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Prevalence and Distribution of *Campylobacter jejuni* in Small-Scale Broiler Operations

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ABSTRACT

Campylobacter jejuni has been recognized as one of the most prevalent causes of foodborne bacterial illnesses in humans. Previous studies have focused on the transmission routes of *C. jejuni* from commercial flock farms to the final retail product. The objective of this study was to determine the prevalence of *C. jejuni* and *Campylobacter* spp. in eggshells, live birds, feed, drinking water, and the rearing environment in a small-scale broiler operation. Broilers were raised under two different production systems: (i) environmentally controlled housing and (ii) open-air housing with two replications. Each week, samples were collected from eggshells, bird feces, feed, drinking water, enclosures (vertical walls of bird housing), and feed troughs for enumeration and isolation testing. All samples were plated on modified charcoal-cefoperazone-deoxycholate agar to determine the log CFU per gram and percent prevalence of *Campylobacter* spp. Isolation of *C. jejuni* was verified with latex agglutination and hippurate hydrolysis tests. The results from this study suggest that vertical transmission of these bacteria from egg surfaces to newly hatched chicks is not a significant risk factor. The results also suggest that the prevalence of *C. jejuni* at time of harvest (week 6) was significantly higher ($P < 0.05$) in the open-air housing broilers than in those in the environmentally controlled housing. Elevated levels of cross-contaminants, especially water and feed, may have played a role in this outcome.

Campylobacter jejuni is a common foodborne bacterial pathogen of humans in the United States and other developed countries. The infection caused by this organism is characterized by self-limiting watery and bloody diarrhea *(1, 10, 31)*. The majority of human *Campylobacter* infections can result from consumption of undercooked chicken or food contaminated by raw chicken *(1, 10, 32)*.

In order to reduce or eliminate *Campylobacter* spp. from poultry, it is necessary to understand the ecological aspects of the infection in the reservoir. On-farm production practices can affect pathogen loads on poultry entering slaughter facilities, resulting in cross-contamination post-harvest.

C. jejuni is highly prevalent in chicken flocks, especially in chickens more than 3 weeks old. The organism is carried in poultry intestinal contents in high amounts, leading to fecal contamination of chicken carcasses in processing plants *(20, 28, 32)*. Despite this high colonization rate, infected chickens show little or no clinical signs of illness *(28, 32)*. The sources of infection and modes of transmission for *C. jejuni* infection in poultry farms are not well understood. Many studies suggest that horizontal transmission from environmental sources is the major mode of chicken flock infection by *C. jejuni (4, 13, 20, 22, 32)*. However, several findings suggest that vertical transmission might also play a role in introducing *C. jejuni* from breeders into broiler flocks *(3, 7, 22, 29)*.

Currently, the ecology of *Campylobacter* spp. in the poultry reservoir is poorly understood, particularly with respect to the sources of infection and routes of transmission. It is thought that both vertical and horizontal transmission may affect the immune status of the poultry host and the environmental conditions in the production system *(9, 24)*. Intervention strategies for *Campylobacter* species infection in poultry should consider the complex nature of its transmission and may require the use of multiple approaches that target different segments of the poultry production system *(11)*. However, most studies have concentrated on the transmission routes from commercial farm flock to carcasses after slaughter and to retail products *(6, 8, 14, 23, 33)*. Interest in animal welfare issues has spurred an increased interest in free-range, small-scale, and local poultry production. With these open-air, less-controlled environments, an increased infection rate of *Campylobacter* spp. might be an issue. Therefore, there is a need to control infection rates and identify potential cross-contamination vectors associated with small-scale poultry production.

The objectives of these experiments were severalfold. One objective was to determine the prevalence of *Campylobacter* spp. and *C. jejuni* on the shells of eggs received from the hatchery during incubation. A second objective was to detect the presence and extent of *Campylobacter* spp. and *C.*

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jejuni in live birds raised in an environmentally controlled housing (ECH) system and an open-air housing (OAH) system over a 6-week period. A third objective was to determine whether and to what extent *Campylobacter* spp. and *C. jejuni* were present in the drinking water, feed, enclosures (vertical walls of bird housing), and feed troughs of the experimental birds.

