Genetic relatedness of a rarely isolated *Salmonella: Salmonella enterica* serotype Niakhar from NARMS animal isolates

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Received 7 July 2005; returned 8 September 2005; revised 3 November 2005; accepted 7 November 2005

Background: In the United States, *Salmonella enterica* serotype Niakhar is infrequently isolated. Between 1997 and 2000, the animal arm of the National Antimicrobial Resistance Monitoring System—Enteric Bacteria (NARMS) assayed a total of 22,383 *Salmonella* isolates from various animal sources (swine, cattle, chickens, turkeys, cats, horses, exotic and dogs) for antimicrobial susceptibility. Isolates originated from diagnostic and non-diagnostic submissions.

Objectives: To study the phenotypic and genotypic characteristics of *Salmonella* Niakhar.

Methods and results: Only five (0.02%) of the 22,383 isolates were identified as *Salmonella* Niakhar. Antimicrobial resistance testing indicated that three isolates were pan-susceptible, one isolate was resistant to ampicillin and one isolate was resistant to ampicillin, chloramphenicol, ciprofloxacin, kanamycin, nalidixic acid, streptomycin, sulfamethoxazole, tetracycline and trimethoprim/sulfamethoxazole. RAPD–PCR analysis, PFGE and ribotyping indicated that two pan-susceptible isolates were genetically similar, whereas the three remaining isolates were genetically different. The one *Salmonella* Niakhar isolate that was multiresistant harboured a class I integron, intI1 and two large plasmids.

Conclusions: This study represents the first report of a ciprofloxacin-resistant *Salmonella* isolate from the animal arm of NARMS.

Keywords: antimicrobial resistance, multiple drug resistance, integrons, PFGE, ribotyping

Introduction

Non-typhoid *Salmonella* is one of the leading causes of foodborne illness in the United States.¹,² Gastroenteritis as a result of salmonellosis has been associated with the consumption of contaminated eggs, poultry, meat products, unpasteurized milk and juice, milk products, contaminated raw fruits and vegetables, direct contact with animals, including reptiles, exotic birds, rodents and insects, contaminated water and soil, and person-to-person contact.¹,³⁻⁵ Currently there are over 2500 different *Salmonella* serotypes.⁶ Although salmonellosis is most often associated with a smaller number of serotypes,⁷ all serotypes have the potential to cause disease. *Salmonella enterica* serotype Niakhar belongs to serogroup V⁶ and is not commonly isolated in the United States and abroad. *Salmonella* Niakhar was first isolated at Niakhar, Senegal, in 1970 from a febrile man with diarrhoea.⁸ Since 1970, *Salmonella* Niakhar has been isolated exclusively from animals in the United States.⁹⁻¹¹ Animal isolates in the United States are tested for susceptibility to antimicrobials as part of the animal arm of the National Antimicrobial Resistance Monitoring System—Enteric Bacteria (NARMS) located in Athens, GA, USA (http://www.ars.usda.gov/Main/docs.htm?docid=6750; 30 September 2005, date last accessed). Isolates originate from a wide variety of animal sources and are submitted to NARMS by veterinary diagnostic laboratories, on-farm studies, and raw product collected from federally inspected slaughter and processing plants.¹² Until 2000, resistance was observed among all of the antimicrobials tested in NARMS with the exception of ciprofloxacin. Ciprofloxacin is primarily used to empirically treat gastroenteritis in human medicine, and similar antimicrobials (enrofloxacin and sarafloxacin) have been used in small animal medicine¹³⁻¹⁵ as well as treatment for airsacculitis in poultry.¹³,¹⁵ Ciprofloxacin belongs...
to the fluoroquinolone class of antimicrobials and resistance occurs as a result of a two-step mutation in the gyrA gene.16,17 Although multiple resistance in Salmonella appears to be increasing such as DT104 and Newport18,19 Salmonella isolates originating from animals in the United States have been susceptible to ciprofloxacin. Between 1997 and 2000, NARMS analysed a total of 22,383 Salmonella isolates from cattle, swine, dogs, horses, turkey, exotic birds, and chickens. Only 5 (0.02%) isolates were identified as S. enterica serotype Niakhar and originated from veterinary diagnostic laboratories. Until submission of the Salmonella Niakhar isolate in 2000, resistance to ciprofloxacin was not observed for any Salmonella serotype tested in the animal arm of NARMS. This study reports the phenotypic and genotypic characteristics of Salmonella Niakhar isolates from NARMS.

