated to provide a similar probability of detecting at least 1 *Salmonella*-positive sample across herd sizes, given the same prevalence of fecal shedding of *Salmonella* spp for all herds.[14] An estimated prevalence of *Salmonella* spp of 7.5% in target cattle (ie, heifer calves receiving milk or milk replacer, cows to be culled within 14 days, cows due to calve within 14 days, cows within 14 days after calving, and cows designated as sick by farm personnel) and 2.5% in other cows (ie, healthy lactating cows) were used in the calculations. Estimates of the number of cattle that would be available at each 2-month interval in the target cattle and healthy lactating cattle groups were made on the basis of the following statistics: 35% cull rate, 13.5-month calving interval, and 5% sick cattle at any time. Resulting numbers of samples were rounded off to multiples of 5 for ease of implementation of the sampling protocol. During each sampling visit, target cattle fecal samples including up to 6, 10, 10, and 15 preweaned heifer calf fecal samples and up to 4, 5, 10, and 10 cow fecal samples from herds with 30 to 49, 50 to 99, 100 to 199, and ≥ 200 cows, respectively, were collected. On smaller farms, the designated number of target cattle was not always available at each sampling visit; therefore, fecal samples from as many target cattle as possible were collected. At each sampling visit, up to 20, 25, 30, and 30 healthy cattle fecal samples from herds with 30 to 49, 50 to 99, 100 to 199, and ≥ 200 cows, respectively, were collected. For healthy cows, systematic sampling was used to collect a representative number of fecal samples from cattle in each pen on the basis of total herd size and numbers in each pen. For target cattle groups, equal numbers (when available) of fecal samples from sick, periparturient, and to-be-culled cows were collected at each visit, and systematic sampling within groups was performed when more than the targeted number of cattle were available. No effort was made to collect samples from the same cattle at subsequent herd visits.

Samples from the environment—Areas to be sampled were wiped with sterile gauze pads soaked in double-strength skim milk, and pads were placed in commercially available bags[a] for transport. This technique has been shown to be effective for preservation of *Salmonella* spp collected from the environment on poultry farms.[15-18] One gauze pad sample from each of the following locations was collected during each sampling visit: calving pen floor, sick pen floor, calf pens or housing, feed alley for lactating cows (without regard to previous cow contact), lagoon or manure storage area, and bird droppings in cattle housing or feed storage areas. Other samples that were collected included 100 mL of water (from a water tank or a pooled water sample from 5 drinking cups in the lactating cow barn), 60 mL of milk from the bulk tank, and a milk line filter. Fluid samples were placed in cylindrical flip-top plastic containers, and milk line filters were placed in commercially available bags[a] or plastic freezer bags. If certain pen types did not exist on a particular farm (eg, no sick pen), no sample was collected. The calving pen was also used as the sick pen on some farms; therefore, only 1 sample was collected and labeled according to the pen's predominant use. When a manure storage area was not used or accessible (eg, frozen), samples were collected from a manure pile or outflow area from the lactating cow barn.

Shipment of samples and isolation of *Salmonella* spp—Samples were taken directly to the laboratory (Michigan) or shipped via overnight delivery in styrofoam boxes containing ice packs (Minnesota, New York, and Wisconsin). Samples were usually shipped on the same day they were collected;

