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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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).

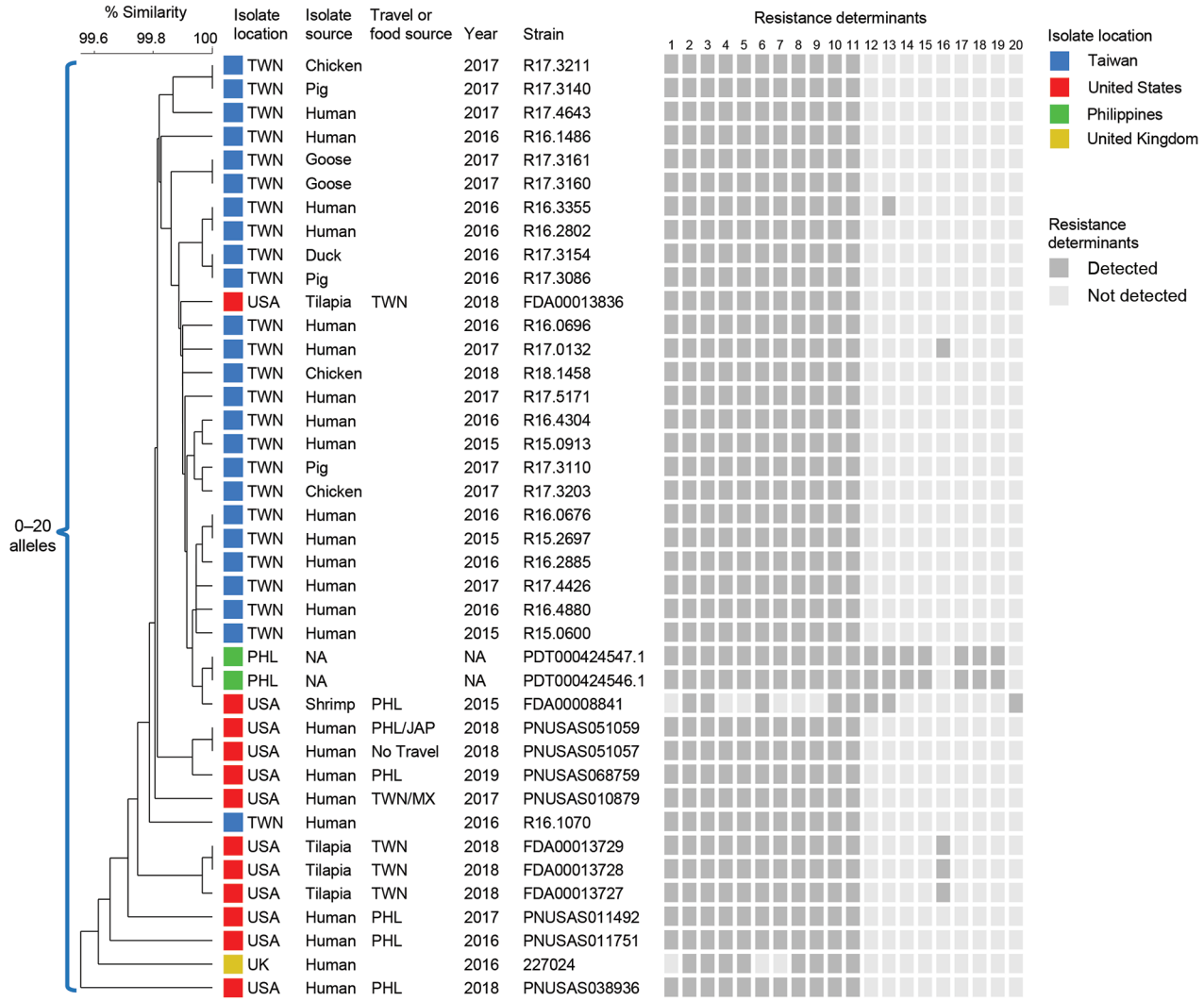

Figure. Core genome multilocus sequence typing (cgMLST) phylogenetic tree of 40 *Salmonella enterica* serotype Anatum isolates, 2015–2019. The tree was constructed by using BioNumerics version 7.6 (Applied Maths, http://www.applied-maths.com). Isolate sources, collection years, and National Center for 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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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 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