Materials and methods

Bacterial isolates

Five isolates of S. enterica serotype Niakhar were identified within the animal arm of NARMS from 1997 to 2000. The isolates originated from on-farm cattle studies in 1997 (designated as isolates A and B), and from veterinary diagnostic laboratories in 2000 (designated as isolates C, D and E). All isolates were serotyped at the National Veterinary Services Laboratories (NVSL), located in Ames, IA, USA. Maintenance of NARMS isolates has been described.12 Establishing and maintaining bacterial isolates for further study was accomplished by following the isolation procedures practised by NARMS.12

Antimicrobial susceptibility testing

Antimicrobial susceptibility was determined using a custom-made panel of antimicrobials in the Sensititre™ semi-automated system (TREK Diagnostics, Inc., Westlake, OH, USA) as per the manufacturer’s instructions. Antibiotics or their classes were selected based on their use in human and veterinary medicine and, where possible, full range MICs were used (http://www.ars.usda.gov/Main/docs.htm?docid=6750; 30 September 2005, date last accessed). Escherichia coli ATCC 25922, Pseudomonas aeruginosa ATCC 27853 and Enterococcus faecalis 29212 were used as quality control strains. Results were interpreted according to the NCCLS guidelines for broth microdilution methods20,21 when available.21

Random amplification of polymorphic DNA analysis

Random amplification of polymorphic DNA analysis (RAPD) analysis was performed using PCR primers 1290 (5’-GTGGATGCGA-3’)22 and 1254 (5’-CCGCGAGCCAA-3’)23 synthesized by OPERON (QIAGEN® Operon, Germantown, MD, USA). The whole cell DNA template for PCR was prepared according to the protocol of Hilton et al.23 with the final 10 μL of reaction consisting of 2 mM MgCl₂ (Gene Mate Plastics, ISC BioExpress), 50 pmol of RAPD oligonucleotide primer, 0.2 mM deoxyribonucleoside triphosphates (Boehringer Mannheim, Indianapolis, IN, USA) and 0.05 U of Tag DNA polymerase (Roche Diagnostics, Indianapolis, IN, USA). The samples were prepared as described by the Idaho Technology Rapidcycler, Idaho Falls, ID, USA.24 Program parameters for the Rapidcycler were (i) denaturation at 92°C for 30 s, (ii) annealing at 36°C for 7 s, and (iii) elongation at 72°C for 70 s, for a total of two cycles; immediately followed by (iv) denaturation at 92°C for 1 s, (v) annealing at 36°C for 7 s, and (vi) elongation at 72°C for 1 min, for a total of 38 cycles. DNA products for the RAPD-PCR were analysed by gel electrophoresis on a 1.5% agarose gel mixed with 1× Tris/aceitic acid/EDTA (TAE) containing ethidium bromide (0.02 mg/L) at 100 V for 30 min. The 100 bp ladder (Roche Diagnostics) served as the molecular weight standard for determining the size of the PCR products.

PFGE

A 24 h Salmonella PFGE procedure was performed as described by Pulse Net: The National Molecular Subtyping Network for Foodborne Disease Surveillance.25 Bacterial genomic DNA plugs were digested using the restriction enzyme, XbaI (Promega, Madison, WI, USA). DNA standards were prepared from S. enterica serotype Newport AM01144. Digested DNA was separated using the CHEF-DRII PFGE system as per the manufacturer’s instructions (Bio-Rad, Hercules, CA, USA). Electrophoresis was carried out for 19 h at 6 V, using 2.2 L of the buffer 0.5x Tris/borate/EDTA (TBE) at a temperature of 14°C, and an initial pulse time of 2.16 s followed by a final switch time of 63.8 s. BioNumerics software (Applied Maths Scientific Software Development, Belgium) was used to normalize the band patterns based on the molecular weight standards included on each gel. The Dice coefficient was used to statistically analyse the band pattern dissemination. A dendrogram was constructed to illustrate the genetic relatedness of the isolates.