MATERIALS AND METHODS

Egg samples. Ninety-six fertilized eggs were incubated at the McNeese State University Agricultural Sciences laboratory in Lake Charles, LA, and evaluated for *C. jejuni*. Each week, 75 eggs were randomly selected and swabbed from the surface of the equator area side by side (4 cm^2) using a sterile rayon-tipped swab. The sample swabs were placed in individual tubes containing 3 ml of sterile tryptone soy broth (TSB) for enumeration and isolation of *Campylobacter* spp. for 3 weeks until hatched.

Housing and care. Two replications, each using 150 Ross × Ross female broiler chickens, were allotted to two housing environments: (i) an ECH (32°C) system with individual pens (Petersime Incubator Co., Gettysburg, OH) with raised wire flooring and (ii) an OAH system that consisted of a covered roof and partially solid and chicken wire walls with exposed soil and wood shavings. Both housing systems were in secure areas that prevent unauthorized persons from entering. The Petersime ECH system was divided into 12 vertical pens of equal size (74.7 by 99.1 by 24.13 cm). Each pen housed 11 or 12 birds. Individual open water and feed troughs were provided for each pen. Each housing system was emptied of birds, feed, and litter and cleaned (ECH was cleaned with a hot water wash and disinfectant and OAH by removal of litter and debris). The animal care givers monitored feed and water and removed litter trays daily. Normal pest and rodent control was maintained throughout the experiment. In the OAH, broilers (150 per replication) were reared together in an area measuring (3.8 by 5.13 by 2.54 m). Heat lamps were suspended 0.4 m above the litter for temperature regulation in the OAH system. The OAH system had commercial open water and feed troughs. The animal care givers monitored the feed and water troughs daily. The temperature and percent relative humidity during the time period were 32°C and 58%, respectively. Feed was procured from the Texas Farm Products Company (Nacogdoches, TX). Starter and grower diets were provided (without antibiotics) to meet or exceed the dietary requirements of the National Research Council *(18)*. For the ECH and the OAH systems, drinking water and feed were supplied ad libitum.

Fecal samples. Two sampling replications, each extending for 6 weeks, for both the ECH and OAH systems were performed. Replication I was initiated in September 2013, and replication II in December 2013. Each week, 75 birds were randomly tested by obtaining cloacal samples with sterile rayon-tipped swabs and assaying them for the presence of *Campylobacter* spp. *(19)*. The swabs were placed in a tube containing 3 ml of sterile TSB for further analysis.

Environment samples. As with the fecal regimen, drinking water sampling underwent two replications, each extending for 6 weeks, for both the ECH and the OAH system. Twelve and six water troughs were present in the ECH and the OAH system, respectively. Six water samples were tested for each trough and placed in sterile bottles. For each sample, 5 ml of water was collected in a sterile bottle for subsequent testing.

In addition to water, feed was also tested for the presence of *Campylobacter* spp. and *C. jejuni*. For these tests, amounts of approximately 3 g of feed were placed in sterile bottles for future analysis. Each newly opened feed bag was assayed. A single sample was tested per bag. For the distribution of feed, 12 and 6 troughs were present in the ECH and the OAH system, respectively. Six feed samples were tested per trough.

Similarly, the enclosures were tested. Twelve pen surfaces and six wall surfaces were present in the ECH and the OAH system, respectively. Each surface was swabbed in an area of approximately 25 cm^2. Each swab was immediately placed into 3 ml of TSB for subsequent analysis.

The feed troughs were also tested. Twelve feed troughs were present in the ECH system, and six feed troughs were present in the OAH system. As was done for the enclosures, each trough was swabbed six times per test.

Bacterial isolation and identification. Eggshell, fecal, and environment samples were collected in sterile containers using aseptic techniques, transported to the laboratory, and analyzed each week. Bacterial counts were determined for *Campylobacter* spp. *(5)*. Immediately upon arrival in the laboratory, all samples were whirl mixed in a shaker incubator (Excella E24/E24R Temperature-Controlled Benchtop Shaker, New Brunswick Scientific, Edison, NJ) for approximately 1 h at 37°C and then mixed with a vortexer for 2 min to release the bacteria.

