MAJOR ARTICLE

Nontyphoidal *Salmonella* from Human Clinical Cases, Asymptomatic Children, and Raw Retail Meats in Yucatan, Mexico

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Background. We report the results of a 3-year *Salmonella* surveillance study of persons with diarrhea; asymptomatic children; and retail pork, poultry, and beef in Yucatan, Mexico.

Methods. Isolates were characterized according to serotype, antimicrobial susceptibility, and genetic relatedness with pulsed-field gel electrophoresis.

Results. *Salmonella* Typhimurium was the most common serotype found in ill humans (21.8% of isolates), followed by *Salmonella* Agona (21% of isolates). *Salmonella* Enteritidis was a minor serotype (4.2% of isolates). Asymptomatic children carried *S.* Agona (12.1% of isolates), *Salmonella* Meleagridis (11.6% of isolates), *Salmonella* Anatum (8% of isolates) and *S.* Enteritidis (5.8% of isolates). A high percentage of retail meat samples contained *Salmonella;* it was most commonly found in pork (58.1% of samples), followed by beef (54% of samples) and poultry (39.7% of samples). Resistance to oral drugs used for the treatment of salmonellosis was observed for ampicillin (14.6% of isolates were resistant), chloramphenicol (14.0% of isolates), and trimethoprim-sulfamethoxazole (19.7% of isolates). Resistance to ceftriaxone emerged in 2002 and was limited to the serotype *S.* Typhimurium. Twenty-seven percent of the isolates were resistant to nalidixic acid, and none were resistant to ciprofloxacin. Multidrug resistance was most common among isolates of serotypes *S.* Typhimurium and *S.* Anatum. Pulsed-field gel electrophoresis showed that strains found in retail meats were genetically identical to strains found in both asymptomatic children and ill patients.

Conclusions. Our study found a high prevalence of *Salmonella* in retail meats and persons with enteric infection; many of these isolates were resistant to clinically important antimicrobials. A random selection of isolates from people and retail meat showed genetic relatedness, which suggests that, in Yucatan, considerable transfer of *Salmonella* occurs through the food chain.

Nontyphoidal *Salmonella* infections are an important public health problem worldwide [1, 2]. *Salmonella* may cause gastroenteritis in people of all ages and severe invasive disease in infants, elderly persons, and immunocompromised persons [1, 2]. During the past 2 decades, the incidence of zoonotic foodborne *Salmonella* infections in industrialized countries has progressively increased [1]. In addition, the frequency of antimicrobial resistance and the number of resistance determinants in *Salmonella* has risen markedly [3]. In response to the growing threat of outbreaks of infection and drug resistance of foodborne pathogens, industrialized nations have established intersectoral, multidisciplinary monitoring programs. They have also implemented numerous and costly interventions designed to reduce or eliminate infection or colonization with *Salmonella* and other foodborne pathogens in food animals and animal-derived foods [4].

Although developing countries carry most of the global burden of diarrheal disease [5], very few have established intersectoral monitoring programs for *Sal*

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monella. In Latin America, monitoring networks are usually limited to samples obtained from people, and most networks rely on deficient passive surveillance systems. Thus, there is little information on the main food-animal reservoirs for *Salmonella* and the modes of transmission. Even less is known about antimicrobial resistance in *Salmonella* strains of food-animal origin, the extent of its transmission to humans, and the public health burden of illness due to *Salmonella* infection.

Yucatan, among the poorest states in Mexico, has one of the highest morbidity rates for infectious intestinal disease in children <5 years of age (322 cases of infectious intestinal disease per 1000 children per year; D. Ruiz, Yucatan State Health Department, personal communication). Food-animal production is one of the major economic activities in Yucatan, and ~95% of all retail meat sold in the state is locally produced. In view of the public health importance of zoonotic foodborne disease, an active surveillance program was established in 2000. The objectives and structure of the surveillance program were based on recommendations from a World Health Organization technical expert committee and adapted to local needs and infrastructure [3]. The main objectives of the program were (1) to determine the prevalence of *Salmonella* in both ill and healthy people and in retail pork, chicken, and beef; (2) to determine the main serovars isolated from each source and their antimicrobial susceptibility patterns; and (3) to determine the genetic relatedness of isolates from people and retail meat. This article describes the results obtained from 2000 to 2002 and their implications for public health and future research.

