In 2011, a *Salmonella enterica* serovar Anatum clone emerged in Taiwan. During 2016–2017, infections increased dramatically, strongly associated with emergence and spread of multidrug-resistant strains with a plasmid carrying 11 resistance genes, including *bla*<sub>DHA-1</sub>. Because these resistant strains infect humans and food animals, control measures are urgently needed.

*Salmonella*, a prevalent foodborne pathogen that causes zoonoses worldwide, comprises 2 species, *Salmonella enterica* and *S. bongori*, and ≈2,600 serovars (1). In Taiwan, salmonellosis has been primarily caused by the *S. enterica* serovars Enteritidis, Typhimurium, Stanley, Newport, and Albany, which together caused 70% of salmonellosis infections during 2004–2012 (2). During this period, *Salmonella* Anatum was not prevalent, causing only 0.4% of the infections. However, since 2015, *Salmonella* Anatum infections have increased, and most isolates are multidrug resistant (MDR). We report the epidemiologic trend of *Salmonella* Anatum infection of humans, the clonal relationships among strains recovered during 2004–2017, and the resistance mechanism of the newly emerging MDR strains.

The Study

To investigate the epidemiologic trend, we analyzed the data in the *Salmonella* fingerprint database constructed by the Taiwan Centers for Disease Control. The database comprises demographic and experimental data, including pulsed-field gel electrophoresis (PFGE) fingerprints obtained by using the PulseNet standardized PFGE protocol (3), serotypes obtained using PFGE pattern comparison and conventional methods (4), and antimicrobial drug susceptibility testing results for isolates collected from hospitals nationwide. We conducted whole-genome sequencing for 68 *Salmonella* Anatum isolates from humans and animals and 9 isolates from chicken carcasses and abattoir environments by using the Illumina MiSeq platform (https://www.illumina.com) and identified resistance genes, incompatibility groups of plasmids, and sequence types by using the whole-genome sequencing data. To investigate clonal relationships and locations of resistance genes, we constructed a dendrogram for *Salmonella* Anatum strains with whole-genome single-nucleotide polymorphism profiles to assess genetic relatedness among strains and determined the complete genomic sequence of *Salmonella* Anatum strain R16.0676 with whole-genome sequencing data generated by using a MinION nanopore sequencer (https://nanoporetech.com/products/minion) and an Illumina MiSeq sequencer. To investigate mobility of resistance plasmids, we conducted conjugation experiments to transfer the resistance genes–carrying (R) plasmid from *Salmonella* Anatum strain R16.0676 into recipient *Escherichia coli* C600 and transferred an R plasmid from an *E. coli* transconjugant back to a rifampin-resistant mutant of *Salmonella* Anatum strain R13.0957 (Appendix, https://wwwnc.cdc.gov/EID/article/25/1/18-1103-App1.pdf).

The *Salmonella* fingerprint database of the Taiwan Centers for Disease Control contained PFGE fingerprints for 34,160 *Salmonella* isolates recovered during 2004–2017, of which antimicrobial drug sensitivity test results were available for 23,018. *Salmonella* Anatum was not a prevalent serovar among those collected during 2004–2014 (Figure 1). However, the number of *Salmonella* Anatum infections increased in 2015 and subsequently underwent another sharp increase in 2016 and 2017. In 2017, *Salmonella* Anatum accounted for 14.2% of *Salmonella* infections in Taiwan and ranked as the third most frequently identified serovar.

Whole-genome single-nucleotide polymorphism analysis of *Salmonella* Anatum recovered from humans during 2004–2017 revealed 3 distinct lineages (Figure 2). Strains of lineage (L) 1 were either pansusceptible or MDR; they mostly appeared during 2004–2009 (Appendix Table 2). L2 comprised only 2 isolates, which emerged in 2005 and were pansusceptible. L3 comprised 2 sublineages; sublineage (SL) 3_1, first detected in 2011, was mostly pansusceptible, whereas SL3_2, which first emerged in 2013, was mostly MDR. The MDR strains of SL3_2 first appeared in 2015 and were resistant or of reduced susceptibility to 10 of the 14 antimicrobial drugs tested. SMX.642 was the predominant MDR strain, but the first 2 isolates recovered...
in 2013 were pansusceptible. Of the 9 isolates from chicken carcasses and abattoir environments, 5 belonged to SL3_1 and 4 to SL3_2. The new clone (L3) accounted for 91.9% of the total Salmonella Anatum infections during 2004–2017 and 99.6% in 2017. MDR strains accounted for 90.3% of the new clone recovered during 2011–2017 and 94.1% in 2017. All Salmonella Anatum isolates sequenced belonged to sequence type 64.