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Appendix

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

CLSI antimicrobial class	Antimicrobial agent	Concentration range, µg/mL	Interpretive categories and MIC breakpoints, µg/mL		
			Susceptible	Intermediate	Resistant
Aminoglycosides	Gentamicin	0.25–16	≤4	8	≥16
	Streptomycin†	2–64	≤16	NA	≥32
β-lactam combination agents	Amoxicillin-clavulanic acid	1/0.5–32/16	≤8/4	16/8	≥32/16
Cephems	Cefoxitin	0.5–32	≤8	16	≥32
	Ceftriaxone	0.25–64	≤1	2	≥4
Folate pathway antagonists	Sulfisoxazole	16–256	≤256	NA	≥512
	Trimethoprim-sulfamethoxazole	0.12/2.38–4/76	≤2/38	NA	≥4/76
Macrolides	Azithromycin†	0.25–32	≤16	NA	≥32
Penems	Meropenem	0.06–4	≤1	2	≥4
Penicillins	Ampicillin	1–32	≤8	16	≥32
Phenicols	Chloramphenicol	2–32	≤8	16	≥32
Quinolones	Ciprofloxacin	0.015–4	≤0.06	0.12–0.5	≥1
	Nalidixic acid	0.5–32	≤16	NA	≥32
Tetracycline	Tetracycline	4–32	≤4	8	≥16

*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

Strain	Plasmid replicons	Resistance determinants
227024	IncC	*aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 qnrB4 sul1 sul2 tet*(A)
FDA00008841	IncC IncI1-Iy	*aph(3")-Ib aph(6)-Id floR sul2 tet(A) aadA1* bla_{TEM-1B} *sul3*
FDA00013727	IncC IncI2	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A) *mcr-1.1*
FDA00013728	IncC IncI2	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A) *mcr-1.1*
FDA00013729	IncC IncI2	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A) *mcr-1.1*
FDA00013836	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
PDT000424546.1	IncC IncHI2 IncHI2A	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A) *aadA1* bla_{TEM-1B} *dfrA1 dfrA12 mph*(A) *oqxAB qnrA6*
PDT000424547.1	IncC IncHI2 IncHI2A	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A) *aadA1* bla_{TEM-1B} *dfrA1 dfrA12 mph*(A) *oqxAB qnrA6*
PNUSAS010879	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
PNUSAS011492	IncC ColE1	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
PNUSAS011751	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
PNUSAS038936	None	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
PNUSAS051057	IncC IncI1-Iy	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
PNUSAS051059	IncC IncI1-Iy	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
PNUSAS068759	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R15.0600	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R15.0913	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R15.2697	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R16.0676	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R16.0696	IncC IncI1-Iy	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R16.1070	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R16.1486	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R16.2802	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)

Strain	Plasmid replicons	Resistance determinants
R16.2885	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R16.3355	IncC IncI1-Iy	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A) bla_{TEM-1B}
R16.4304	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R16.4880	IncC IncX4	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.0132	IncC IncI2 IncX4	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A) *mcr-1.1*
R17.3086	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.3110	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.3140	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.3154	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.3160	IncC IncFII(p96A)	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.3161	IncC IncFII(p96A)	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.3203	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.3211	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.4426	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.4643	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R17.5171	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)
R18.1458	IncC	*aadA2 aph(3")-Ib aph(6)-Id* bla_{DHA-1} *dfrA23 floR lnu*(F) *qnrB4 sul1 sul2 tet*(A)

Strain no.