MATERIALS AND METHODS

Specimen collection. During the first year, surveillance was limited to ill persons and asymptomatic children; retail pork and chicken were added to surveillance in 2001, and beef was added in 2002. The asymptomatic children were included to give a broader perspective of the transmission and carriage rate of *Salmonella* in the general population. Fecal samples were collected from patients with diarrhea who were treated in the oral rehydration unit or the pediatric emergency department of a major state referral hospital located in the capital city, or at a primary care health center in a nearby town, and from asymptomatic children attending day care centers or kindergartens throughout the state of Yucatan. For study purposes, a case of diarrhea was defined as at least 3 loose bowel movements in 24 h. Healthy children who regularly attended kindergarten or day care and who did not present with diarrhea within 7 days prior to submitting a sample of fecal matter were considered to be asymptomatic. The Hospital General O'Horan internal review board and ethics committee approved the protocol, and written informed consent was obtained from all participants or their guardians. Retail chicken, pork, and beef were purchased at supermarkets, butcher shops, and/or open markets in the cities where the ill persons and asymptomatic children resided.

Microbiology. Isolation and identification of *Salmonella* from samples of human feces and retail meat were performed according to methods described elsewhere [6]. Up to 4 colonies of *Salmonella* were picked from the primary isolation plates for identification; isolates biochemically confirmed to be *Salmonella* were serotyped according to the Kauffmann-White scheme [7]. All isolates were tested with the disk diffusion method for susceptibility to ampicillin, chloramphenicol, ceftriaxone, ciprofloxacin, gentamicin, kanamycin, nalidixic acid, streptomycin, sulfisoxazole, trimethoprim-sulfamethoxazole, and tetracycline. MICs were determined by broth microdilution for selected isolates, according to the protocols and interpretive criteria of the Clinical and Laboratory Standards Institute (formerly NCCLS) [8, 9].

PFGE. To determine the genetic relatedness of *Salmonella* isolates found in samples from our human subjects and in retail meats, a subset of isolates underwent PFGE analysis, performed according to the protocol developed by the Centers for Disease Control and Prevention [10]. PFGE results were analyzed using BioNumerics software, version 3.0 (Applied-Maths, Kortrijk, Belgium), and banding patterns were compared using Dice coefficients with a 1.5% band position tolerance.

Data analysis. Whonet software, version 5.2 (World Health Organization) was used to enter data and analyze susceptibility patterns by serotype.

RESULTS

Epidemiological surveillance. Fecal samples were collected from 621 patients with diarrhea (aged 1 month–26 years) who were hospitalized at the Hospital General O'Horan or treated at a nearby primary care health clinic and from 1812 asymptomatic children (aged 4 months–7 years) who attended 28 different schools or day care centers in 2 major cities and 6 towns in Yucatan. A total of 295 chicken samples, 339 pork samples, and 126 beef samples were purchased from 78 supermarkets, butcher shops, or markets at the 8 locations (table 1). Retail pork had the highest prevalence of *Salmonella* (58.1% samples), followed by beef (54%) and poultry (39.7%). Pork contained >1 serotype per sample, more frequently than did retail chicken or beef (table 1). The prevalence of *Salmonella* in poultry from open markets was 60% (55 of 91 samples), compared with 46% (37 of 81) for samples from butcher shops and 24% (29 of 123) for samples from supermarkets. The prevalence of *Salmonella* in pork was 78% (94 of 120) for samples from markets, 81% (62 of 77) for samples from butcher shops, and 29% (41 of 142) for samples from supermarkets, . The prevalence of *Salmonella* in beef was 94% (31 of 33) from markets, 91% (21 of 23) from butcher shops, and 23% (16 of 70) from supermarkets.

Table 1. Prevalence of *Salmonella* infection in humans and contamination in retail meat from Yucatan, Mexico, 2000–2002.

Source of samples	No. of patients or samples tested	No. (%) of patients or samples positive for *Salmonella*			
		Total	By no. of serotypes isolated		
			1	2	⩾3
Persons with diarrhea[a]	621	116 (18.7)	113 (18.2)	3 (0.5)	0 (0)
Asymptomatic children[a]	1812	207 (11.4)	192 (10.6)	13 (0.7)	2 (0.1)
Retail poultry[b]	295	117 (39.7)	94 (31.9)	20 (6.8)	3 (1)
Retail pork[b]	339	197 (58.1)	115 (33.9)	66 (19.5)	16 (4.7)
Retail beef[c]	126	68 (54)	40 (31.7)	20 (15.9)	8 (6.3)

[a] Samples collected from 2000 to 2002.
[b] Samples collected from 2001 to 2002.
[c] Samples collected during 2002.