Ribotyping

Ribotyping was performed using the automated RiboPrinter® microbrial characterization system (DePont Qualicon™, Wilmington, DE, USA) as per the manufacturer’s directions. In brief, colonies were picked from 24 h SBA plates, the cells were lysed and DNA was digested using the restriction enzyme, PvuII. Samples were then loaded into the RiboPrinter®, and restriction fragments were separated by electrophoresis and simultaneously transferred onto a nylon membrane. The DNA probe for Salmonella species was then hybridized to the genomic DNA of each isolate on the membrane. Bound labelled antibodies were captured using a chemiluminescence detection system containing a charged-coupled device camera. Once analysed, the band patterns were manually assigned to ribogroups. Restriction patterns were combined by similarity to form an individualized ribogroup which could be used to establish genetic relatedness of the isolates.26–28 Based on the results of normalized band patterns, BioNumerics software version 3.5 constructed a dendrogram using Pearson’s coefficient to determine genetic relatedness.

PCR amplification

DNA probes were generated using PCR specific primers for classes 1, 2, 3 and 4 integrons (intI1, intI2, intI3 and intI4, respectively) as described (Table 1). Oligonucleotides were synthesized by OPERON (QIAGEN® Operon). Template preparation from whole cell DNA was obtained as described previously.23 Samples were prepared as described (Idaho Technology Rapidcycler). Rapidcycler program parameters for the integrons were (i) denaturation at 94°C for 15 s, (ii) annealing at 55°C for 15 s, and (iii) elongation at 72°C for 35 s, for a total of 30 cycles. The PCR products were purified using the CONCERT Rapid PCR Purification system (Gibco BRL, Life Technologies) and analysed by gel electrophoresis using 1.5% agarose mixed in 1× TAE plus ethidium bromide (0.02 mg/L) at 100 V for 30 min. The 100 bp ladder served as the molecular weight standard.

Southern transfer and hybridization

Following PFGE, the gel was placed in the CL-1000 Crosslinker (UVP Laboratory Products, Upland, CA, USA) where ultraviolet light at 60 mJ of energy was applied to separate DNA into single strands. The single-stranded DNA was transferred to a positively charged,
nylon membrane (Roche Diagnostics) using the Model 785 Vacuum Blotter and Pump (Bio-Rad). The procedures for DNA–DNA hybridization and detection were carried out as described (Genius 3 kit, Boehringer Mannheim). Hybridization of DNA occurred at 65°C. Hybridizing DNA fragments were detected by using an anti-digoxigenin antibody–alkaline phosphatase conjugate mixed with a colour substrate solution of 4-nitroblue tetrazolium chloride and 5-bromo-4-chloro-3-indolylphosphate (Genius system, Boehringer Mannheim). Hybridization of DNA occurred at 65°C. Blotter and Pump (Bio-Rad). The procedures for DNA–DNA hybridization were carried out as described above. Small plasmid hybridization were carried out as described. Plasmid analysis. For large plasmids, DNA was cut using the S1 nuclease enzyme.30,31 Electrophoresis of the 1.2% agarose gel occurred in two blocks. Block 1 involved running the gel for 14 h at 6 V, including a pulse time of 45 s for both the initial and final time. In Block 2, the gel was run for 6 h at 6 V, having a pulse time of 25 s for both the initial and final time. For these two blocked times, 2.2 L of 0.5× TBE buffer was used at a temperature of 14°C. Following electrophoresis, Southern transfer and hybridization were carried out as described above. Small plasmid detection was conducted as described using the QIA prep spin miniprep kit (Qiagen, Inc., Valencia, CA, USA). Gel electrophoresis was done on a 0.8% agarose gel at 80 V for 45 min. Supercoiled DNA (Invitrogen, Life Technologies) was used as the molecular weight standard. The gel was placed in ethidium bromide (0.01 mg/L) for 20 min to allow for staining, followed by 10 min in nanopure water to eliminate excess ethidium bromide.