Each sample, consisting of 0.1 ml of the respective material, was aseptically transferred and spread onto modified charcoal-cefoperazone-deoxycholate agar. The inoculated plates were then incubated at 42°C for 48 h under a microaerophilic environment (5% O_2, 10% CO_2, and 85% N_2).

From cultured samples, *Campylobacter* spp. were verified via latex agglutination *(16, 17)* with a Microgen M46 *Campylobacter* Assay Kit (Microgen Bioproducts Ltd., Camberley, Surrey, UK) according to the manufacturer's instructions and *C. jejuni* was confirmed via hippurate hydrolysis *(12)*.

Statistical analysis. Statistical procedures were performed using SAS Windows *(27)*. Day-old broilers were randomly allotted to two treatments (housing type) with two replications. All calculations were performed with Proc GLM procedures *(27)* using a P value of 0.05 for the significance of the least-squares means with a model of housing type and week of testing. When a difference was detected between treatments, specific comparisons between treatment means at that time point were made with the PDIFF option of LSMEANS.

RESULTS

Egg samples. Each week during the 3-week incubation period until hatching, 75 egg surface (4 cm^2) swab samples were tested for *Campylobacter* spp. and *C. jejuni*. No *Campylobacter* species or *C. jejuni* growth was detected (0%, 0 of 225) from weeks 1 through 3.

Drinking water. *Campylobacter* species counts in drinking water from the ECH system ranged from nondetectable to 2.10 log CFU/ml and from the OAH system ranged from nondetectable to 3.05 log CFU/ml (Fig. 1). The counts of *Campylobacter* spp. in drinking water increased from week 1 to week 6 in both housing systems (Fig. 1).

The prevalence of *Campylobacter* spp. in drinking water ranged from 0% (0 of 24) to 66.7% (16 of 24) in the

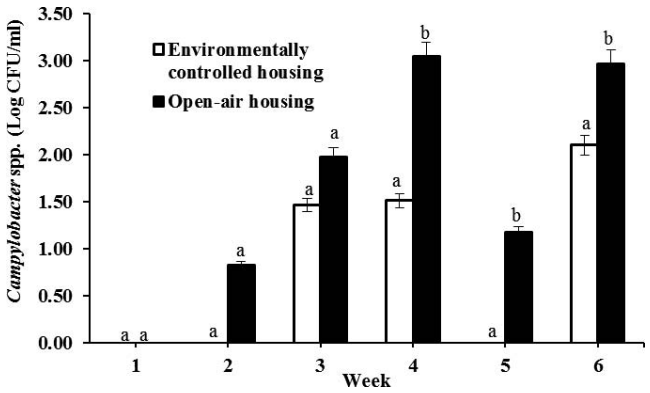

FIGURE 1. Campylobacter *species bacterial counts in drinking water from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6. Data are means from two replications; SEM = 1.7784. Treatment means with different letters (a and b) for the same week are significantly different (*$P < 0.05$*).*

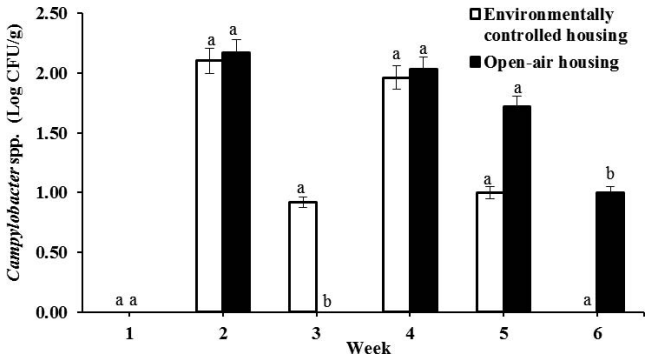

FIGURE 2. Campylobacter *species bacterial counts in feed from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6. Data are means from two replications; SEM = 1.6439. Treatment means with different letters (a and b) for the same week are significantly different (*$P < 0.05$*).*