The chromosomal sequence of strain R16.0676 was 4,674,190 bp (GenBank accession no. CP029800) and was not noted to carry any horizontally transferable resistance gene. R16.0676 harbored 2 plasmids, which were designated pR16.0676_90k (90,137 bp; IncC; accession no. CP029802) and pR16.0676_34k (34,063 bp; IncN3; accession no. CP029801). pR16.0676_90k harbored 11 resistance genes, aadA2, bla_DHA-1, dfrA23, floR, lnu(F), qnrB4, strA, strB, sul1, sul2, and tet(A), which were distributed in 2 antimicrobial resistance islands, ARI1 and ARI2 (Appendix Figure, panel A). ARI1 carried 5 resistance genes, floR, strA, strB, sul2, and tet(A), and was found in many IncC plasmids in the National Center for Biotechnology Information database (5). ARI2 carried the other 6 resistance genes, aadA2, bla_DHA-1, dfrA23, lnu(F), qnrB4, and sul1. The resistance genes could confer resistance to cefoxitin, cefotaxime, cepazidime, ampicillin, chloramphenicol, streptomycin, sulfonamide, tetracycline, and trimethoprim and reduced susceptibility to ciprofloxacin as shown by antimicrobial susceptibility testing (Figure 2). pR16.0676_90k shared 79% sequence identity with a 272-kb plasmid, pECAZ155_KPC (GenBank accession no. CP019001.1), which harbored only the sequence of ARI1 but not ARI2. pR16.0676_34k did not carry any resistance gene (Appendix Figure, panel B), but it shared 98% sequence identity with a 34.8-kb plasmid, pN-Cit (GenBank accession no. JQ996149.1).

All MDR SL3_2 isolates, including the 4 isolates recovered from the abattoirs, harbored an IncC plasmid and the same 11 resistance genes identified in strain R16.0676. Strain R17.0132 acquired an additional mcr-1 gene and was resistant to colistin (Figure 2). We did not obtain any transconjugants with pR16.0676_90k, but we did obtain a transconjugant with a composite plasmid, which had the same sequences as pR16.0676_90k and pR16.0676_34k (Appendix Figure, panel C). This 125-kb composite plasmid probably resulted from insertion of pR16.0676_90k into pR16.0676_34k through an insertion sequence 26–mediated transposition process. The resulting plasmid acquired an additional copy of insertion sequence 26 and an 8-bp tandem repeat in the insertion site. More than a dozen genes are typically required for conjugation (6). pR16.0676_90k harbored only 3 genes, and pR16.0676_34k contained at least 12 genes related to conjugation. Fusion of the 2 plasmids caused the composite plasmid to become self-transmissible. When the composite plasmid was transferred back into a rifampin-resistant mutant of Salmonella Anatum strain R13.0957, we obtained transconjugants harboring only a 58-kb or 83-kb R plasmid, which were derived from the 125-kb plasmid through deletions (Appendix Figure, panel C). Accordingly, the composite plasmid was unstable in Salmonella Anatum.

Conclusions

We identified a new Salmonella Anatum clone that emerged in Taiwan in 2011. During 2011–2014, strains of the new clone were not resistant and caused few infections. The dramatic increase in Salmonella Anatum infections that occurred during 2016–2017 was strongly associated with the emergence of MDR strains in 2015. The most crucial concern regarding emergence of the MDR...
Salmonella Anatum clone was that all MDR strains carry \( \text{bla}_{\text{DHA-1}} \), which encodes AmpC \( \beta \)-lactamase and confers resistance to \( \beta \)-lactam drugs, including third-generation cephalosporins. This resistance cannot be overcome by using \( \beta \)-lactam inhibitors. Because these MDR strains can cause numerous infections in humans and are prevalent in animals used for food, urgent control measures are needed.

