of the bacteria (10). The novel *Ehrlichia* sp. strain La Dormida is phylogenetically related to the ruminant pathogen *E. ruminantium* and represents a potential risk for veterinary and public health because *A. neumanni* ticks parasitize domestic and wild ruminants and bite humans.

Acknowledgments
We thank Federico Ruiz and Aníbal Gomez for their support with field work and Federico Prandi.

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Multidrug-Resistant *Salmonella* Serotype Anatum in Travelers and Seafood from Asia, United States

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A multidrug-resistant *Salmonella enterica* serotype Anatum strain reported in Taiwan was isolated in the United States from patients and from seafood imported from Asia. Isolates harbored 11 resistance determinants, including quinolone and inductible cephalosporin resistance genes. Most patients had traveled to Asia. These findings underscore the need for global One Health resistance surveillance.

A sharp increase in *Salmonella enterica* serotype Anatum infections reported in Taiwan during 2016–2017 was associated with emergence of
multidrug-resistant (MDR) strains harboring 11 resistance genes: *aadA2*, *bla*<sub>DHA-1</sub>, *dfrA23*, *floR*, *lnu*(F), *qnrB4*, *strA*, *strB*, *sul1*, *sul2*, and *tet*(A) (1). Isolates had intermediate susceptibility to ciprofloxacin and resistance to many antimicrobial agents, including third-generation cephalosporins. We report human cases and related isolates in the United States.

We found 43 isolates genetically related to MDR *Salmonella* Anatum from Taiwan in the National Center for Biotechnology Information Pathogen Detection Isolates Browser (http://www.ncbi.nlm.nih.gov/pathogens). We analyzed genome assemblies for resistance determinants and plasmids by using databases adapted from ResFinder and PlasmidFinder (Center for Genomic Epidemiology, https://cge.cbs.dtu.dk). To assess strain relatedness, we constructed a core genome multilocus sequence typing (cgMLST) phylogenetic tree and pairwise matrix of allele differences by using BioNumerics version 7.6 (Applied Maths, http://www.applied-maths.com). We contacted US health departments to obtain patient information and isolates for susceptibility testing by broth microdilution (Appendix Table 1, http://wwwnc.cdc.gov/EID/article/26/5/19-0992-App1.pdf).

**Figure.** Core genome multilocus sequence typing (cgMLST) phylogenetic tree of 40 *Salmonella enterica* serotype Anatum isolates, 2015–2019. The tree was constructed by using BioNumerics version 7.6 (Applied Maths, http://www.applied-maths.com). Isolate sources, collection years, and National Center for Biotechnology Information strain or isolate numbers are shown. For isolates from the United States, international travel destinations of patients and sources of imported foods are provided. Dark gray boxes indicate resistance determinants detected: 1) *aadA2*; 2) *aph(3’)-lb* (strA); 3) *aph(6’)-Id* (strB); 4) *bla*<sub>DHA-1</sub>; 5) *dfrA23*; 6) *floR*; 7) *lnu*(F); 8) *qnrB4*; 9) *sul1*; 10) *sul2*; 11) *tet*(A); 12) *aadA1*; 13) *bla*<sub>TEM-1B</sub>; 14) *dfrA1*; 15) *dfrA12*; 16) *mcr-1*; 17) *mph*(A); 18) *opxA*B; 19) *qnrA6*; 20) *sul3*. Scale bar indicates percentage similarity.

JAP, Japan; MX, Mexico; NA, not available; PHL, Philippines; TWN, Taiwan; UK, United Kingdom; USA, United States.
We created a cgMLST phylogenetic tree showing resistance determinants detected for 40 isolates with >99.5% similarity and 0–20 allele differences (Figure; Appendix Figure). We excluded 3 more distantly related isolates. A total of 25 isolates were from Taiwan (16 from humans, 3 each from chickens and pigs, 2 from geese, and 1 from a duck); 12 were from the United States (7 from humans, 4 from tilapia imported from Taiwan, and 1 from shrimp imported from the Philippines). We detected IncC plasmids in all isolates, except PNUSA038936; 15 had additional plasmids (Appendix Table 2). Most (38/40) had the previously reported 11 resistance genes (I). Two isolates from the Philippines had additional resistance genes, including mph(A), qnrA6, and qoxAB; 3 isolates from tilapia in the United States and 1 human isolate from Taiwan had mcr-1.1. We found no quinolone resistance–determining region mutations.