ECH system and from 0% (0 of 12) to 83.3% (10 of 12) in the OAH system (Table 1). Additionally, the prevalence of *C. jejuni* in drinking water ranged from 0% (0 of 24) to 16.7% (4 of 24) in the ECH system and from 0% (0 of 12) to 83.3% (10 of 12) in the OAH system (Table 1). The prevalence of *C. jejuni* in drinking water was significantly higher ($P < 0.05$) in the OAH system (83.3%, 10 of 12) than in the ECH system (8.3%, 2 of 24) in week 4 (Table 1).

Feed. Fresh feed from each newly opened bag was tested for *Campylobacter* spp. and *C. jejuni*. All samples were negative. For the distributed feed, the counts of *Campylobacter* spp. ranged from nondetectable to 2.10 log CFU/g in the ECH system and from nondetectable to 2.17 log CFU/g in the OAH system (Fig. 2).

The prevalence of *Campylobacter* spp. ranged from 0% (0 of 24) to 83.3% (20 of 24) in feed from the ECH system and from 0% (0 of 12) to 33.3% (4 of 12) in feed from the OAH system (Table 2). Additionally, the prevalence of *C. jejuni* ranged from 0% (0 of 24) to 33.3% (8 of 24) in feed from the ECH system and from 0% (0 of 12) to 33.3% (4 of 12) in feed from the OAH system (Table 2). The prevalence of *C. jejuni* in feed in the OAH system was not significantly different ($P > 0.05$) (33.3%, 4 of 12) from that in the ECH system (25.0%, 6 of 24) in week 4 (Table 2).

Enclosures. *Campylobacter* spp. were detected on the surface of enclosures in both systems. During the 6-week period of testing, the *Campylobacter* species counts from enclosures ranged from nondetectable levels to 1.30 log CFU/25 cm^2 in the ECH system and from nondetectable levels to 2.34 log CFU/25 cm^2 in the OAH system (Fig. 3).

Campylobacter spp. were not detected in weeks 1, 2, 5, and 6 in the ECH and the OAH systems (Table 3). However, *Campylobacter* spp. were found during the third week at 16.7% (4 of 24) in the ECH system and during the fourth week at 58.3% (7 of 12) in the OAH system (Table 3). Additionally, *C. jejuni* was not found in the ECH system. However, *C. jejuni* was found in the OAH system at 16.7% (2 of 12) (Table 3). *C. jejuni* in enclosures was significantly higher ($P < 0.05$) in the OAH system (16.7%; 2 of 12) compared to the ECH system (0%; 0 of 24) in week 4 (Table 3).

Feed troughs. *Campylobacter* species counts in this study ranged from non-detectable levels to 1.55 log CFU/25 cm^2 in the ECH system and from non-detectable levels to

TABLE 1. *The prevalence of* Campylobacter *spp. and* C. jejuni *in drinking water from the environmentally controlled housing and the open-air housing systems for weeks 1 through 6*[a]

Week	No. (%) of drinking water troughs testing positive for *Campylobacter* species in:		No. (%) of drinking water troughs testing positive for *C. jejuni* in:	
	ECH	OAH	ECH	OAH
1	0/24 (ND) A	0/12 (ND) A	0/24 (ND) A	0/12 (ND) A
2	0/24 (ND) A	8/12 (66.7) B	0/24 (ND) A	0/12 (ND) A
3	16/24 (66.7) A	8/12 (66.7) A	4/24 (16.7) A	6/12 (50.0) B
4	12/24 (50.0) A	10/12 (83.3) B	2/24 (8.3) A	10/12 (83.3) B
5	0/24 (ND) A	6/12 (50.0) B	0/24 (ND) A	6/12 (50.0) B
6	10/24 (41.7) A	4/12 (33.3) A	4/24 (16.7) A	4/12 (33.3) A

[a] Each positive result represents one water trough. Data are sum totals from two replications. SEM for *Campylobacter* spp. = 0.0747; SEM for *C. jejuni* = 0.0680. ECH, environmentally controlled housing; OAH, open-air housing; ND, nondetectable. Treatment totals with different letters (A and B) for the same week are significantly different ($P < 0.05$).