Conjugation

Salmonella Niakhar isolate D possessing resistance to nine antimicrobials served as the donor strain. One isolate of Salmonella Heidelberg and one isolate of Salmonella Cerro retrieved from the 2001 Salmonella NARMS isolates were used as recipient strains. Both of these strains were resistant to apramycin, an antimicrobial to which isolate D developed susceptibility. Nine antimicrobials (ampicillin, chloramphenicol, ciprofloxacin, kanamycin, nalidixic acid, streptomycin, sulfamethoxazole, tetracycline and trimethoprim/sulfamethoxazole) served as the selective markers based on the antibiotic resistance phenotype of isolate D. Conjugation was achieved by mating a fresh culture of the donor strain (Salmonella Niakhar) and recipient strains (Salmonella Heidelberg and Salmonella Cerro separately) in tubes containing 5 mL of TSB for 18–24 h in a 37°C aeration incubator. The transconjugants were evaluated by the results obtained from three donor/recipient dilutions: 1 : 1, 1 : 2 and 1 : 5. The serotype combinations were centrifuged for 2 min at 4950 rpm so that the serotypes would have close contact with one another during the incubation period. After the incubation period of the mating mixture, 100 μL of the donor/recipients at 1 : 1, 1 : 2 and 1 : 5 dilutions were spread equally using a sterilized bacterial cell spreader (VWR Scientific, West Chester, PA, USA) on the appropriately labelled TSA plates containing combinations of the selective antibiotics [32 μg of apramycin and 32 μg of ampicillin; 32 μg of apramycin and 32 μg of chloramphenicol; 32 μg of apramycin and 64 μg of kanamycin; 32 μg of apramycin and 32 μg of nalidixic acid; 32 μg of apramycin and 64 μg of streptomycin; 32 μg of apramycin and 512 μg of sulfamethoxazole; 32 μg of apramycin and 16 μg of tetracycline; 32 μg of apramycin, 4 μg of trimethoprim and 76 μg of sulfamethoxazole; 32 μg of apramycin (served as control); and the appropriate amount of all previously mentioned antimicrobials with the exception of apramycin in a TSB plate (served as other controls)]. Thirty-six hours later, transconjugants were examined for antimicrobial susceptibility profiles. PFGE analyses, as described earlier, were performed and evaluated on Salmonella Niakhar, Salmonella Heidelberg, Salmonella Cerro and transconjugants.

Table 1. PCR primers used to generate probes for detection of integrons and resistance genes

<table>
<thead>
<tr>
<th>Gene</th>
<th>Template source</th>
<th>Oligonucleotide sequencesa</th>
<th>Product size (bp)</th>
<th>Reference or source</th>
</tr>
</thead>
<tbody>
<tr>
<td>intI1</td>
<td>Salmonella Typhimurium DT104</td>
<td>L: 5'-ACATGTGATTGCGACGAGCA-3'</td>
<td>568</td>
<td>Ploy et al.60</td>
</tr>
<tr>
<td>intI2</td>
<td>E. coli J53.3::Tn7</td>
<td>L: 5'-CAGGATATGCGACAAAAAGT-3'</td>
<td>788</td>
<td>Ploy et al.60</td>
</tr>
<tr>
<td>intI3</td>
<td>E. coli AK9873</td>
<td>L: 5'-GCCCTCCGACGCCGACTTC-3'</td>
<td>979</td>
<td>Ploy et al.60</td>
</tr>
<tr>
<td>intI4</td>
<td>Vibrio cholerae</td>
<td>L: 5'-GTGGAAGATGCCTGTTCT-3'</td>
<td>526</td>
<td>this study</td>
</tr>
<tr>
<td>intCS</td>
<td></td>
<td>F: 5'-GGATCCAAGCAAGCA-3'</td>
<td>variablec</td>
<td>Levesque and Roy59</td>
</tr>
<tr>
<td>1290b</td>
<td></td>
<td>5'-GGATTTTCCATCTTTC-3'</td>
<td>variable</td>
<td>Hopkins and Hilton22</td>
</tr>
<tr>
<td>1254b</td>
<td></td>
<td>5'-CCGCACGCAA-3'</td>
<td>variable</td>
<td>Hilton et al.23</td>
</tr>
</tbody>
</table>

aL, C and F = forward primer; D and R = reverse primer.

bRAPD primer number.
cRange for band fragments to occur is variable.
RUNNER software (Hastings Software, Inc.). Analyses of the sequence in order to determine the antibiotic resistance genes located within the gene cassette of the integron were accomplished using BLAST software (National Center for Biotechnology Information, Bethesda, MD, USA).