however, samples were occasionally stored at 4°C for 12 to 36 hours before shipping. Primary *Salmonella* isolation was performed at 1 investigator's laboratory at Michigan State University. Tetrathionate enrichment broth[b] was added directly to all samples (fecal and environmental) at an approximate ratio of 1:10 (sample:broth); the mixture was mixed manually and incubated for 48 hours at 37°C. After incubation, the sample-broth mixture was streaked onto **xylose lysine desoxycholate 4 (XLT-4)** selective medium,[b] and plates were incubated for 24 hours at 37°C. Bacterial colonies with black centers were inoculated into triple sugar iron agar,[b] and slants were incubated for 24 hours at 37°C. More than 1 isolate/sample was selected when bacterial colonies on XLT-4 medium differed morphologically but were characteristic of *Salmonella* spp. Isolates in triple sugar iron slants that yielded a positive reaction for *Salmonella* spp were tested by use of slide agglutination with polygroup antisera[b] or serogrouped by use of antisera for somatic groups B, C1, C2, D1, E1, E3, and K.[b] Isolates with negative results of slide agglutination and serogrouping were inoculated into lysine iron agar[b] and streaked on Simmon citrate medium,[b] and slants were incubated for 24 hours at 37°C to verify the identity of isolates as *Salmonella* spp. All isolates with a positive reaction with somatic group or polygroup antisera or with lysine iron agar and Simmon citrate medium were classified as *Salmonella* isolates. The polygrouping process placed isolates into 1 of 5 groups (A, B, C, D, and E); this procedure was discontinued in May 2001. Isolates from samples collected after May 2001 were serogrouped, as were previous isolates with polygroup results that indicated the isolate could be one of the following somatic groups: B, C1, C2, D1, E1, E3, or K. The serogroup was classified as other for any isolate that was considered a *Salmonella* sp on the basis of a positive reaction on lysine iron agar and Simmon citrate medium or polygrouping but that did not react with antisera for somatic groups B, C1, C2, D1, E1, E3, or K or that would not have reacted with these antisera on the basis of a polygroup test result (the serogroups of interest corresponded with polygroups A, B, and C only). The 7 serogroups were chosen because they correspond with the following 10 serotypes of *S enterica* commonly isolated from healthy and sick cattle[9,19]: group B, *Salmonella* serotype Typhimurium; group C1, *S* Montevideo; group C2, *S* Newport and *S* Kentucky; group D1, *S* Dublin; group E1, *S* Anatum, *S* Muenster, and *S* Meleagridis; group E3, *S* Menhaden; and group K, *S* Cerro.

Data and statistical analyses—Seasons were defined as follows: winter (January through March), spring (April through June), summer (July through September), and fall (October through December). Median within-herd prevalence of *Salmonella* spp in cattle was the median prevalence over 5 visits for each of the 110 farms, resulting in 110 median within-herd prevalences. Maximum within-herd prevalence of *Salmonella* spp in cattle was the maximum prevalence over 5 visits for each of the 110 farms, resulting in 110 maximum within-herd prevalences.

Logistic regression methods were used to test the association between herd size, season, and farm type (organic vs conventional) and the dependent variable of within-herd prevalence by visit (number of *Salmonella*-positive cattle per number of cattle sampled). Independent variables of interest were also adjusted for effects of state of origin. The generalized estimating equations approach was used to adjust for the correlation of multiple sampling occasions for each herd.[c] For all comparisons, values of $P < 0.05$ (on the basis of the generalized estimating equations parameter estimate [*t* test]) were considered significant.

The Pearson χ^2 test was used to assess differences in the detection of *Salmonella* spp on farms between visits. A commercial software program[c] was used. Values of $P < 0.05$ were considered significant.

Results

Samples were collected on 84 conventional and 26 organic farms in 4 herd size categories (**Table 1**). Approximately equal numbers of herds were enrolled in each state. Few organic farms with at least 100 cows were enrolled because such farms were not available. Eight of 110 farms reported confirmed *Salmonella* infections in cattle during the 2 years prior to commencement of the study.

At least 1 *Salmonella*-positive fecal sample or environmental sample was detected over 5 sampling visits on 102 of 110 (92.7%) farms (Table 1). One hundred (90.9%) farms had at least 1 *Salmonella*-positive fecal sample, and 56 (50.9%) farms had at least 1 *Salmonella*-positive environmental sample. Although *Salmonella* spp were found on > 90% of farms, almost all of the positive farms (99/102 [97.1%]) had at least 1 visit in which no *Salmonella* organisms were isolated from any samples collected and 68 of 102 farms had no *Salmonella* organisms isolated from samples collected on 3, 4, or 5 visits. At least 1 *Salmonella*-positive fecal sample was identified on 30.9% to 54.5% of farms on individual visits (**Figure 1**). On a cumulative visit

Table 1—Proportion (%) of farms, classified on the basis of farm type (conventional and organic) and herd size, that had at least 1 *Salmonella*-positive fecal or environmental sample over 5 sampling visits.

Herd size (No. of cows)*	Organic	Conventional	Total
30–49	10/10 (100)	9/9 (100)	**19/19 (100)**
50–99	7/9 (77.8)	21/22 (95.4)	**28/31 (90.3)**
100–199	4/4 (100)	23/24 (95.8)	**27/28 (96.4)**
≥ 200	3/3 (100)	25/29 (86.2)	**28/32 (87.5)**
Total	**24/26 (92.3)**	**78/84 (92.8)**	**102/110 (92.7)**

*Includes lactating and nonlactating cows.