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Dr. Chiou is a principal investigator at the Centers for Disease Control, Ministry of Health and Welfare, Taiwan. His research interests include genotyping, molecular epidemiology, and antimicrobial resistance of foodborne bacterial pathogens.

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EID SPOTLIGHT TOPIC

Antimicrobial Resistance

Antibiotics and similar drugs, together called antimicrobial agents, have been used for the past 70 years to treat patients who have infectious diseases. Since the 1940s, these drugs have greatly reduced illness and death from infectious diseases. However, these drugs have been used so widely and for so long that the infectious organisms the antibiotics are designed to kill have adapted to them, making the drugs less effective.

Each year in the United States, at least 2 million people become infected with bacteria that are resistant to antibiotics and at least 23,000 people die each year as a direct result of these infections.

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http://wwwnc.cdc.gov/eid/page/resistance-spotlight
New Multidrug-Resistant *Salmonella enterica* Serovar Anatum Clone, Taiwan, 2015–2017

Appendix

**Experimental Methods**

**Antimicrobial susceptibility testing**

We performed antimicrobial susceptibility testing for Salmonella isolates using the microbroth dilution method and custom-made Sensititre® 96 well susceptibility plates (TREK Diagnostic Systems Ltd., West Sussex, UK). The antimicrobials for the custom-made Sensititre plates changed several times during 2004—2016. The test was performed according to the manufacturer's instructions, and the interpretation of MIC results was followed the guidelines of the Clinical and Laboratory Standards Institute (CLSI) (1). The CLSI interpretive criteria were used for all of the antimicrobials except streptomycin, for which MIC$\geq$32 μg/ml was used for streptomycin resistance.

**Whole genome sequencing and sequence analysis**

We conducted whole genome sequencing of *S. Anatum* isolates using Illumina MiSeq sequencing platform (Illumina Inc. USA) with MiSeq Reagent Kit v3 (2X 300 bp). Appendix Table lists the sequencing data (coverage and N50) and the NCBI accession numbers for the isolates with WGS data. We used the CLC Genomics Workbench software (Qiagen Bioinformatics, Germany) to assemble the Illumina reads for all isolates, identified resistance genes and incompatibility groups of plasmids using the ResFinder and PlasmidFinder tools provided by the Center for Genomic Epidemiology (http://www.genomicepidemiology.org/), and determined sequence type using the plugin tool provided in BioNumerics version 7.6.3 (Applied Maths Inc.).
**Sequencing of complete genome of S. Anatum strain R16.0676 and plasmids**

We used a MinION nanopore sequencer (Oxford Nanopore Technologies, UK) to obtain long reads for S. Anatum strain R16.0676 and plasmids from transconjugants, an Albacore basecaller (Oxford Nanopore Technologies) to execute base calling of nanopore reads, Canu (2) to assemble reads, Pilon (3) to polish the Canu-assembled contigs with the Illumina reads, and Nanopolish (https://github.com/jts/nanopolish) to polish the Canu-assembled contigs with raw nanopore reads. Subsequently, we used PCR and Sanger sequencing techniques to correct the uncertain sequences and RAST (http://rast.nmpdr.org/) to annotate the complete chromosome and plasmid sequences of the strain R16.0676 (4).

**Construction of a dendrogram for S. Anatum strains using wgSNP profiles**

We used the tools provided in BioNumerics version 7.6.3 for construction of a dendrogram with wgSNP profiles of S. Anatum strains. The sequences of raw reads were mapped to the reference genomic sequence of S. Anatum strain GT-38 (GenBank accession no. CP013226) and the mapped sequences of strains and the reference were aligned for SNP calling by using the option of strict SNP filtering (closed SNP set). By using this SNP calling criteria, SNPs are called by removing positions with at least one ambiguous base (non-ATGC base), one unreliable base (N), one gap and non-informative SNPs. Each retained SNP position has minimum 5x coverage, at least covered once in both forward and reverse direction. The minimum distance between retained SNP position is 12 bp. A dendrogram was constructed with the whole genome SNP profiles using the categorical (SNPs) option for similarity coefficient and single linkage algorithm for cluster analysis.