Strain (strain no.)	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40
227024 (1)	0	11	20	9	9	14	15	16	12	8	17	11	11	11	11	11	12	14	14	10	12	12	12	11	12	11	13	12	11	12	12	12	12	11	13	12	12	15	10	10
PNUSAS010879 (2)	11	0	15	4	4	11	10	11	7	3	12	6	6	6	6	6	7	10	9	5	8	8	7	6	7	7	8	7	7	8	8	7	7	6	9	7	7	10	5	6
PNUSAS038936 (3)	20	15	0	11	11	17	16	17	13	11	18	13	13	13	13	13	14	17	16	12	15	15	14	13	14	14	15	14	14	15	15	14	14	13	16	14	14	16	14	15
PDT000424546.1 (4)	9	4	11	0	0	7	6	7	3	1	8	4	2	2	2	2	3	6	5	1	4	4	3	2	3	3	4	3	3	4	4	3	3	2	5	3	3	6	3	4
PDT000424547.1 (5)	9	4	11	0	0	7	6	7	3	1	8	4	2	2	2	2	3	6	5	1	4	4	3	2	3	3	4	3	3	4	4	3	3	2	5	3	3	6	3	4
FDA00013727 (6)	14	11	17	7	7	0	1	1	7	8	14	10	7	7	7	7	7	11	10	6	9	9	8	7	8	8	9	10	8	8	8	8	10	7	12	7	8	13	10	10
FDA00013728 (7)	15	10	16	6	6	1	0	0	6	7	13	9	6	6	6	6	7	10	8	5	8	8	7	6	7	7	8	9	7	7	7	7	9	6	10	7	7	11	9	9
FDA00013729 (8)	16	11	17	7	7	1	0	0	6	7	13	8	7	7	7	7	8	11	9	6	8	8	8	7	7	7	9	10	7	8	8	8	10	7	11	8	8	11	8	8
FDA00013836 (9)	12	7	13	3	3	7	6	6	0	4	9	6	3	3	3	3	4	7	6	2	5	5	4	3	4	4	5	6	4	4	4	4	6	3	8	4	4	8	6	6
FDA00008841 (10)	8	3	11	1	1	8	7	7	4	0	8	2	3	3	3	3	4	6	6	2	5	5	4	3	4	4	5	4	4	5	5	4	4	3	6	2	4	7	2	2
PNUSAS011751 (11)	17	12	18	8	8	14	13	13	9	8	0	10	10	10	10	10	11	14	13	9	11	11	11	10	11	10	12	11	10	11	11	11	11	10	13	10	11	13	10	10
PNUSAS068759 (12)	11	6	13	4	4	10	9	8	6	2	10	0	6	6	6	6	6	10	9	5	8	8	7	6	7	7	8	7	7	8	8	7	7	6	9	7	7	9	2	2
R15.0600 (13)	11	6	13	2	2	7	6	7	3	3	10	6	0	2	2	2	3	6	5	1	4	4	3	2	3	3	4	5	3	4	4	3	5	2	7	3	3	8	5	6
R15.0913 (14)	11	6	13	2	2	7	6	7	3	3	10	6	2	0	2	2	3	6	5	1	4	4	1	2	3	3	2	5	3	4	4	1	5	2	7	3	3	8	5	6
R15.2697 (15)	11	6	13	2	2	7	6	7	3	3	10	6	2	2	0	0	3	6	5	1	4	4	3	2	3	3	4	5	3	4	4	3	5	2	7	3	3	8	5	6
R16.0676 (16)	11	6	13	2	2	7	6	7	3	3	10	6	2	2	0	0	3	6	5	1	4	4	3	2	3	3	4	5	3	4	4	3	5	2	7	3	3	8	5	6
R16.0696 (17)	12	7	14	3	3	7	7	8	4	4	11	6	3	3	3	3	0	7	6	2	5	5	4	3	4	4	5	6	4	5	5	4	6	3	8	4	4	9	5	6
R16.1070 (18)	14	10	17	6	6	11	10	11	7	6	14	10	6	6	6	6	7	0	9	5	8	8	7	6	7	7	8	9	7	8	8	7	9	6	11	7	7	12	9	10
R16.1486 (19)	14	9	16	5	5	10	8	9	6	6	13	9	5	5	5	5	6	9	0	4	7	7	6	5	6	6	7	8	6	7	7	6	8	5	10	5	6	10	8	9