Results

Antimicrobial resistance

Demographics, source and antimicrobial resistance patterns for each isolate are shown in Table 2. Isolates A, B and E were susceptible to all antimicrobials evaluated, whereas isolate C was only resistant to ampicillin. However, isolate D exhibited multiple resistance (defined as resistance to two or more antimicrobials) to ampicillin, chloramphenicol, ciprofloxacin, kanamycin, nalidixic acid, streptomycin, sulfamethoxazole, tetracycline and trimethoprim/sulfamethoxazole.

RAPD analyses

RAPD–PCR results are shown in Figure 1. RAPD–PCR primers 1290 (lanes 2–8) and 1254 (lanes 10–16) were used. Using RAPD primer 1290, isolates A (lane 3) and B (lane 4) were genetically similar, whereas isolates C, D and E (lanes 5, 7 and 6, respectively) were genetically unrelated to all isolates. Using RAPD primer 1254, isolates A (lane 11) and B (lane 12) were genetically similar, whereas isolates C, E and D (lanes 13, 14 and 15, respectively) were genetically different. E. coli (lanes 2 and 10) and Salmonella Typhimurium DT104 (lanes 8 and 16) isolates were used to represent a distant and similar banding pattern, respectively.

PFGE

E. coli (lane 2) and Salmonella Typhimurium DT104 (lane 8) isolates served as controls as described for Figure 1. Using visual and dendrogram analyses (Figure 2a and b), isolates A and B were genetically identical to one another. Isolates C, D and E (Figure 2a) were genetically unrelated. A greater than seven band pattern difference between isolates was used to classify isolates as dissimilar.32 Dendrogram results (Figure 2b) indicated that isolates C and D exhibited 77% similarity, whereas isolate E and E. coli exhibited 79% similarity, and Salmonella Typhimurium DT104 exhibited 68% similarity to all isolates including E. coli.

Ribotyping analysis

Ribotype patterns were compared using Pearson’s coefficient and a dendrogram was constructed (Figure 3). Banding patterns showed a high degree of relatedness (95%) between isolates A and B.

Table 2. Demographics, source and antimicrobial resistance patterns for each S. enterica serotype Niakhar isolate

<table>
<thead>
<tr>
<th>Isolate</th>
<th>Year</th>
<th>Source</th>
<th>Location</th>
<th>Region</th>
<th>Antimicrobial resistance pattern</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>1997</td>
<td>on-farm—dairy cattle</td>
<td>Southeastern United States</td>
<td>2</td>
<td>none</td>
</tr>
<tr>
<td>B</td>
<td>1997</td>
<td>on-farm—dairy cattle</td>
<td>Western United States</td>
<td>5</td>
<td>none</td>
</tr>
<tr>
<td>C</td>
<td>2000</td>
<td>veterinary diagnostic laboratory—cattle</td>
<td>Northeastern United States</td>
<td>1</td>
<td>AMP</td>
</tr>
<tr>
<td>D</td>
<td>2000</td>
<td>veterinary diagnostic laboratory—cattle</td>
<td>North Central Midwestern United States</td>
<td>3</td>
<td>AMP, CHL, CIP, KAN, NAL, STR, SUL, TET, SXT</td>
</tr>
<tr>
<td>E</td>
<td>2000</td>
<td>veterinary diagnostic laboratory—dog</td>
<td>South Central United States</td>
<td>4</td>
<td>none</td>
</tr>
</tbody>
</table>

aIdentification of state by region: region 1 = ME, VT, NH, NY, MA, CT, RI, PA, MD, DE, NJ, OH, IN, MI; region 2 = VA, KY, TN, NC, SC, GA, AL, WV, FL, PR; region 3 = ND, SD, NE, KS, MN, IA, MO, WI, IL; region 4 = OK, AR, LA, TX, MS; region 5 = WA, MT, OR, ID, WY, CO, UT, NM, AZ, NV, CA.

bAMP, ampicillin; CHL, chloramphenicol; CIP, ciprofloxacin; KAN, kanamycin; NAL, nalidixic acid; STR, streptomycin; SUL, sulfamethoxazole; TET, tetracycline; SXT, trimethoprim/sulfamethoxazole.