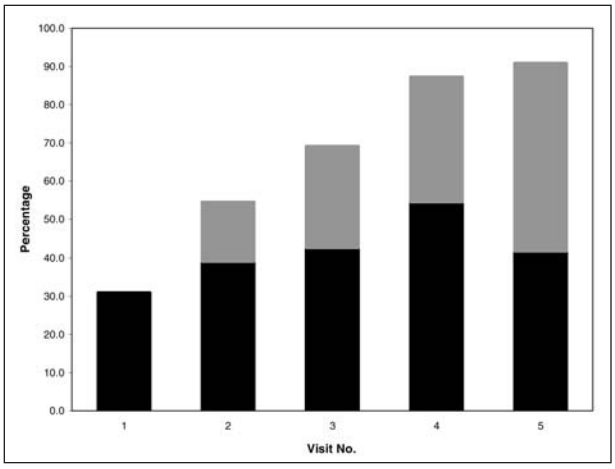

Figure 1—Percentage of 110 conventional and organic farms that had at least 1 *Salmonella*-positive fecal sample on an individual-visit basis (black bar) and cumulative-visit basis (black and gray bar). The cumulative data represent a running total of the number of farms with at least 1 *Salmonella*-positive fecal sample, with each farm only counted once. On a cumulative-visit basis, the percentage of farms with at least 1 *Salmonella*-positive fecal sample was significantly different between visits 1 and 2 ($P < 0.001$), 2 and 3 ($P < 0.03$), and 3 and 4 ($P < 0.001$) but not 4 and 5.

basis, the number of farms with at least 1 *Salmonella*-positive fecal sample (ie, a running total of the number of farms with at least 1 *Salmonella*-positive fecal sample, with each farm only counted once) increased significantly between each successive visit, with the exception of between visits 4 and 5.

Overall, 1,083 of 22,417 (4.8%) fecal samples (**Table 2**) and 269 of 4,570 (5.9%) environmental samples were *Salmonella*-positive. Use of logistic regression methods that used the proportion of *Salmonella*-positive cattle per farm visit as the outcome and after adjustment for the correlation of multiple sampling occasions per herd and effects of herd size, season, and state revealed that cattle on farms with ≥ 200 cows and 100 to 199 cows had significantly higher **odds ratios (ORs)** for *Salmonella* shedding of 3.1 (95% **confidence interval** [**CI**], 1.2 to 8.2) and 2.3 (95% CI, 1.1 to 5.2), respectively, compared with cattle on farms with 30 to 49 cows. There was no significant difference in ORs for *Salmonella* shedding between farms with 50 to 99 cows and farms with 30 to 49 cows. After adjustment for effects of herd size, season, state, and for the correlation of multiple sampling occasions per herd, no significant difference in ORs was found for *Salmonella* shedding between cattle on conventional versus organic farms ($P = 0.99$), and there was no significant interaction between herd size and farm type. After adjustment for herd size, state, and the multiple sampling occasions per herd, the ORs for *Salmonella* shedding in cattle (compared with winter) were 2.4 (95% CI, 1.4 to 4.0) in summer, 2.1 (95% CI, 1.3 to 3.4) in spring, and 1.8 (95% CI, 1.1 to 3.2) in fall.

Of the 7 serogroups identified (B, C1, C2, D1, E1, E3, and K [excluding the other group]), serogroup B was most common at the farm level in both fecal and environmental samples (ie, more farms had at least 1 serogroup B isolate than any other serogroup; 43.0% of 100 fecal-positive farms and 42.9% of 56 environment-positive farms had at least 1 group B isolate; **Table 3**). Among the 7 serogroups identified, serogroup E1 was most common at the sample level in both fecal and environmental samples (ie, serogroup E1 was identified in more samples than was any other serogroup, 32.2% of 1,561 isolates were from fecal samples, and 32.8% of 399 were environmental isolates). With the other serogroup category counted as a single serogroup, the highest number of serogroups found in fecal samples on a single visit to a farm was 7, whereas the highest number for environmental samples was 4. Of the 102 *Salmonella*-positive farms, 78 (76.4%) farms had > 1 serogroup isolated from fecal or environmental samples, and 50 (49.0%) farms had ≥ 4 serogroups isolated.