TABLE 2. *The prevalence of* Campylobacter *spp. and* C. jejuni *in feed from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6*[a]

Week	No. (%) of feed troughs testing positive for *Campylobacter* spp. in:		No. (%) of feed troughs testing positive for *C. jejuni* in:	
	ECH	OAH	ECH	OAH
1	0/24 (ND) A	0/24 (ND) A	0/24 (ND) A	0/12 (ND) A
2	20/24 (83.3) A	4/12 (33.3) B	8/24 (33.3) A	0/12 (ND) B
3	10/24 (41.7) A	0/12 (ND) B	6/24 (25.0) A	0/12 (ND) B
4	16/24 (66.7) A	4/12 (33.3) B	6/24 (25.0) A	4/12 (33.3) A
5	2/24 (8.3) A	1/12 (8.3) A	2/24 (8.3) A	1/12 (8.3) A
6	0/24 (ND) A	1/12 (8.3) A	0/24 (ND) A	0/12 (ND) A

[a] Each positive result represents one feed trough. Data are sum totals from two replications. SEM for *Campylobacter* spp. = 0.0781; SEM for *C. jejuni* = 0.0573. ECH, environmentally controlled housing; OAH, open-air housing; ND, nondetectable. Treatment totals with different letters (A and B) for the same week are significantly different ($P < 0.05$).

2.26 log CFU/25 cm^2 in the OAH system (Fig. 4). These data indicate that levels of *Campylobacter* spp. in the troughs were relatively low.

Campylobacter spp. were not detected in feed troughs in the ECH system during weeks 1, 3, 5, and 6, but were detected in weeks 2 and 4 at 66.7% (16 of 24) and 50.0% (12 of 24), respectively (Table 4). *Campylobacter* spp. were not detected in feed troughs in the OAH system in weeks 1, 5, and 6, but were detected in weeks 2, 3, and 4 at 16.7% (2 of 12), 25.0% (3 of 12), and 16.7% (6 of 12), respectively (Table 4). Additionally, *C. jejuni* was detected in feed troughs in weeks 3 and 4 in the OAH system at 25.0% (3 of 12) and 8.3% (1 of 12), respectively (Table 4). *C. jejuni* in feed troughs was not detected in the ECH system. The prevalence of *C. jejuni* in feed troughs was significantly higher ($P < 0.05$) in the OAH system (25.0%; 3 of 12) compared with the ECH system (0%; 0 of 24) in week 3 (Table 4).

Fecal samples. *Campylobacter* species fecal counts increased from week 1 to week 6 in both the ECH and the OAH systems. The counts of *Campylobacter* spp. in the ECH system increased from an initial value of 1.70 log CFU per broiler in week 1 to 4.91 log CFU per broiler in week 6 (Fig. 5). In the OAH system, counts increased from a nondetectable level in week 1 to 5.31 log CFU per broiler in week 6 (Fig. 5). Although these results found that *Campylobacter* species counts in the OAH system (5.31 CFU per broiler) were significantly higher ($P < 0.05$) than those of the ECH system (4.91 CFU per broiler) at week 6 (Fig. 5), they do not suggest biological significance.

Detection of *Campylobacter* spp. in individual chickens from the ECH system ranged from 5.3% (8 of 150) to 83.3% (125 of 150) (Table 5). From the OAH system, *Campylobacter* species detection ranged from 0% (0 of 150) to 93.3% (140 of 150) (Table 5). In both housing systems, the prevalence of *Campylobacter* spp. in individual broilers peaked during the third week. Specifically, there was a prevalence of 93.3% (140 of 150) in the OAH birds and 83.3% (125 of 150) in the ECH birds (Table 5). Additionally, the prevalence of *C. jejuni* ranged from 5.3% (8 of 150) to 50.0% (75 of 150) in the ECH system and from 0% (0 of 150) to 70.7% (106 of 150) in the OAH system (Table 5). The prevalence of *C. jejuni* in week 6 was significantly higher ($P < 0.05$) in the OAH system (37.3%;