Figure 1. Comparison of genetic relatedness of the five Niakhar isolates using RAPD-PCR analysis. RAPD–PCR primers were 1290 (lanes 2–8) and 1254 (lanes 10–16). Standard sizes in base pairs are located to the left of the figure. Lanes 1, 9 and 17, 100 bp ladder; lanes 2 and 10, E. coli (negative control); lanes 3 and 11, isolate A; lanes 4 and 12, isolate B; lanes 5 and 13, isolate C; lanes 6 and 14, isolate E; lanes 7 and 15, isolate D; and lanes 8 and 16, Salmonella Typhimurium DT104 (positive control).
Isolates D and E were also related although to a lesser degree (86%). Isolate C showed only a 37% similarity to the four other Salmonella Niakhar isolates. Collectively, isolates A and B and isolates D and E were even less related (65% similarity). Salmonella Typhimurium DT104 was 43% similar to isolates A, B, D and E, whereas E. coli was only 37% genetically similar. However, isolate C was more closely related to E. coli than the four other isolates (65% similarity). These results are very similar.

**Figure 2.** Comparison of genetic relatedness of five Niakhar isolates using PFGE. DNA was digested using XbaI. (a) Standard sizes in kilobases are indicated to the left of the figure. Lanes 1 and 9, S. enterica serotype Newport standard strain AM01144; lane 2, E. coli (negative control); lane 3, isolate A; lane 4, isolate B; lane 5, isolate C; lane 6, isolate E; lane 7, isolate D; and lane 8, Salmonella Typhimurium DT104 (positive control). (b) A dendrogram was constructed from the PFGE band patterns using BioNumerics software.

**Figure 3.** Comparison of genetic relatedness among five Niakhar isolates using automated ribotyping (Qualicon). Ribotype profiles were obtained after digestion with PvuII enzyme. From the band patterns, a dendrogram was constructed to illustrate the genetic relatedness of the isolates.
PFGE. Use of Southern blotting showed that *Salmonella* Typhimurium DT104 (lanes 7 and 8). The integron on the chromosome of isolate D was localized to an ~12 kb *XbaI* fragment using PFGE. Use of Southern blotting showed that *intI1* was located on the chromosome of isolate D (data not shown; J. D. Tankson, P. Fedorka Cray and C. Jackson). Using PCR primers to the 5′ (*intCSF*) and 3′ (*intCSR*) conserved region of *intI1*, a 1.2 kb fragment was amplified from isolate D. Sequencing of the 5′ and 3′ conserved region revealed that it contained *aadA*-1, a spectinomycin resistance gene, conferring resistance to the aminoglycoside antibiotic class. Therefore, the spectinomycin resistance gene was the only resistance gene located within the 5′ and 3′ conserved region of the integron.

Only isolate D contained two large plasmids which localized to ~220 and 60 kb fragments (Figure 5). There were no small plasmids isolated in any of the Niakhar isolates. Further work is warranted in order to determine the location of the other eight resistance genes. Work is in progress for determining the resistance genes located within the two plasmids.