Salmonella was recovered from 18.7% of persons with diarrhea (116 of 621) , with the highest monthly rates of recovery (45%–63% of persons) registered from June to October. Although the average rate of recovery in asymptomatic children during the study period was 11.4%, there was considerable variation in the rates of recovery among the different schools (range, 0%–37%). However, there was no clustering by city or socioeconomic level. Three children with diarrhea and 13 asymptomatic children were found to carry 2 different *Salmonella* serotypes, and 3 different serotypes were found in each fecal sample from 2 other asymptomatic children.

The top 10 most common serovars isolated from ill persons, asymptomatic children, and retail meats are shown in table 2. *Salmonella* Agona and *Salmonella* Meleagridis were the most common serovars isolated from all of the 5 sources of samples. Among retail meats, *Salmonella* Typhimurium was mainly isolated from pork (5.1% of isolates) and *Salmonella* Enteritidis was the second most prevalent serotype in chicken (16.8% of isolates).

Antimicrobial resistance. The percentages of isolates from the different sources that were resistant to antimicrobials are given in table 3. Overall, the most common antimicrobial to which the different serovars of *Salmonella* were resistant was streptomycin (73.6% of the isolates were resistant), followed by tetracycline (72.1%), sulfisoxazole (45.9%), and nalidixic acid (26.9%). Lower rates were seen for therapeutically important oral drugs, such as ampicillin (14.6%), chloramphenicol (14.0%), and trimethoprim-sulfamethoxazole (19.7%). Resistance to third-generation cephalosporins was detected for the first time in 2002 and was restricted to *S.* Typhimurium (23% of the isolates were resistant). No isolates were resistant to ciprofloxacin. Resistance to ampicillin, chloramphenicol, and trimethoprim-sulfamethoxazole was most common among isolates from persons with diarrhea and isolates from pork. Re-

Table 2. *Salmonella* serotypes most commonly isolated in infected persons and food sources in Yucatan, Mexico, 2000–2002.

Ranking[a]	Serotypes isolated, by source									
	Patients with diarrhea (*n* = 119)		Asymptomatic children (*n* = 224)		Retail poultry (*n* = 143)		Retail pork (*n* = 296)		Retail beef (*n* = 106)	
	Serotype	No. (%) of isolates	Serotype	No. (%) of isolates	Serotype	No. (%) of isolates	Serotype	No. (%) of isolates	Serotype	No. (%) of isolates
1	*S.* Typhimurium	26 (21.8)	*S.* Agona	27 (12.1)	*S.* Albany	26 (18.2)	*S.* Meleagridis	45 (15.2)	*S.* Meleagridis	29 (27.9)
2	*S.* Agona	25 (21.0)	*S.* Meleagridis	26 (11.6)	*S.* Enteritidis	24 (16.8)	*S.* Havana	38 (12.8)	*S.* Anatum	17 (16.3)
3	*S.* Anatum	7 (5.8)	*S.* Anatum	18 (8.0)	*S.* Agona	14 (9.8)	*S.* Agona	37 (12.5)	*S.* Reading	11 (10.6)
4	*S.* Adelaide	6 (5.0)	*S.* Enteritidis	13 (5.8)	*S.* Meleagridis	14 (9.8)	*S.* Anatum	37 (12.5)	*S.* Agona	9 (8.7)
5	*S.* Meleagridis	6 (5.0)	*S.* Reading	13 (5.8)	*S.* Stanleyville	7 (4.9)	*S.* Reading	20 (6.8)	*S.* Worthington	7 (6.7)
6	*S.* Panama	6 (5.0)	*S.* Albany	11 (4.9)	*S.* Braenderup	6 (4.2)	*S.* Worthington	18 (6.1)	*S.* Cerro	6 (5.8)
7	*S.* Enteritidis	5 (4.2)	*S.* Infantis	11 (4.9)	*S.* Cannstatt	5 (3.5)	*S.* Typhimurium	15 (5.1)	*S.* Havana	4 (3.8)
8	*S.* Albany	4 (3.4)	*S.* Havana	8 (3.6)	*S.* Reading	5 (3.5)	*S.* Adelaide	11 (3.7)	*S.* Albany	3 (2.9)
9	*S.* Derby	4 (3.4)	*S.* Adelaide	7 (3.1)	*S.* Adelaide	4 (2.8)	*S.* Infantis	10 (3.4)	*S.* Derby	3 (2.9)
10	*S.* Stanleyville	3 (2.5)	*S.* Typhimurium	6 (2.7)	*S.* Havana	4 (2.8)	*S.* Derby	8 (2.7)	*S.* Infantis	3 (2.9)