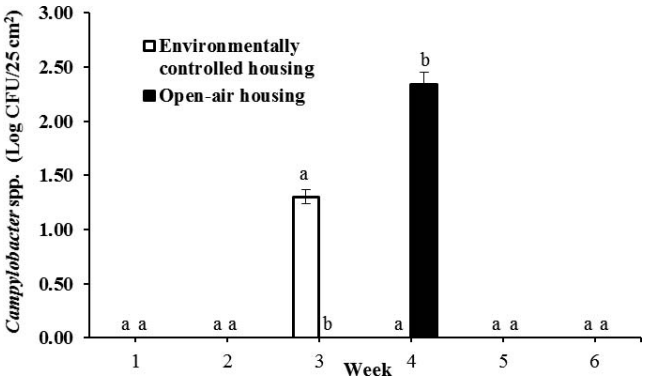

FIGURE 3. Campylobacter *species bacterial counts from enclosures from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6. Data are means from two replications; SEM = 1.3931. Treatment means with different letters (a and b) for the same week are significantly different (*$P < 0.05$*).*

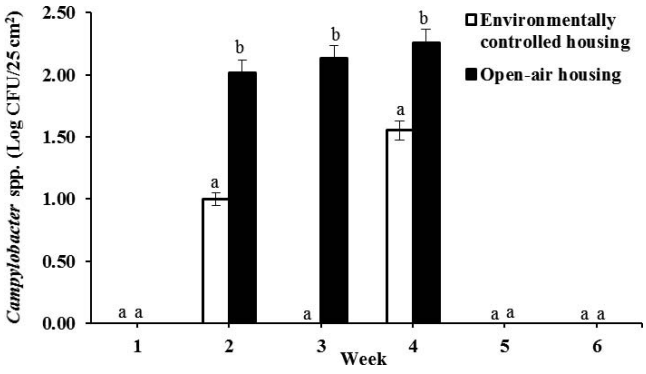

FIGURE 4. Campylobacter *species bacterial counts from feed troughs from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6. Data are means from two replications; SEM = 1.7571. Treatment means with different letters (a and b) for the same week are significantly different (*$P < 0.05$*).*

TABLE 3. *The prevalence of* Campylobacter *spp. and* C. jejuni *from enclosures from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6*[a]

	No. (%) of enclosures testing positive for *Campylobacter* spp. in:		No. (%) of enclosures testing positive for *C. jejuni* in:	
Week	ECH	OAH	ECH	OAH
1	0/24 (ND) A	0/12 (ND) A	0/24 (ND) A	0/12 (ND) A
2	0/24 (ND) A	0/12 (ND) A	0/24 (ND) A	0/12 (ND) A
3	4/24 (16.7) A	0/12 (ND) B	0/24 (ND) A	0/12 (ND) A
4	0/24 (ND) A	7/12 (58.3) B	0/24 (ND) A	2/12 (16.7) B
5	0/24 (ND) A	0/12 (ND) A	0/24 (ND) A	0/12 (ND) A
6	0/24 (ND) A	0/12 (ND) A	0/24 (ND) A	0/12 (ND) A

[a] Each positive result represents one feed trough. Data are sum totals from two replications. SEM for *Campylobacter* spp. = 0.0557; SEM for *C. jejuni* = 0.0324. ECH, environmentally controlled housing; OAH, open-air housing; ND, nondetectable. Treatment totals with different letters (A and B) for the same week are significantly different ($P < 0.05$).

56 of 150) than in the ECH system (26.0%; 39 of 150) (Table 5).

DISCUSSION

It has been proposed that the vertical transmission of *Campylobacter* spp. from eggs to broilers might be due to abiotic factors *(26)*. However, our results suggest that the possibility of vertical transmission of *Campylobacter* spp. specifically from the surface of eggs to newly hatched chicks is not a significant risk factor in small commercial settings. These results are consistent with at least one previous study *(25)*.