**Location of antimicrobial resistance genes**

The integrons (*intI1, intI2, intI3* and *intI4*) and their expected base pair size are shown in Table 1. After probing, only isolate D possessed an integron, *intI1*. Figure 4 shows the presence of *intI1* amplifying at the 568 bp PCR fragment for isolate D and *Salmonella* Typhimurium DT104 (lanes 7 and 8). The integron from isolate D was localized to an ~12 kb *XbaI* fragment using PFGE. Use of Southern blotting showed that *intI1* was located on the chromosome of isolate D (data not shown; J. D. Tankson, P. Fedorka Cray and C. Jackson). Using PCR primers to the 5′ (*intCSF*) and 3′ (*intCSR*) conserved region of *intI1*, a 1.2 kb fragment was amplified from isolate D. Sequencing of the 5′ and 3′ conserved region revealed that it contained *aadA*-1, a spectinomycin resistance gene, conferring resistance to the aminoglycoside antibiotic class. Therefore, the spectinomycin resistance gene was the only resistance gene located within the 5′ and 3′ conserved region of the integron.

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**Discussion**

*S. enterica* serotype Niakhar is infrequently isolated in both the United States and elsewhere. In this study, the significance of the serotype lies not with its infrequent isolation, but rather with its acquisition of resistance to ciprofloxacin. Interestingly, prior to 2000, the animal arm of NARMS did not report resistance to ciprofloxacin among *Salmonella* serotypes. Conversely, the human arm of NARMS reported a 0.1–0.4% resistance to ciprofloxacin from 1988 to 2000 (www.cdc.gov/narms/reports.htm; 30 September 2005, date last accessed). However, none of the ciprofloxacin-resistant human isolates was identified as *Salmonella* Niakhar (www.cdc.gov/narms/reports.htm; 30 September 2005, date last accessed). Therefore, this is a first observation of ciprofloxacin resistance among the NARMS animal collection of isolates.

Dairy cattle were implicated as the source for isolates A and B. Although both isolates originated from on-farm collections (http://www.aphis.usda.gov/vs/ceah/ncahs/nahms/index.htm; 30 September 2005, date last accessed), they were in disparate geographic locations (Southeastern and Western United States). It is interesting to note that they were pan-susceptible even though cattle are long-lived and likely to have seen at least some type of antimicrobial in feed for either prophylaxis or therapeutic means. Further support can also be inferred from isolates C and E. Although these isolates were also from disparate regions of the United States (Northeastern and South Central Midwest), they originated from clinical submissions, one from cattle (isolate C) and one from a dog (isolate E). Isolate C was only resistant to ampicillin whereas isolate E was pan-susceptible. Since diagnostic submissions are most probably a result of overt clinical illness (morbidity and/or mortality), it is probable that both animals were previously treated with some class of antimicrobial. Even though the status of the cow meat was unknown, seriously ill cattle are not sold as food for human consumption. Therefore, the probability of this submission making it through the preparation process to be sold for human consumption is relatively low. However, a dog is usually considered a companion for man and is likely to have been treated when illness occurred. Additionally, household pets (dogs, cats, etc.) are common on the farm and freely move around animal production environments. Therefore, they may also serve as vectors to those who come into contact with them, including both animals and humans. Although it is difficult to estimate antimicrobial exposure, the lack of resistance (especially clinical submissions) suggests that the development of resistance within a serotype may be dependent upon factors other than...
antimicrobial use or exposure. These may include acquisition of transmissible elements or a newly introduced clone.

However, it is interesting to note that isolate D originated in cattle and it is multiresistant to antimicrobials implicated in both the multiresistant Salmonella Typhimurium DT104 and Salmonella Newport serotypes. Submissions from the diagnostic laboratories, as observed for isolates C, D and E, typically include major species identification (cattle, swine, dog, chicken, turkey, etc.) but rarely include differentiation within species such as dairy and beef cattle, or chick, broiler or broiler breeder for chicken isolates. The major reservoir for Salmonella Typhimurium DT104 and Salmonella Newport is cattle, particularly dairy cattle. Because cattle are less confined during production than other food animals, it is probable that isolates A, B, C and D were introduced into the herd by a vector such as a bird, fly, rodent or other wildlife or through movement of cattle during transport. Birds, flies, rodents and wildlife are known vectors of Salmonella,