To provide a summary measure of *Salmonella* prevalence for each farm during the course of the study, the median within-herd prevalence of *Salmonella* spp over 5 visits for each of the 110 farms was determined. The analysis was restricted to fecal samples for ease of interpretation and comparison with previous studies; fecal samples represent shedding from a single animal, whereas environmental samples could be representative of multiple animals or environmental contamination. Of the 110 farms, 74 (67%) had a median within-herd prevalence of *Salmonella* spp over 5 visits of 0%, and 36 (33%) had a median within-herd prevalence of *Salmonella* spp > 0%. The highest median within-herd prevalence of *Salmonella* spp over 5 visits was 50.0%. The 90th percentile for median within-herd prevalence of *Salmonella* spp was 9.1%, and the 75th percentile was 2.0%. Farms with a median within-herd prevalence of *Salmonella* spp at or above the 90th percentile accounted for 50.9% and 50.8% of the *Salmonella*-positive fecal and environmental samples, respectively, and farms at or above the 75th percentile accounted for 76.3% and 76.3% of the *Salmonella*-positive fecal and environmental samples, respectively.

The maximum within-herd prevalence of *Salmonella* spp in cattle was also identified for the 110 farms. The highest prevalence in fecal samples for a single visit was 68.5%. The 90th percentile for maximum within-herd prevalence of *Salmonella* spp was 29.1%, and the 75th percentile was 13.6%.

High-prevalence farms were characterized by use of the 90th percentile for median within-herd prevalence of *Salmonella* spp in cattle over 5 visits (**Figure 2**). Eight of these 11 farms had at least 100 cows, and 9 of 11 were conventional farms. Four farms had at least 10% prevalence in fecal samples for all 5 visits, and all 11 farms had at least 2 visits with a prevalence of ≥ 10%. Some farms had predominance and persistence of a single serogroup; 6 of 11 farms had 1 serogroup that persisted for 4 or 5 visits and represent-

Table 2—Proportion (%) of fecal samples collected over 5 sampling visits that were *Salmonella*-positive on farms classified on the basis of farm type (conventional and organic) and herd size.

Herd size (No. of cows)*	Conventional	Organic	Total
30–49	31/1,110 (2.8)	35/1,267 (2.8)	**66/2,377 (2.8)**
50–99	96/3,748 (2.6)	46/1,446 (3.2)	**142/5,194 (2.7)**
100–199	297/5,367 (5.5)	17/836 (2.0)	**314/6,203 (5.1)**
≥ 200	456/7,839 (5.8)	105/804 (13.1)	**561/8,643 (6.5)**
Total	**880/18,064 (4.9)**	**203/4,353 (4.7)**	**1,083/22,417 (4.8)**

*Includes lactating and nonlactating cows.
No significant ($P < 0.05$) difference in percentage of *Salmonella*-positive samples between conventional and organic farms was found.

Table 3—Number (%) of farms with at least 1 *Salmonella*-positive fecal or environmental sample and number (%) of *Salmonella*-positive isolates from fecal and environmental samples classified on the basis of serogroup.

	Farms		Isolates[a]	
Serogroup	Fecal	Environmental	Fecal	Environmental
B	43 (43.0)	24 (42.9)	203 (13.0)	68 (17.1)
C1	31 (31.0)	19 (33.9)	169 (10.8)	54 (13.5)
C2	16 (16.0)	11 (19.6)	160 (10.3)	40 (10.0)
D1	18 (18.0)	1 (1.8)	50 (3.2)	4 (1.0)
E1	36 (36.0)	18 (32.1)	502 (32.2)	131 (32.8)
E3	24 (24.0)	10 (17.9)	41 (2.6)	13 (3.3)
K	10 (10.0)	0 (0.0)	21 (1.3)	0 (0.0)
Other	83 (83.0)	38 (67.9)	415 (26.6)	89 (22.3)
Total	**100 (100.0)**	**56 (100.0)**	**1561 (100.0)**	**399 (100.0)**

[a]More than 1 isolate/sample was serogrouped when colonies on xylose lysine desoxycholate 4 medium were characteristic of *Salmonella* spp but differed morphologically. Therefore, the number of fecal isolates (1,561) differs from the number of *Salmonella*-positive fecal samples (1,083), and the number of environmental isolates (399) differs from the number of *Salmonella*-positive environmental samples (269).