An important potential source of *Campylobacter* gastroenteritis outbreaks is contaminated water *(22)*. The presence of *Campylobacter* spp. in drinking water stations has been reported in other studies. One study *(2)* reported that the presence of *Campylobacter* spp. in broiler house drinking water samples was as high as 88%. In our study, drinking water in the OAH system experienced significantly higher levels of *Campylobacter* spp. than drinking water in the ECH system during at least part of the experimental period. Drinking water in OAH was provided through an open single communal system that lay in close proximity to the soil and therefore, could become contaminated by chicken feces and other pollutants. Under conditions like these, sediments and biofilms may form that serve as an environmental reservoir for *Campylobacter* spp.

Although our findings do not suggest that the drinking water is the primary source of infection, it remains a potential source of cross-contamination. These results are consistent with previous studies *(15, 22)*. Our findings suggest that drinking water should be clean and free of chicken feces, which sustain the growth of *Campylobacter* bacteria. The drinking water system must be monitored. Having fewer birds per drinking water station also may mitigate this problem.

Owing to its low moisture content, fresh feed is an unlikely primary source of *Campylobacter* bacteria. *(2)*. However, our results suggest that feed had become cross-contaminated for most of the experimental period in both the ECH and the OAH system. A likely source for contamination is via defecation in feeders *(30)*. As with the water supply, it is imperative to maintain clean feed when producing broilers to prevent cross-contamination. To that end, fresh dry feed, stored in closed containers, should be used. Additionally, feed should not be supplied in overabundance so that it becomes fallow.

Because the bacterium cannot survive on dry surfaces, enclosures typically are not considered primary sources of *Campylobacter* colonization. However, enclosures can become contaminated from feces of vermin *(20)*. It is uncertain why the enclosures in each setting showed evidence of *Campylobacter* contamination for only one week during the six weeks of testing. Although this may

TABLE 4. *The prevalence of* Campylobacter *spp. and* C. jejuni *from feed troughs from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6*[a]

	No. (%) of feed troughs testing positive for *Campylobacter* spp. in:		No. (%) of feed troughs testing positive for *C. jejuni* in:	
Week	ECH	OAH	ECH	OAH
1	0/24 (ND) A	0/12 (ND) A	0/24 (ND) A	0/12 (ND) A
2	16/24 (66.7) A	2/12 (16.7) B	0/24 (ND) A	0/12 (ND) A
3	0/24 (ND) A	3/12 (25.0) B	0/24 (ND) A	3/12 (25.0) B
4	12/24 (50.0) A	2/12 (16.7) B	0/24 (ND) A	1/12 (8.3) A
5	0/24 (ND) A	0/12 (ND) A	0/24 (ND) A	0/12 (ND) A
6	0/24 (ND) A	0/12 (ND) A	0/24 (ND) A	0/12 (ND) A

[a] Each positive result represents one feed trough. Data are sum totals from two replications. SEM for *Campylobacter* spp. = 0.0661; SEM for *C. jejuni* = 0.0425. ECH, environmentally controlled housing; OAH, open-air housing; ND, nondetectable. Treatment totals with different letters (A and B) for the same week are significantly different ($P < 0.05$).

TABLE 5. *The prevalence of* Campylobacter *spp. and* C. jejuni *in live broilers from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6*[a]

Week	No. (%) of broilers testing positive for *Campylobacter* spp. in:		No. (%) of broilers testing positive for *C. jejuni* in:	
	ECH	OAH	ECH	OAH
1	8/150 (5.3) A	0/150 (ND) B	8/150 (5.3) A	0/150 (ND) B
2	86/150 (57.3) A	48/150 (32.0) B	66/150 (44.0) A	48/150 (32.0) B
3	125/150 (83.3) A	140/150 (93.3) B	28/150 (18.7) A	106/150 (70.7) B
4	115/150 (76.7) A	123/150 (82.0) B	35/150 (23.3) A	35/150 (23.3) A
5	75/150 (50.0) A	60/150 (40.0) B	75/150 (50.0) A	60/150 (40.0) B
6	39/150 (26.0) A	56/150 (37.3) B	39/150 (26.0) A	56/150 (37.3) B