NOTE. The *n* values are the number of isolates from patients or meat samples that tested positive for *Salmonella*.
[a] Ranked, for each class of source, from most commonly isolated serotype (1) to least commonly isolated serotype (10).

Table 3. Antimicrobial resistance in *Salmonella* isolates from human feces and retail meat in Yucatan, Mexico, 2000–2002.

Source of isolates	No. of isolates	Percentage of isolates resistant,[a] by antimicrobial										
		AMP	CHL	CIP	CRO	GEN	KAN	NAL	STR	SU	SXT	TET
Persons with diarrhea	119	17.6	21.0	0	0.8	1.7	5.0	19.3	80.7	48.1	19.3	71.5
Asymptomatic children	223	11.2	8.9	0	0	5.8	3.1	22.0	64.6	30.3	13.0	59.7
Chicken	143	2.8	5.6	0	0.7	2.8	2.1	35.7	63.0	35.9	11.2	65.8
Pork	296	21.3	19.3	0	2.7	14.2	8.1	24.7	77.0	53.2	24.0	77.3
Beef	106	15.9	13.1	0	0.9	8.4	6.6	40.6	87.8	56.1	33.7	92.5
All sources	893	14.6	14.0	0	1.3	7.9	2.1	26.9	73.6	45.9	19.7	72.1

NOTE. Surveillance data for patients with diarrhea and asymptomatic children was collected from 2000 to 2002; for chicken and pork, from 2001 to 2002; and for beef, during 2002 only. AMP, ampicillin; CHL, chloramphenicol; CIP, ciprofloxacin; CRO, ceftriaxone; GEN, gentamicin; KAN, kanamicin; NAL, nalidixic acid; STR, streptomycin; SU, sulfisoxazole; SXT, trimethoprim-sulfamethoxazole; TET, tetracycline.

[a] Includes resistant and intermediately susceptible isolates.

sistance to gentamicin was most common among isolates from pork, and resistance to nalidixic acid was most common among isolates from chicken and beef.

Specific *Salmonella* serovars presented distinct resistance patterns. Isolates belonging to some serovars were almost all pansusceptible: *Salmonella* Infantis, *Salmonella* Weltevreden, and *Salmonella*Braenderup. The percentage of isolates resistant to nalidixic acid, a precursor to fluoroquinolone resistance, was very high among *Salmonella* Albany isolates (66.7%) and *S.* Enteritidis isolates (47.4%) from our human subjects, and among *S.* Albany (50%) and *S.* Enteritidis (62.5%) isolates from chicken. Multidrug resistance was most common in *S.* Anatum and *S.* Typhimurium isolates. Sixty-eight percent of the *S.* Anatum isolates ($n = 81$) and 52% of the *S.* Typhimurium isolates ($n = 50$) were resistant to at least 5 antimicrobials; and 6% of the multidrug-resistant *S.* Anatum isolates and 24% of the multidrug-resistant *S.* Typhimurium isolates were resistant to $\geqslant 9$ antimicrobials. The rates of resistance among *S.* Typhimurium isolates from ill patients, asymptomatic children, and pork are shown in table 4 and are compared with available data from other countries in North America and Latin America [11–14].

PFGE. A random sample of 16 *S.* Typhimurium isolates, 31 *S.* Agona isolates, 18 *S.* Albany isolates, and 17 *S.* Enteritidis isolates from human subjects and retail meat ($n = 82$) were selected for molecular analysis. PFGE patterns showed 4 clusters (A–D) that were segregated according to serotype (figure 1). Groups of identical isolates from human subjects and retail meat samples were found for each serotype. Seven pansusceptible *S.* Agona strains with identical PFGE patterns (figure 1, *pattern 1*) were isolated from ill patients and asymptomatic children, as well as from pork and chicken, which demonstrates a wide distribution of this serotype. A second *S.* Agona cluster

Table 4. Antimicrobial resistance in *Salmonella* Typhimurium isolated from ill persons and retail meat in North America and Latin America, 2001–2002.