**Conjugation**

We conducted conjugation experiments to transfer the resistance genes-carrying (R) plasmid from strain R16.0676 into *Escherichia coli* C600 recipients by using LB medium with 50 mg/L ampicillin and 2,000 mg/L streptomycin for transconjugant selection. Subsequently, we transferred an R plasmid from an *E. coli* transconjugant back to a rifampicin-resistant mutant of S. Anatum strain R13.0957 by using LB medium with 50 mg/L ampicillin and 150 mg/L rifampicin for transconjugant selection. The
plasmids and their sizes were estimated using a S1-PFGE method (5). The sequences of R plasmids from transconjugants were determined using MinION nanopore sequencer or illumina MiSeq sequencer.

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Appendix Table 1. The NCBI accession numbers for the whole genome sequences of Salmonella enterica serovar Anatum isolates and plasmids investigated in this study*

| Strain/Plasmid | BioProject | BioSample | SRA       | Coverage (X) | N50 (bp) |
|---------------|------------|-----------|-----------|--------------|----------|
| CA08.145      | PRJNA478278| SAMN09788957| SRR7665411| 29.4         | 332,460  |
| CC04.028      | PRJNA478278| SAMN09788958| SRR7665410| 47.4         | 733,275  |
| CC06.031      | PRJNA478278| SAMN09788959| SRR7665409| 33           | 432,006  |
| CF09.078      | PRJNA478278| SAMN09788960| SRR7665408| 39.1         | 640,112  |
| CH05.023      | PRJNA478278| SAMN09788961| SRR7665415| 44.3         | 695,804  |
| CH07.062      | PRJNA478278| SAMN09788962| SRR7665414| 50.5         | 741,255  |
| CI07.001      | PRJNA478278| SAMN09788963| SRR7665413| 73.3         | 741,487  |
| CS182         | PRJNA478278| SAMN09788964| SRR7665412| 29.9         | 374,704  |
| D013          | PRJNA478278| SAMN09788965| SRR7665406| 44.7         | 699,584  |
| D020          | PRJNA478278| SAMN09788966| SRR7665405| 41           | 643,641  |
| EA04.039      | PRJNA478278| SAMN09788967| SRR7665354| 42.8         | 678,360  |
| EA04.047      | PRJNA478278| SAMN09788968| SRR7665353| 49.1         | 733,283  |
| MS32850       | PRJNA478278| SAMN09788969| SRR7665356| 33.3         | 434,923  |
| MS32915       | PRJNA478278| SAMN09788970| SRR7665355| 38.2         | 551,024  |
| NC04.178      | PRJNA478278| SAMN09788971| SRR7665358| 45.9         | 732,987  |
| Strain/Plasmid | BioProject | BioSample | SRA      | Coverage (X) | N50 (bp) |
|---------------|-----------|-----------|----------|-------------|----------|
| NJ08.181      | PRJNA478278 | SAMP09788972 | SRR7665357 | 35.9 | 531,861   |
| NK04.008      | PRJNA478278 | SAMP09788973 | SRR7665360 | 36.3 | 532,082   |
| NL05.024      | PRJNA478278 | SAMP09788974 | SRR7665359 | 44.2 | 695,569   |
| P049          | PRJNA478278 | SAMP09788975 | SRR7665351 | 54.1 | 741,359   |
| P164          | PRJNA478278 | SAMP09788976 | SRR7665350 | 31  | 399,915   |
| P165          | PRJNA478278 | SAMP09788977 | SRR7665385 | 24.6 | 173,037   |
| P593          | PRJNA478278 | SAMP09788978 | SRR7665386 | 28.9 | 319,346   |
| R13.0957      | PRJNA478278 | SAMP09788979 | SRR7665387 | 40.3 | 643,625   |
| R13.1215      | PRJNA478278 | SAMP09788980 | SRR7665388 | 35.7 | 495,112   |
| R13.1671      | PRJNA478278 | SAMP09788981 | SRR7665381 | 29.3 | 332,460   |
| R13.2266      | PRJNA478278 | SAMP09788982 | SRR7665382 | 83.7 | 741,735   |
| R14.1408      | PRJNA478278 | SAMP09788983 | SRR7665383 | 44.2 | 695,795   |
| R15.0600      | PRJNA478278 | SAMP09788984 | SRR7665384 | 54.5 | 741,397   |