The 7 patients from the United States were 19–71 (median 48) years of age; 3 were women and 4 men. Among 5 patients with data on race, 3 were Asian and 2 white. All patients reported illness, including diarrhea (7/7), abdominal pain (4/7), nausea (2/7), and fever (1/7). None were hospitalized or died. Four became ill ≤3 days after returning from travel to the Philippines; 1 visited Japan before the Philippines. Two additional patients reported travel before illness onset; 1 traveled to the Philippines and the other to Taiwan and Mexico, but travel and illness onset dates were unavailable.

One patient had never travelled internationally. Her isolate was indistinguishable from 1 from a patient who traveled to Asia and differed by only 2 alleles from an isolate from shrimp imported from the Philippines. Before illness onset, she ate at several restaurants and had shrimp at an Asian restaurant and sushi bar.

In patient isolates from the United States, bla<sub>DHA-1</sub> appeared to be carried in a complex integron, with the regulatory ampR gene positioned upstream and qnrB4 downstream. Six isolates had IncC plasmids similar to pR16.0676.90k (GenBank accession no. CP029802) (I), which likely carried all 11 resistance genes, but long-reading sequence is required for confirmation. Isolate PNUSA038936 lacked the IncC plasmid replicon but appeared to have an IS26-mediated integration of the entire resistance region from the plasmid (≈60 kb) into the chromosome.

We performed antimicrobial susceptibility testing on 6 patient isolates, including PNUSA038936. All had intermediate susceptibility to ciprofloxacin (MIC 0.25 µg/mL) and were resistant to amoxicillin/clavulanic acid, ampicillin, cefoxitin, chloramphenicol, streptomycin, sulfisoxazole, tetracycline, and trimethoprim/sulfamethoxazole. One isolate had intermediate susceptibility to ceftriaxone (MIC 2 µg/mL) and 5 were ceftriaxone susceptible; 1 had a MIC of ≤0.25 µg/mL, 3 MICs of 0.5 µg/mL, and 1 a MIC of 1 µg/mL.

The emergence and spread of <i>Salmonella</i> carrying <i>bla<sub>DHA-1</sub></i> has both clinical and public health implications. Unlike most plasmid-mediated AmpC β-lactamase genes, <i>bla<sub>DHA-1</sub></i> is inducible (2,3), which can complicate detection and treatment. Isolates can appear susceptible to third-generation cephalosporins in vitro, but treatment may fail if AmpC induction occurs (3,4). The co-occurrence of <i>qnr</i>A6; the plasmid-mediated quinolone resistance gene <i>qnr</i>B4; and in the isolates from the Philippines, <i>mph(A)</i>, a macrolide-resistance gene, is worrisome because third-generation cephalosporins (e.g., ceftriaxone), fluoroquinolones (e.g., ciprofloxacin), and the macrolide azithromycin are recommended for <i>Salmonella</i> infections requiring treatment (5,6). In addition, the presence of <i>mcr-1.1</i>, which confers resistance to colistin, a drug of last resort for treating MDR gram-negative bacterial infections, is concerning.

Our findings underscore the need for global, One Health surveillance. Most infections likely were acquired during travel in Asia. International travel, particularly to Asia, has been associated with acquisition of <i>Salmonella</i> with clinically important resistance (7,8). Resistance also can be disseminated via food and animals. Imported food likely was the source of infection for 1 patient without international travel. Among imported foods tested by the US Food and Drug Administration, seafood from Asia is a frequently reported source of antimicrobial-resistant <i>Salmonella</i> (9,10). Given the extent of international travel and trade, data sharing among human health, animal health, and food production sectors and across geographic borders is essential to detect MDR strains and inform strategies and interventions to prevent spread.