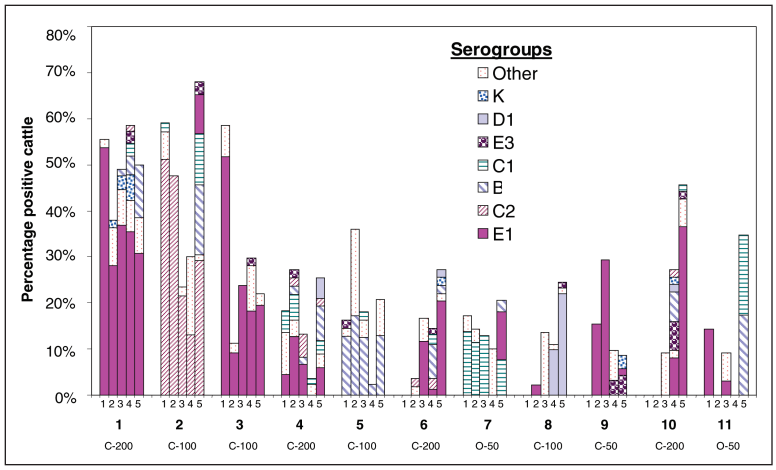

Figure 2—Prevalence of *Salmonella* spp in cattle (fecal samples) and classification of isolates on the basis of serogroup at each of 5 sampling visits to 11 high-prevalence farms (farms at or above the 90th percentile for median within-herd prevalence of *Salmonella* spp in cattle over 5 visits). C = Conventional farm. O = Organic farm. 200 = At least 200 cows. 100 = 100 to 199 cows. 50 = 50 to 99 cows. For some samples, > 1 isolate was identified, which resulted in > 1 serogroup identified for some samples. When > 1 serogroup was identified for a sample, the serogroup percentages for that particular farm were adjusted proportionately to the number of positive fecal samples.

ed most of the isolates from that herd. Nine of 11 farms had 1 serogroup that represented most of the isolates from that herd, but there was also considerable diversity among the serogroups, with up to 7 different serogroups detected on the same farm for 1 visit.

Discussion

Particular strengths of our study included the longitudinal approach used and the large number of participating herds distributed over 4 states, including 3 of the top 5 milk-producing states in the United States.[20] Conventional herds were randomly selected from among those eligible for inclusion in our study; participating herds represented a diversity of management characteristics. For organic herds, the sampling frame approximated a census of all known organic herds within 150 miles of each university. This study design allowed us to describe the prevalence of *Salmonella* spp on dairy farms in the Midwest and Northeast United States over a period of time.

Our results revealed that *Salmonella* spp can be detected on nearly all dairy farms. Sampling of farms on 5 occasions resulted in the detection of 100 of 110 (90.9%) farms with at least 1 *Salmonella*-positive fecal sample. Smith et al[21] reported that 75% of 60 California dairy farms had serologic evidence of recent exposure to *Salmonella* spp, which also supports the conclusion that *Salmonella* organisms are commonly found on dairy farms. Results of a nationwide study[9] revealed that 27.5% of 91 dairy farms had at least 1 *Salmonella*-positive cow (on the basis of bacteriologic culture of feces) when 40 to 70 healthy cattle were sampled once on each farm. Of 105 dairy farms in Ohio, 31.4% had at least 1 *Salmonella*-positive cow (on the basis of bacteriologic culture of feces) when all adult cattle > 2 years old were sampled once on each farm.[10] On an individual-visit basis, 30.9% to 54.5% of farms in our study had at least 1 *Salmonella*-positive fecal sample. Collection of a larger number of samples at each visit would likely have resulted in a larger number of *Salmonella*-positive farms at each visit. However, because of the ubiquitous nature of *Salmonella* spp and the many opportunities for their introduction onto farms, it is likely that a larger number of farms would be found to be *Salmonella*-positive when sampled over time rather than at 1 point in time.

Although > 90% of herds had at least 1 *Salmonella*-positive fecal sample, > 97% of these herds also had at least 1 visit in which *Salmonella* spp were not isolated from fecal samples. The inability to consistently detect *Salmonella* spp in these herds can be attributed, solely or in combination, to a true absence of *Salmonella* spp in the herd at the time of sampling, limitations of bacteriologic culture for *Salmonella* spp, intermittent shedding in individual cattle, or other factors. Within-herd sample size can also explain variation in prevalence across visits; larger numbers of samples would have resulted in less variation. Because *Salmonella* spp can be shed intermittently, it was not unexpected to have fecal bacteriologic culture results that were negative for *Salmonella* spp, given the frequency of sampling used.