Evidence to support this includes the rarity of the serotype, the rarity of resistance within the serotype, and the observation that only one isolate was obtained by source, region and year. This further suggests that unlike Salmonella Typhimurium DT104 and Salmonella Newport are genetically different from one another. However, it is interesting to note that isolate D originated in cattle and it is multiresistant to antimicrobials implicated in both the multiresistant Salmonella Typhimurium DT104 and Salmonella Newport serotypes. Submissions from the diagnostic laboratories, as observed for isolates C, D and E, typically include major species identification (cattle, swine, dog, chicken, turkey, etc.) but rarely include differentiation within species such as dairy and beef cattle, or chick, broiler or broiler breeder for chicken isolates. The major reservoir for Salmonella Typhimurium DT104 and Salmonella Newport is cattle, particularly dairy cattle. Because cattle are less confined during production than other food animals, it is probable that isolates A, B, C and D were introduced into the herd by a vector such as a bird, fly, rodent or other wildlife or through movement of cattle during transport. Birds, flies, rodents and wildlife are known vectors of Salmonella, and the conditions associated with cattle production increase the likelihood of contact between cattle and a vector. It is less likely that direct use of antimicrobials affected the multiresistance observed for this Salmonella Niakhar isolate. Evidence to support this includes the rarity of the serotype, the rarity of resistance within the serotype, and the observation that only one isolate was obtained by source, region and year. This further suggests that unlike Salmonella Typhimurium DT104 and Salmonella Newport, Salmonella Niakhar is not a virulent serotype and would be less likely to expand within a population.

Annual data compiled by NVSL also confirmed Niakhar is an uncommon serotype. NVSL reported Niakhar was isolated in 1993, 1997 and 2000 (one isolate, two isolates and two isolates, respectively). Even though the NVSL report of Niakhar isolation did not coincide with NARMS, it is important to recognize that the NARMS programme does not test every animal isolate submitted to NVSL for antimicrobial resistance. Therefore, while this observation of ciprofloxacin resistance is unique, it is only unique among the isolates tested. Although there were no reports of Salmonella Niakhar in 2001 or 2002, further monitoring in both animal and human populations is warranted as this may be an emerging and clinically significant serotype.

PFGE analysis suggests that Niakhar isolates from regions 5 and 2 (isolates A and B, respectively) are identical or genetically similar. Niakhar isolates from regions 1, 3 and 4 (isolates C, D and E, respectively) are genetically different from one another. Therefore, even though these isolates are from different geographic regions, the serotype is not clonal. Literature has emphasized the need for more detailed genetic typing studies for Salmonella. PFGE analysis suggests that Niakhar isolates from regions 5 and 2 (isolates A and B, respectively) are identical or genetically similar. Niakhar isolates from regions 1, 3 and 4 (isolates C, D and E, respectively) are genetically different from one another. Therefore, even though these isolates are from different geographic regions, the serotype is not clonal. Literature has emphasized the need for more detailed genetic typing studies for Salmonella.

Antimicrobial resistance patterns (Table 2) indicated that three isolates (isolates A, B and E) were pan-susceptible, one isolate (isolate C) was resistant to ampicillin and one isolate (isolate D) was resistant to ciprofloxacin. Multiple resistance determinants are most often associated with the presence of plasmids and integrons. Plasmids and integrons are defined as mobile, extra- chromosomal pieces of DNA that have the ability to horizontally disseminate antimicrobial resistance genes (and multiresistance genes) rapidly and efficiently between serotypes, bacterial species or bacterial genera. Integrons contain gene cassettes that harbour the antimicrobial resistance genes. Enterobacteriaceae have been reported to carry integrons, especially class I (intI1) integrons. Isolate D, which was multiresistant, harboured intI1 and two large plasmids. This is similar to reports for Salmonella Typhimurium DT104 which also harbours plasmids and integrons. However, unlike DT104, most of the Salmonella Niakhar resistance genes are not chromosomally integrated, but located on plasmids. However, further characterization of these genes is warranted.

We would like to thank Leena Jain, Jovita Haro and Takiyah Ball for their excellent technical assistance, and Dr John Maurer for the Vibrio cholerae isolate containing the intI4 integron gene and the Escherichia coli isolates containing the intI2 and intI3 integron genes. Note: The mention of trade names or commercial products in this manuscript is solely for the purpose of providing specific information and does not imply recommendation or endorsement by the US Department of Agriculture.

None to declare.

References