Country	Source of isolate	No. of isolates	Percentage of isolates resistant,[a] by antimicrobial						
			AMP	CHL	SXT	NAL	CRO, CTX	TIO	Reference
Brazil	Humans	23	9	13	17	18	ND	ND	[11]
Brazil	Food	54	16.6	61.1	16.6	64.8	ND	ND	[11]
Canada	Humans	610	45.7	33	6.8	1.3	0	1.7	[12]
Chile	Humans	203	22	21	8	2	0	ND	[11]
Colombia	Humans	55	68	26	51	6	2	ND	[11]
Mexico	Humans	25	36	44	36	12	8	8	PR
Mexico	Pork meat	15	60	60	53	53	53	53	PR
United States	Humans	2009	13	9	1	2	0.2	4	[13]
United States	Chicken	60	16.7	0	0	0	0	10	[14]
United States	Turkey	74	16.2	1.4	1.4	8.1	0	8.1	[14]
United States	Pork	10	40	40	20	0	0	20	[14]
United States	Beef	9	22	22	0	0	0	22	[14]

NOTE. AMP, ampicillin; CHL, chloramphenicol; CRO, ceftriaxone; CTX, cefotaxime; NAL, nalidixic acid; ND, not determined; PR, present report; SXT, trimethoprim-sulfamethoxazole; TIO, ceftiofur.

[a] Resistance rates do not include the intermediate category.