Salmonella spp were isolated from at least 1 fecal sample on every visit in only 7 (6.4%) herds. Six of these herds were high-prevalence herds. Therefore, it is possible that farms from which *Salmonella* spp can be routinely isolated may be more likely to have high within-herd prevalence of *Salmonella* spp.

Results of our study (with regard to percentage of *Salmonella*-positive fecal samples) were similar to those of studies by Wells et al[9] and Huston et al.[10] In our study, 4.8% of fecal samples were *Salmonella*-positive, compared with 5.4%[9] and 5.9%,[10] in the other studies. There was a significant difference in *Salmonella* shedding between herds with ≥ 200 and 100 to 199 cows, compared with herds with 30 to 49 cows. These results were not unexpected because the association between herd size and *Salmonella* shedding has been well-documented.[9,10,22,23] Specific factors associated with larger herd sizes most likely account for the greater probability of *Salmonella* spp shedding in larger herds, and more work needs to be done to identify those factors. There was no significant difference in *Salmonella* shedding between cattle in conventional and organic herds. On the basis of the results of our study, it can be hypothesized that organic and conventional farms have similar differences in *Salmonella* shedding between large and small farms. Although large organic farms (≥ 200 cows) had a higher proportion of *Salmonella*-positive fecal samples, compared with similarly sized conventional farms, there was no significant difference in *Salmonella* shedding in cattle between organic and conventional farms after adjust-

ment for effects of herd size, season, and state and for the multiple sampling visits per herd. It is possible that large organic farms have a greater risk of *Salmonella* shedding in cattle, compared with conventional farms; however, a larger number of large organic farms would be needed to make this comparison. Large organic dairy herds in the Midwest United States are uncommon[24]; this complicates comparisons of conventional and organic dairy herds.

Serogroup E1 was the most common serogroup identified in fecal samples in our study. In the National Animal Health Monitoring System Dairy '96 study, serogroup E was also most common in fecal samples, although across farms, serogroup C1 was most common and 14.3% of *Salmonella*-positive dairy farms had at least 1 C1 isolate in cattle; the second most common serogroup was serogroup E.[9] In contrast, serogroup B was most common across farms in our study, with 43% of fecal-positive farms with at least 1 serogroup B isolate in feces; the second most common serogroup was serogroup E1. One possible explanation for this difference may be geographic; the National Animal Health Monitoring System study was conducted in herds across the United States, and farms in our study were limited to the Midwest and Northeast. Different time periods for collection of samples and different study designs could also account for the difference; a longitudinal approach is likely to detect a greater number of serogroups because a greater number of samples are collected. Of the *Salmonella* serotypes that are classified in serogroup B, *S* Typhimurium is of most concern because it is the most commonly reported serotype that causes disease in both humans[25] and cattle.[26]

The fact that the farms at or above the 75th percentile of farms ranked by the median within-herd prevalence of *Salmonella* spp accounted for > 75% of all positive samples in our study indicates that a relatively small percentage of farms accounts for most *Salmonella* spp found on dairy farms. These results suggest that focusing control efforts on relatively few farms with high prevalences of *Salmonella* spp would be the most effective means of *Salmonella* control in dairy herds. If the focus of control is on farms with high prevalences of *Salmonella* spp, determination of herd-level *Salmonella* status (positive or negative) has questionable value, except in terms of what it can indicate regarding the prevalence of *Salmonella* spp on the farm.

Salmonella spp have a wide host range, including warm- and cold-blooded vertebrates and invertebrates (including snails, earthworms, and arthropods[11]), and are able to survive and multiply in the environment; therefore, it is not surprising that *Salmonella* spp can be found on most farms. It is apparent from results of our study that *Salmonella* spp can be highly prevalent on some farms at 1 point in time or across time; this has also been determined in many other studies.[9,27-31] The extent to which on-farm prevalence of *Salmonella* spp plays a role in the risk of contamination of food products destined for human consumption is not well understood. As has been suggested[32] and practiced in the Danish *Salmonella* surveillance and control program,[33,34] targeting high-prevalence farms, in combination with other factors along the farm-to-table continuum, should be an important focus of *Salmonella* control efforts.

[a]Whirl Pak bag, NASCO, Fort Atkinson, Wis.
[b]BD Diagnostic Systems, Sparks, Md.
[c]SAS, version 8, SAS Institute Inc, Cary, NC.

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