| R15.0695      | PRJNA478278 | SAMP09788985 | SRR7665378 | 56.5 | 741,426   |
| R15.0913      | PRJNA478278 | SAMP09788986 | SRR7665379 | 37.6 | 533,333   |
| R15.1294      | PRJNA478278 | SAMP09788987 | SRR7665364 | 35.7 | 495,179   |
| R15.1365      | PRJNA478278 | SAMP09788988 | SRR7665363 | 37.3 | 533,154   |
| R15.1977      | PRJNA478278 | SAMP09788989 | SRR7665362 | 31.4 | 405,893   |
| R15.2697      | PRJNA478278 | SAMP09788990 | SRR7665361 | 27.9 | 289,505   |
| R16.0274      | PRJNA478278 | SAMP09788991 | SRR7665368 | 30.9 | 399,664   |
| R16.0348      | PRJNA478278 | SAMP09788992 | SRR7665367 | 30.8 | 399,652   |
| R16.0460      | PRJNA478278 | SAMP09788993 | SRR7665366 | 43.3 | 694,259   |
| R16.0569      | PRJNA478278 | SAMP09788994 | SRR7665365 | 36.4 | 532,231   |
| R16.0696      | PRJNA478278 | SAMP09788995 | SRR7665370 | 34.5 | 454,735   |
| R16.1070      | PRJNA478278 | SAMP09788996 | SRR7665369 | 66.1 | 741,485   |
| R16.1231      | PRJNA478278 | SAMP09788997 | SRR7665397 | 33.6 | 452,715   |
| R16.1486      | PRJNA478278 | SAMP09788998 | SRR7665396 | 37.6 | 533,690   |
| R16.2802      | PRJNA478278 | SAMP09788999 | SRR7665393 | 30.1 | 387,305   |
| R16.2821      | PRJNA478278 | SAMP09789000 | SRR7665394 | 30  | 383,318   |
| R16.2885      | PRJNA478278 | SAMP09789001 | SRR7665391 | 38.6 | 639,698   |
| R16.3115      | PRJNA478278 | SAMP09789002 | SRR7665392 | 54.1 | 741,397   |
| R16.3355      | PRJNA478278 | SAMP09789003 | SRR7665389 | 56.3 | 741,426   |
| R16.3623      | PRJNA478278 | SAMP09789004 | SRR7665390 | 36.6 | 532,391   |
| R16.3927      | PRJNA478278 | SAMP09789005 | SRR7665403 | 33.5 | 437,722   |
| R16.4304      | PRJNA478278 | SAMP09789006 | SRR7665404 | 31.9 | 406,851   |
| R16.4391      | PRJNA478278 | SAMP09789007 | SRR7665376 | 38.3 | 551,278   |
| R16.4880      | PRJNA478278 | SAMP09789008 | SRR7665372 | 51  | 741,359   |
| R17.0132      | PRJNA478278 | SAMP09789009 | SRR7665349 | 41.6 | 643,695   |
| R17.3086      | PRJNA478278 | SAMP09789010 | SRR7665397 | 80.2 | 741,599   |
| R17.3110      | PRJNA478278 | SAMP09789011 | SRR7665375 | 33.6 | 454,461   |
| R17.3140      | PRJNA478278 | SAMP09789012 | SRR7665373 | 101 | 742,067   |
| R17.3154      | PRJNA478278 | SAMP09789013 | SRR7665380 | 79.4 | 741,597   |
| R17.3160      | PRJNA478278 | SAMP09789014 | SRR7665377 | 83.4 | 741,599   |
| R17.3161      | PRJNA478278 | SAMP09789015 | SRR7665352 | 81.1 | 741,599   |
| R17.3203      | PRJNA478278 | SAMP09789016 | SRR7665371 | 107.6 | 782,067   |
| R17.3211      | PRJNA478278 | SAMP09789017 | SRR7665407 | 95.4 | 741,778   |
| R17.4426      | PRJNA478278 | SAMP09789018 | SRR7665398 | 30.2 | 399,562   |
| R17.4643      | PRJNA478278 | SAMP09789019 | SRR7665399 | 50  | 733,496   |
| R17.5171      | PRJNA478278 | SAMP09789020 | SRR7665400 | 45.5 | 719,281   |
| Strain/Plasmid | BioProject | BioSample | SRA         | Coverage (X) | N50 (bp) |
|---------------|------------|-----------|-------------|--------------|----------|
| SA11.164      | PRJNA478278| SAMN09789021 | SRR7655401 | 32.7         | 427,327  |
| SG06.139      | PRJNA478278| SAMN09789022 | SRR7655402 | 46.5         | 733,111  |
| SN08.005      | PRJNA478278| SAMN09789023 | SRR7655374 | 25.8         | 209,293  |
| R16.0676      | PRJNA474787| SAMN09373897 | SRR7655457 | 35.2         | 465,526  |
| R18.1457      | PRJNA478278| SAMN09914824 | SRR7755901 | 82.7         | 741,599  |
| R18.1458      | PRJNA478278| SAMN09914823 | SRR7755902 | 41.6         | 643,774  |

