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.

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References

1. Brouqui P, Matsumoto K. Bacteriology and phylogeny of Anaplasmataceae. In: Raoul, D, Parola P, editors. Rickettsial diseases. New York; Informa; 2007. p. 179–198.
2. Dumler JS, Barbet AF, Bekker CP, Dasch GA, Palmer GH, Ray SC, et al. Reorganization of genera in the families Rickettsiaceae and Anaplasmataceae in the order Rickettsiales: unification of some species of *Ehrlichia* with *Anaplasma*, *Cowdria* with *Ehrlichia* and *Ehrlichia* with *Neorickettsia*, descriptions of six new species combinations and designation of *Ehrlichia equi* and 'HGE agent' as subjective synonyms of *Ehrlichia phagocytophila*. Int J Syst Evol Microbiol. 2001;51:2145–65. https://doi.org/10.1099/00207713-51-6-2145
3. Aguiar DM, Ziliani TF, Zhang X, Melo AL, Braga IA, Witter R, et al. A novel *Ehrlichia* genotype strain distinguished by the TRP36 gene naturally infects cattle in Brazil and causes clinical manifestations associated with ehrlichiosis. Ticks Tick Borne Dis. 2014;5:537–44. https://doi.org/10.1016/j.ttbdis.2014.03.010
4. Eberhardt AT, Fernandez C, Fargnoli L, Beldomenico PM, Monje LD. A putative novel strain of *Ehrlichia* infecting *Amblyomma tigrinum* associated with Pampas fox (*Lycalopex gymnocercus*) in Esteros del Iberá ecoregion, Argentina. Ticks Tick Borne Dis. 2020;11:101318.
5. Cicuttin GL, De Salvo MN, Nava S. Two novel *Ehrlichia* strains detected in *Amblyomma tigrinum* ticks associated to dogs in peri-urban areas of Argentina. Comp Immunol Microbiol Infect Dis. 2017;53:40–4. https://doi.org/10.1016/j.cimid.2017.07.001
6. Lopes MG, Muñoz-Leal S, de Lima JTR, Fournier GFDSR, Acosta IDCL, Martins TF, et al. Ticks, rickettsial and ehrlichial infection in small mammals from Atlantic forest remnants in northeastern Brazil. Int J Parasitol Parasites Wildl. 2018;7:380–5. https://doi.org/10.1016/j.ijppaw.2018.10.001
7. Nava S, Venzal JM, Gonzalez-Acuña DA, Martins TF, Guglielmone AA, editors. Ticks of the Southern Cone of America: diagnosis, distribution and hosts with taxonomy, ecology and sanitary importance. London: Elsevier; 2017. p. 135–42.
8. Monje LD, Costa FB, Colombo VC, Labruna MB, Antoniazzi LR, Gamietea I, et al. Dynamics of exposure to *Rickettsia parkeri* in cattle in the Paraná River delta, Argentina. J Med Entomol. 2016;53:660–5. https://doi.org/10.1093/jme/tjv250
9. Monje LD, Fernandez C, Percara A. Detection of *Ehrlichia* sp. strain San Luis and *Candidatus* Rickettsia andeanae in *Amblyomma parvum* ticks. Ticks Tick Borne Dis. 2019;10:111–4. https://doi.org/10.1016/j.ttbdis.2018.09.008
10. Allsopp BA. Natural history of *Ehrlichia ruminantium*. Vet Parasitol. 2010;167:123–35. https://doi.org/10.1016/j.vetpar.2009.09.014

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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 inducible 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_{DHA-1}, *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).