R16.2885 (20)	10	5	12	1	1	6	5	6	2	2	9	5	1	1	1	1	2	5	4	0	3	3	2	1	2	2	3	4	2	3	3	2	4	1	6	2	2	7	4	5
R16.2802 (21)	12	8	15	4	4	9	8	8	5	5	11	8	4	4	4	4	5	8	7	3	0	0	5	4	5	1	6	7	1	6	6	5	7	4	9	5	5	10	6	8
R16.3355 (22)	12	8	15	4	4	9	8	8	5	5	11	8	4	4	4	4	5	8	7	3	0	0	5	4	5	1	6	7	1	6	6	5	7	4	9	5	5	10	6	8
R16.4304 (23)	12	7	14	3	3	8	7	8	4	4	11	7	3	1	3	3	4	7	6	2	5	5	0	3	4	4	3	6	4	5	5	2	6	3	8	4	4	9	6	7
R16.4880 (24)	11	6	13	2	2	7	6	7	3	3	10	6	2	2	2	2	3	6	5	1	4	4	3	0	3	3	4	5	3	4	4	3	5	2	7	3	3	8	5	6
R17.0132 (25)	12	7	14	3	3	8	7	7	4	4	11	7	3	3	3	3	4	7	6	2	5	5	4	3	0	4	5	6	4	5	5	4	6	3	8	4	4	9	6	7
R17.3086 (26)	11	7	14	3	3	8	7	7	4	4	10	7	3	3	3	3	4	7	6	2	1	1	4	3	4	0	5	6	0	5	5	4	6	3	8	4	4	9	5	7
R17.3110 (27)	13	8	15	4	4	9	8	9	5	5	12	8	4	2	4	4	5	8	7	3	6	6	3	4	5	5	0	7	5	6	6	1	7	4	9	5	5	10	7	8
R17.3140 (28)	12	7	14	3	3	10	9	10	6	4	11	7	5	5	5	5	6	9	8	4	7	7	6	5	6	6	7	0	6	7	7	6	0	5	4	6	6	9	6	7
R17.3154 (29)	11	7	14	3	3	8	7	7	4	4	10	7	3	3	3	3	4	7	6	2	1	1	4	3	4	0	5	6	0	5	5	4	6	3	8	4	4	9	5	7
R17.3160 (30)	12	8	15	4	4	8	7	8	4	5	11	8	4	4	4	4	5	8	7	3	6	6	5	4	5	5	6	7	5	0	0	5	7	4	9	5	5	9	6	8
R17.3161 (31)	12	8	15	4	4	8	7	8	4	5	11	8	4	4	4	4	5	8	7	3	6	6	5	4	5	5	6	7	5	0	0	5	7	4	9	5	5	9	6	8
R17.3203 (32)	12	7	14	3	3	8	7	8	4	4	11	7	3	1	3	3	4	7	6	2	5	5	2	3	4	4	1	6	4	5	5	0	6	3	8	4	4	9	6	7
R17.3211 (33)	12	7	14	3	3	10	9	10	6	4	11	7	5	5	5	5	6	9	8	4	7	7	6	5	6	6	7	0	6	7	7	6	0	5	4	6	6	9	6	7
R17.4426 (34)	11	6	13	2	2	7	6	7	3	3	10	6	2	2	2	2	3	6	5	1	4	4	3	2	3	3	4	5	3	4	4	3	5	0	7	3	3	8	5	6
R17.4643 (35)	13	9	16	5	5	12	10	11	8	6	13	9	7	7	7	7	8	11	10	6	9	9	8	7	8	8	9	4	8	9	9	8	4	7	0	8	8	11	7	9
R17.5171 (36)	12	7	14	3	3	7	7	8	4	2	10	7	3	3	3	3	4	7	5	2	5	5	4	3	4	4	5	6	4	5	5	4	6	3	8	0	4	9	6	7
R18.1458 (37)	12	7	14	3	3	8	7	8	4	4	11	7	3	3	3	3	4	7	6	2	5	5	4	3	4	4	5	6	4	5	5	4	6	3	8	4	0	9	6	7
PNUSAS011492 (38)	15	10	16	6	6	13	11	11	8	7	13	9	8	8	8	8	9	12	10	7	10	10	9	8	9	9	10	9	9	9	9	9	9	8	11	9	9	0	8	9
PNUSAS051057 (39)	10	5	14	3	3	10	9	8	6	2	10	2	5	5	5	5	5	9	8	4	6	6	6	5	6	5	7	6	5	6	6	6	6	5	7	6	6	8	0	0
PNUSAS051059 (40)	10	6	15	4	4	10	9	8	6	2	10	2	6	6	6	6	6	10	9	5	8	8	7	6	7	7	8	7	7	8	8	7	7	6	9	7	7	9	0	0

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.