Acknowledgments

We thank state and local health departments in California, Colorado, Hawaii, and Virginia for sequencing and submitting the human <i>Salmonella</i> isolates described in this report and for collecting and sharing public health investigation information for patients with us. At the US Food and Drug Administration, we acknowledge the Office of Regulatory Affairs for collecting and testing the seafood samples and sequencing isolates; the GenomeTrakr program in the Center for Food Safety and Applied Nutrition for processing and submitting isolate data to the National Center for Biotechnology Information (NCBI); and National Antimicrobial Resistance Monitoring System colleagues at the Center for Veterinary Medicine for telling us about the isolates. We also thank PulseNet for processing and submitting human isolate data to NCBI, and NCBI staff for making the Pathogen Detection Isolates Browser publicly available.
The findings and conclusions in this report are those of the authors and do not necessarily represent the official position of the Centers for Disease Control and Prevention.

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Fatal Rodentborne Leptospirosis in Prison Inmates, South Africa, 2015

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Leptospirosis is a neglected zoonotic disease. In 2015, 
leptospirosis was diagnosed in 2 prison inmates in South Africa. Using real-time PCR and DNA sequencing, we 
identified 
Leptospira interrogans 
serogroup Icterohaemorrhagiae in rodents and water samples within the prison. Leptospirosis might be frequently underdiagnosed in 
South Africa.

Although leptospirosis, a bacterial zoonosis, is 
responsible for ≈1 million cases per year worldwide, 
estimates of its incidence in Africa are limited by a lack of quality-assured studies (1). Humans be 
come infected through mucosal membranes or skin 
breaks by direct contact with reservoir animals or ex 
position to urine-contaminated soil or water. We de 
scribe an outbreak of leptospirosis in prison inmates in Cape Town, South Africa, and identification of 
probable animal sources and environmental routes of infection.

In September 2015, the South Africa Department of Correctional Services requested the National Institu 
te for Communicable Diseases to assist with investiga 
tion and management of leptospirosis infections in 2 
inmates at a maximum-security prison in Cape Town. The National Health Laboratory Service Animal Ethics 
Committee clearance 131/11 granted approval for rodent trapping and testing; ethical clearance certifi 
cate no. M160667 from the Human Research Ethics Committee (Medical) of the University of the Wit 
watersrand covered the outbreak investigation.

Case-patient 1, a 52-year-old man, was admit 
ted to a hospital in Cape Town. He had jaundice, 
overwhelming sepsis, disseminated intravascular
Multidrug Resistant Salmonella Serotype Anatum in Travelers and Seafood from Asia, United States

Appendix

Appendix Table 1. Antimicrobial agents, concentration ranges, and breakpoints used for susceptibility testing of Salmonella Anatum isolates, United States, 2016–2019*

<table>
<thead>
<tr>
<th>CLSI antimicrobial class</th>
<th>Antimicrobial agent</th>
<th>Concentration range, µg/mL</th>
<th>Interpretive categories and MIC breakpoints, µg/mL</th>
</tr>
</thead>
<tbody>
<tr>
<td>Aminoglycosides</td>
<td>Gentamicin</td>
<td>0.25–16</td>
<td>&lt;4  8  &gt;16</td>
</tr>
<tr>
<td></td>
<td>Streptomycin†</td>
<td>2–64</td>
<td>&lt;16  NA  &gt;32</td>
</tr>
<tr>
<td>β-lactam combination</td>
<td>Amoxicillin-clavulanic acid</td>
<td>1/0.5–32/16</td>
<td>≤B/4  16/8  &gt;32/16</td>
</tr>
<tr>
<td>Cephalosporins</td>
<td>Cefoxitin</td>
<td>0.5–32</td>
<td>≤8  16  &gt;32</td>
</tr>
<tr>
<td></td>
<td>Ceftriaxone</td>
<td>0.25–64</td>
<td>≤1  2   &gt;4</td>
</tr>
<tr>
<td>β-Lactam antagonists</td>
<td>Sulfisoxazole</td>
<td>16–256</td>
<td>≤256  NA  &gt;512</td>
</tr>
<tr>
<td>Folate pathway</td>
<td>Trithemoprim-</td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>sulfamethoxazole</td>
<td>0.12/2.38–4/76</td>
<td>≤2/38  NA  &gt;4/76</td>
</tr>
<tr>
<td>Macrolides</td>
<td>Azithromycin†</td>
<td>0.25–34</td>
<td>≤16  NA  &gt;32</td>
</tr>
<tr>
<td>Penem</td>
<td>Meropenem</td>
<td>0.06–4</td>
<td>≤1   2   &gt;4</td>
</tr>
<tr>
<td>Penicillins</td>
<td>Ampicillin</td>
<td>1–32</td>
<td>≤8  16  &gt;32</td>
</tr>
<tr>
<td>Phenicols</td>
<td>Chloramphenicol</td>
<td>2–32</td>
<td>≤8  16  &gt;32</td>
</tr>
<tr>
<td>Quinolones</td>
<td>Ciprofloxacin</td>
<td>0.015–4</td>
<td>≤0.06  0.12–0.5  &gt;1</td>
</tr>
<tr>
<td></td>
<td>Nalidixic acid</td>
<td>0.5–32</td>
<td>≤16  NA  &gt;32</td>
</tr>
<tr>
<td>Tetracyclines</td>
<td>Tetracycline</td>
<td>4–32</td>
<td>≤4  8   &gt;16</td>
</tr>
</tbody>
</table>