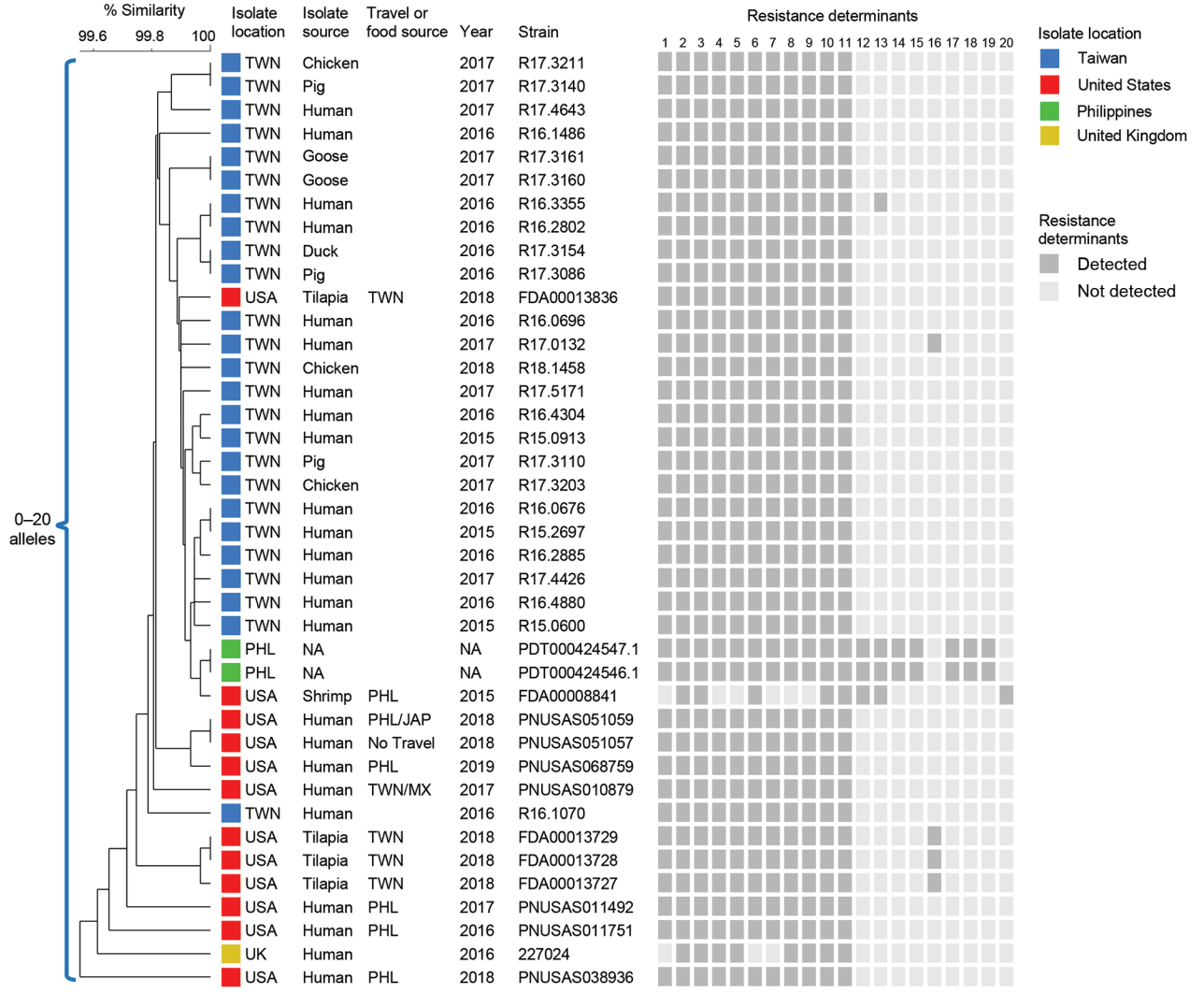

Figure. Core genome multilocus sequence typing (cgMLST) phylogenetic tree of 40 *Salmonella enterica* serotype Anatum isolates, 2015–2019. The tree was constructed by using BioNumerics version 7.6 (Applied Maths, http://www.applied-maths.com). Isolate sources, collection years, and National Center for 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")-Ib* (*strA*); 3) *aph(6)-Id* (*strB*); 4) bla_{DHA-1}; 5) *dfrA23*; 6) *floR*; 7) *lnu*(F); 8) *qnrB4*; 9) *sul1*; 10) *sul2*; 11) *tet*(A); 12) *aadA1*; 13) bla_{TEM-1B}; 14) *dfrA1*; 15) *dfrA12*; 16) *mcr-1.1*; 17) *mph*(A); 18) *oqxAB*; 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 PNUSAS038936; 15 had additional plasmids (Appendix Table 2). Most (38/40) had the previously reported 11 resistance genes (*1*). Two isolates from the Philippines had additional resistance genes, including *mph*(A), *qnrA6*, and *oqxAB*; 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_{DHA-1} 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) (*1*), which likely carried all 11 resistance genes, but long-read sequencing is required for confirmation. Isolate PNUSAS038936 lacked the IncC plasmid replicon but appeared to have an IS*26*-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 PNUSAS038936. 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 *Salmonella* carrying bla_{DHA-1} has both clinical and public health implications. Unlike most plasmid-mediated AmpC β-lactamase genes, bla_{DHA-1} 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 bla_{DHA-1}; the plasmid-mediated quinolone resistance gene *qnrB4*; and in the isolates from the Philippines, *mph*(A), a macrolide-resistance gene, is worrisome because third-generation cephalosporins (e.g., ceftriaxone), fluoroquinolones (e.g., ciprofloxacin), and the macrolide azithromycin are recommended for *Salmonella* infections requiring treatment (*5*,*6*). In addition, the presence of *mcr-1.1*, 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 *Salmonella* 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 *Salmonella* (*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.