[a] Each positive result represents one feed trough. Data are sum totals from two replications. SEM for *Campylobacter* spp. = 0.0228; SEM for *C. jejuni* = 0.0266. ECH, environmentally controlled housing; OAH, open-air housing; ND, nondetectable. Treatment totals with different letters (A and B) for the same week are significantly different ($P < 0.05$).

appear to be an anomaly, the presence of *Campylobacter* on enclosures, even for a short period of time, can have major consequences. That is, cross-contamination, as with drinking water and feed, can occur rapidly through this vector. Therefore, regular sanitation practices designed to clean and disinfect cages should be employed.

As is the case for drinking water, feed, and enclosures, troughs might be a source for *Campylobacter* cross-contamination. Both systems in our study had trough contamination for at least several weeks during the experimental period. Our results suggest that contamination was more severe in the OAH system than in the ECH system. One likely explanation is that troughs in the OAH are more readily exposed to cross-contaminating vectors (especially chicken feces) than are those in the ECH. That is, the likely route here appears to be from feces to beak to trough.

Our study found that the *Campylobacter* species counts in bird feces from the OAH system were significantly higher than those of the ECH system. Additionally, the results from this study indicate that the presence of *Campylobacter* spp. in drinking water, feed, enclosures, and troughs was elevated in the samples taken in the OAH system compared with those taken in the ECH system. As these are probable vectors in the cross-contamination of *Campylobacter* spp., it is reasonably postulated that they contributed to the elevated levels of *Campylobacter* species contamination found in the OAH birds.

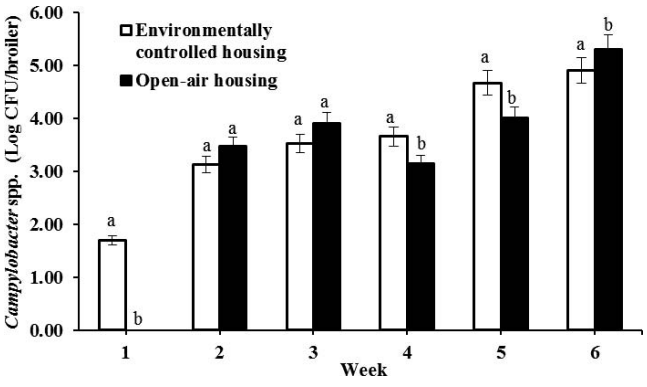

FIGURE 5. Campylobacter *species bacterial counts in live broilers from the environmentally controlled housing and the open-air housing systems from weeks 1 through 6. Data are means from two replications; SEM = 3.2807. Treatment means with different letters (a and b) for the same week are significantly different (*$P < 0.05$*).*

The prevalence of *C. jejuni* in the OAH broilers peaked in week 3, followed by a decline. In the ECH system, the prevalence peaked in week 5 and also was followed by a decline. This pattern is consistent with other studies that have shown that the prevalence of *Campylobacter* spp. peaks and then declines over time *(25)*. Similar findings *(21)* posited that this decline might be due to maturation of antibodies passed from hens to their chicks. As was the case in counts of *Campylobacter* spp. noted above, the prevalence of *C. jejuni* at the time of harvest at week 6 also was significantly higher in the OAH broilers than in those in the ECH. Once again, the elevated levels of cross-contaminants here may have played a role in this outcome.

In summary, this study revealed that abiotic factors have the potential to contribute to horizontal cross-contamination of *C. jejuni*. Most notably, water and feed represent likely sources for cross-contamination. Therefore, sound sanitation practices are of paramount concern in small-scale poultry farming. Although other sources have suggested that eggshells might provide a vertical means of cross-contamination, this research found this not to be the case. Understanding the factors that affect *C. jejuni* in ECH and OAH systems in small-scale poultry operations might help improve the development of risk management strategies for producers. Ultimately, these findings might help reduce the risks to the consumer associated with campylobacteriosis.

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