*CLSI, Clinical and Laboratory Standards Institute; NA, not applicable (no intermediate MIC range exists)
†CLSI breakpoints are not established for azithromycin and streptomycin; interpretive standards used are breakpoints established by the National Antimicrobial Resistance Monitoring System for resistance monitoring and should not be used to predict clinical efficacy.

Appendix Table 2. Plasmid replicons and resistance determinants detected among 40 Salmonella Anatum isolates

<table>
<thead>
<tr>
<th>Strain</th>
<th>Plasmid replicons</th>
<th>Resistance determinants</th>
</tr>
</thead>
<tbody>
<tr>
<td>227024</td>
<td>IncC</td>
<td>aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 qnrB4 sul1 sul2 tet(A)</td>
</tr>
<tr>
<td>FDA00008841</td>
<td>IncC IncI1-ly</td>
<td>aph(3’)-Ib aph(6)-Ib floR sul2 tet(A) aadA1 blbTEM-1B sul3</td>
</tr>
<tr>
<td>FDA00013727</td>
<td>IncC IncI2</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A) mcr-1.1</td>
</tr>
<tr>
<td>FDA00013728</td>
<td>IncC IncI2</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A) mcr-1.1</td>
</tr>
<tr>
<td>FDA00013729</td>
<td>IncC IncI2</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A) mcr-1.1</td>
</tr>
<tr>
<td>FDA00013836</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A) mcr-1.1</td>
</tr>
<tr>
<td>PDT000424546.1</td>
<td>IncC IncHil2 IncHil2A</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, aadA1 blbTEM-1B dfrA1 dfrA12 mph(A) qoxAB qnrA6</td>
</tr>
<tr>
<td>PDT000424547.1</td>
<td>IncC IncHil2 IncHil2A</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, aadA1 blbTEM-1B dfrA1 dfrA12 mph(A) qoxAB qnrA6</td>
</tr>
<tr>
<td>PNUAS001492</td>
<td>IncC CoIE1</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>PNUAS001751</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>PNUAS0038936</td>
<td>None</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>PNUAS0051057</td>
<td>IncC IncI1-ly</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>PNUAS0051059</td>
<td>IncC IncI1-ly</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>R15.0600</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>R15.0891</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>R15.2897</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>R16.0676</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>R16.0696</td>
<td>IncC IncI1-ly</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>R16.1070</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>R16.1486</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
<tr>
<td>R16.2802</td>
<td>IncC</td>
<td>aadA2 aph(3’)-Ib aph(6)-Ib blaOXA-1, dfrA23 floR IuF sulB1 sul2 tet(A)</td>
</tr>
</tbody>
</table>
Appendix Figure. Core genome multilocus sequence typing (cgMLST) pairwise matrix of allele differences for 40 *Salmonella* Anatum isolates. Cell values indicate the number of allele differences between isolates. The matrix was constructed by using BioNumerics version 7.6 (Applied Maths, http://www.applied-maths.com). Based on the number of allele differences, cells are shaded from dark blue (0 allele differences) to red (20 allele differences). National Center for Biotechnology Information strain or isolate numbers are shown.