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References

1. Chiou CS, Hong YP, Liao YS, Wang YW, Tu YH, Chen BH, et al. New multidrug-resistant *Salmonella enterica* serovar Anatum clone, Taiwan, 2015–2017. Emerg Infect Dis. 2019;25:144–7. PubMed https://doi.org/10.3201/eid2501.181103
2. Hennequin C, Ravet V, Robin F. Plasmids carrying DHA-1 β-lactamases. Eur J Clin Microbiol Infect Dis. 2018;37:1197–209. https://doi.org/10.1007/s10096-018-3231-9
3. Jacoby GA. AmpC β-lactamases. Clin Microbiol Rev. 2009;22:161–82. https://doi.org/10.1128/CMR.00036-08
4. Polsfuss S, Bloemberg GV, Giger J, Meyer V, Böttger EC, Hombach M. Practical approach for reliable detection of AmpC beta-lactamase-producing Enterobacteriaceae. J Clin Microbiol. 2011;49:2798–803. PubMed https://doi.org/10.1128/JCM.00404-11
5. American Academy of Pediatrics. *Salmonella* infections. In: Kimberlin DW, Brady MT, Jackson MA, Long SS, editors. Red Book: 2018 report of the committee on infectious diseases. 31st ed. Itasca (IL): The Academy; 2018. p. 711–8.
6. Shane AL, Mody RK, Crump JA, Tarr PI, Steiner TS, Kotloff K, et al. 2017 Infectious Diseases Society of America clinical practice guidelines for the diagnosis and management of infectious diarrhea. Clin Infect Dis. 2017;65:1963–73. https://doi.org/10.1093/cid/cix959
7. Barlow RS, Debess EE, Winthrop KL, Lapidus JA, Vega R, Cieslak PR. Travel-associated antimicrobial drug-resistant nontyphoidal Salmonellae, 2004–2009. Emerg Infect Dis. 2014;20:603–11. PubMed https://doi.org/10.3201/eid2004.131063
8. Williamson DA, Lane CR, Easton M, Valcanis M, Strachan J, Veitch MG, et al. Increasing antimicrobial resistance in nontyphoidal *Salmonella* isolates in Australia from 1979 to 2015. Antimicrob Agents Chemother. 2018;62:e02012–7. http://dx.doi.org/10.1128/AAC.02012-17
9. Bae D, Kweon O, Khan AA. Isolation and characterization of antimicrobial-resistant nontyphoidal *Salmonella enterica* serovars from imported food products. J Food Prot. 2016;79:1348–54. https://doi.org/10.4315/0362-028X.JFP-15-564
10. Zhao S. Antimicrobial-resistant food-borne pathogens in imported food. In: Doyle MP, Erickson MC, editors. Imported food: microbiological issues and challenges. Washington: ASM Press; 2008. p. 159–85.

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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 become infected through mucosal membranes or skin breaks by direct contact with reservoir animals or exposure to urine-contaminated soil or water. We describe 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 Institute for Communicable Diseases to assist with investigation 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 certificate no. M160667 from the Human Research Ethics Committee (Medical) of the University of the Witwatersrand covered the outbreak investigation.

Case-patient 1, a 52-year-old man, was admitted to a hospital in Cape Town. He had jaundice, overwhelming sepsis, disseminated intravascular