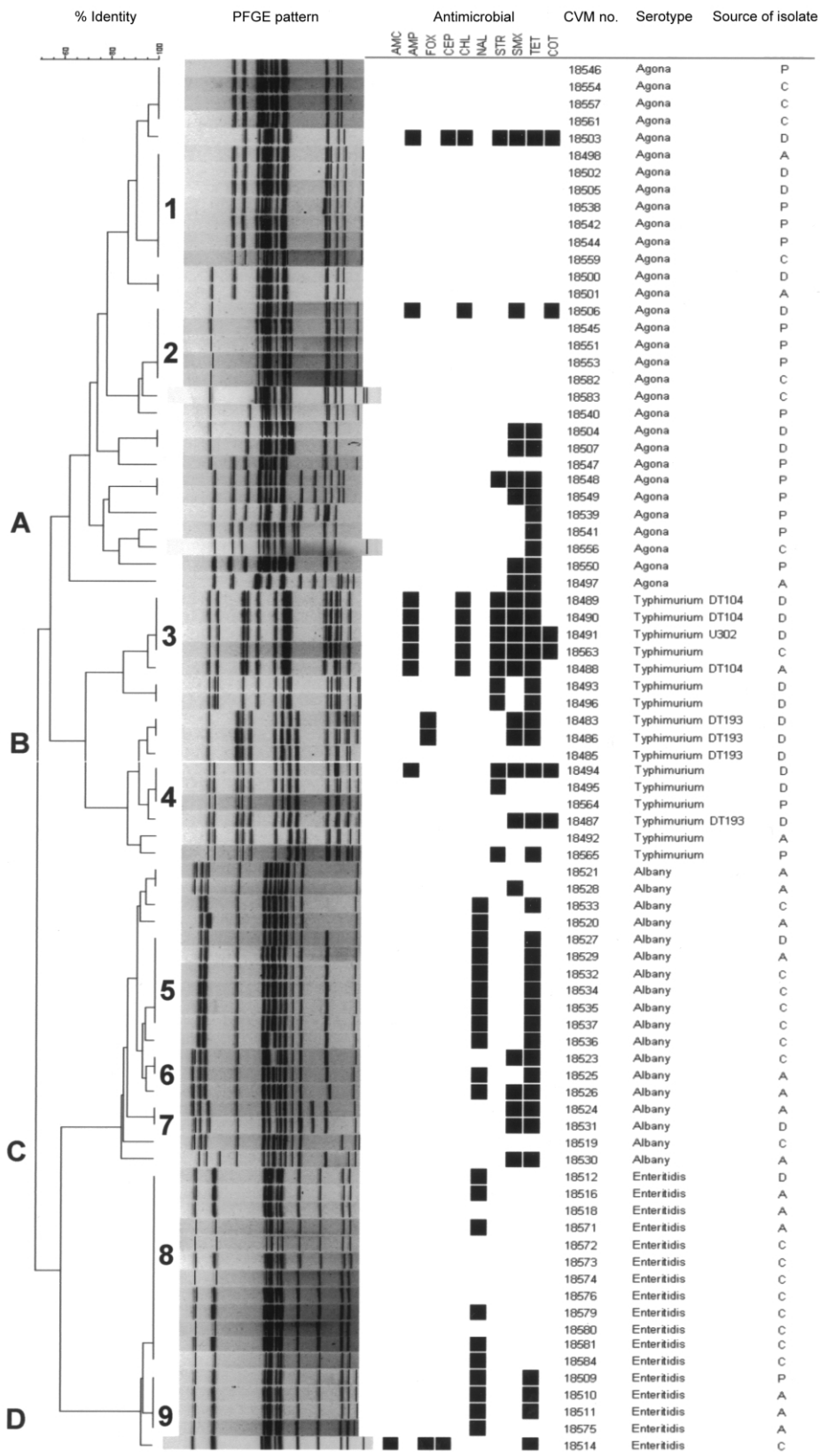

Figure 1. Dendrogram of PFGE patterns for selected isolates of *Salmonella* from Yucatan, Mexico. Antimicrobial resistance, indicated by a black box, was present for amoxicillin-clavulanate (AMC), ampicillin (AMP), cefoxitin (FOX), cephalothin (CEP), chloramphenicol (CHL), nalidixic acid (NAL), streptomycin (STR), sulfamethoxazole (SMX), tetracycline (TET), and trimethoprim-sulfamethoxazole (COT). The sources of the isolates tested were asymptomatic children (A), persons with diarrhea (D), retail pork meat (P), and retail chicken meat (C).

of 5 strains found in isolates from chicken, pork, and an ill person displayed identical PFGE patterns. The isolates in this cluster were pansusceptible except for CVM 18506, which was resistant to 4 antimicrobials. The 4 *S.* Typhimurium isolates from cluster B, 1 from a retail chicken sample and 3 from samples from persons with diarrhea, all had identical PFGE patterns *(pattern 3)* and the resistance phenotype typical of *S.* Typhimurium DT104 (i.e., resistance to the drugs ampicillin, chloramphenicol, streptomycin, sulfamethoxazole, and tetracycline). A second cluster of 3 *S.* Typhimurium isolates with identical PFGE patterns *(pattern 4)* and similar antibiograms was recovered from 1 pork sample and 2 samples from ill persons.

Cluster C contained 18 related *S.* Albany isolates with at least 80% pattern identity. PFGE patterns 5, 6, and 7 include isolates that were recovered from chicken meat and human subjects and that had identical PFGE profiles and similar antibiograms. Among *S.* Enteritidis isolates, PFGE patterns 8 and 9 are very closely related (>95% identity) and account for 16 of 17 strains with ⩽2 resistance phenotypes, which were isolated from chicken meat and asymptomatic children.

DISCUSSION

Our study detected a high prevalence of *Salmonella* in retail meats as well as in ill persons and asymptomatic children from Yucatan. The serotypes most commonly isolated from retail meat were also present to a large extent in the human subjects, and PFGE analysis of a random subset of isolates from human subjects and meat demonstrated identical DNA banding patterns. Furthermore, a considerable proportion of the isolates were resistant to clinically important antimicrobial agents, and certain serotypes, such as *S.* Anatum and *S.* Typhimurium, contained up to 10 resistance determinants. Our data do not allow us to determine whether the transfer of *Salmonella* strains from retail meats to humans occurred at a high frequency. Nevertheless, the high prevalence of *Salmonella*, including antimicrobial-resistant strains, in both humans and meats, as well as the correlation of both serotypes and genotypes from these sources, make this a likely possibility. An equally significant finding was the high rate of asymptomatic carriage in children, which is most likely the result of continuous exposure via foods. This strongly suggests that humans constitute a very large and important reservoir for this zoonotic organism and have a higher degree of immunity than is seen in more developed countries.

Our study had several important limitations. The data for humans and retail meats were collected over a relatively short time span, and the collection of samples was not uniform for all sources throughout the 3-year study period. Moreover, the number of isolates of each serotype was very small. Therefore, we had a limited capacity for establishing differences between sources and the multiple serotypes.

Despite the limitations in the study design, we believe that our sample accurately reflects the epidemiology of *Salmonella* infection and colonization in Yucatan. The retail meat and human fecal samples were collected from 8 different geographic locations throughout the state; these locations represent ~60% of the population. Most of the retail meat in the state is supplied by local producers, and, to date, we have not observed major shifts in either the prevalence of *Salmonella* infection and colonization or in the serotypes of *Salmonella* isolated from people or meat (data not shown). Moreover, because our hospital is a regional referral center, it is reasonable to assume that our ill subjects are characteristic of the patients with *Salmonella* infection throughout the state who require hospitalization.

To our knowledge, this is the first report from Latin America to simultaneously determine the prevalence of *Salmonella* in both humans and food from the same geographic region. A literature search of the last 11 years [15–35] shows that there are few data available that establish an association between the prevalence of *Salmonella* in retail meats and the prevalence of *Salmonella*-associated diarrhea. Moreover, there appear to be no consistent patterns of infection by region. Studies from industrialized countries such as Switzerland [24] and Italy [29] report that as much as 12% and 19%, respectively, of all hospital-based cases of diarrhea were *Salmonella*-associated, but studies in developing countries such as Nigeria [28] or Trinidad and Tobago [15] reported rates of 3.3% and 1.7%, respectively. It is important to emphasize that most of these studies collected samples from referral hospitals and therefore could not estimate the incidence of *Salmonella*-associated diarrhea in the general population—a limitation shared by our current study.

Likewise, on a global level, there are few scientific data that discern whether the serotypes most commonly found in retail meats are those most commonly found in ill humans, or whether the serotypes found in ill humans are a more virulent subset of all circulating *Salmonella* serotypes. Sarwari et al. [36] used a mathematical model to compare *Salmonella* serotypes in ill humans with those isolated from food animals. There was a mismatch between the expected and observed distribution of serotypes, which led the investigators to question whether the risk of transmission to humans is equal for all food product categories and whether all *Salmonella* serotypes have the same ability to cause disease. Other studies [11, 37, 38] document inconsistencies between the predominant serotypes found in food animals and those isolated from humans. Specific examples include *Salmonella* Kentucky in poultry, *Salmonella* Dublin in cattle, and *S.* Infantis and *Salmonella* Senftenberg in swine. These inconsistencies in serotype distributions will be difficult to resolve through routine surveillance, and they emphasize the need for prospective, population-based studies to

determine the relative contribution of the different *Salmonella* serotypes to human disease.

In addition to the high prevalence of *Salmonella* serotypes in both meats and humans, our study also found that the rates of antimicrobial resistance in Yucatan were significantly higher than rates in industrialized countries. For example, rates of resistance to nalidixic acid among *S.* Enteritidis isolates from chicken meat in Denmark and the United States during 2002 were 23% and 0%, respectively, and ~4% among isolates from ill humans from both countries, compared with the resistance rates of 62.5% and 47% among isolates from chicken meat and humans, respectively, found in our study [13, 39]. Likewise, as shown in table 4, the rates of resistance to trimethoprim-sulfamethoxazole and nalidixic acid of *S.* Typhimurium from humans and from food appear to be higher in Latin American countries than in the United States and Canada. The differences in antimicrobial resistance patterns among serotypes demonstrate the need for more thorough investigation of antimicrobial use at the human and veterinary levels and the modes of transmission through the food chain.

Assuming that, in our region, frequent transfer of *Salmonella* occurs through the food chain, we will need to closely monitor the public health impact of emerging multidrug resistance and ceftriaxone resistance. We anticipate a scenario similar to what has happened in Europe and North America, where recent studies [40–42] have documented an association between infection with antimicrobial-resistant *Salmonella* and a greater risk of hospitalization, bloodstream infection, and mortality. It is likely that infants, who are the most susceptible to diarrheal disease and have not yet acquired sufficient immunity, will suffer the greatest impact.

The transfer of *Salmonella* and other zoonotic pathogens to humans via the food supply is an ongoing public health concern worldwide. Our study underscores the need for developing countries to establish integrated surveillance systems for monitoring the prevalence of *Salmonella* and its resistance patterns in people, meat, and food animals. Specific research questions that need to be addressed include the public health significance of the different *Salmonella* serotypes and the public health impact of emerging antimicrobial resistance.

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