* R16.0676, GenBank accession no. CP029800; pR16.0676_34k, GenBank accession no. CP029802; pConj125k, GenBank accession no. MK033499; pConj58k, GenBank accession no. MK033500; pConj58k, GenBank accession no. MK033501.

**Appendix Table 2.** Distribution of PFGE types and clonal lineages for *Salmonella enterica* serovar Anatum isolates collected during 2004–2017*

| Lineage, sublineage, PFGE type | Distribution of isolates, by year |
|-------------------------------|----------------------------------|
|                               | 2004 | 2005 | 2006 | 2007 | 2008 | 2009 | 2010 | 2011 | 2012 | 2013 | 2014 | 2015 | 2016 | 2017 | Total |
| L1                            |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |       |
| SMX.082                       | 9    | 4    | 4    | 6    | 2    | 2    | 1    | 1    | 1    | 1    |      |      |      |      |      | 30     |
| SMX.087                       | 6    | 3    | 2    | 4    | 3    | 2    | 2    | 2    | 3    |      |      |      |      |      |      | 27     |
| SMX.099                       | 2    | 2    |      |      |      |      |      |      |      |      |      |      |      |      | 1     | 5      |
| SMX.092                       | 1    |      |      |      |      |      |      |      |      |      |      | 1    |      |      |      | 3      |
| Other 21                      | 11   | 2    | 2    | 3    | 4    |      |      |      |      |      |      |      |      |      |      | 24     |
| Subtotal                      | 27   | 11   | 8    | 15   | 10   | 4    | 0    | 0    | 1    | 2    | 2    | 3    | 3    | 3    |      | 89     |
| L3                            |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |       |
| SL3_1                         |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |       |
| SMX.768                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      | 1      |
| SMX.871                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      | 1      |
| SL3_2                         |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |
| SMX.642                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      | 2      |
| SMX.903                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      | 22     |
| SMX.1052                      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      | 168    |
| SL3_1 and SL3_2               |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      | 544    |
| Other 54 types                |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      | 736    |
| Subtotal                      | 0    | 0    | 0    | 0    | 0    | 0    | 0    | 1    | 1    | 6    | 4    | 36   | 250  | 732  | 1,030  |
| L2                            |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      |       |
| SMX.098                       |      |      |      |      |      |      |      |      |      |      |      |      |      |      |      | 2      |
| Total S. Anatum               | 27   | 13   | 8    | 15   | 10   | 4    | 0    | 1    | 2    | 8    | 6    | 39   | 253  | 735  | 1,121  |
| All Salmonella collected      | 2,535| 2,326| 2,071| 3,766| 2,284| 1,923| 1,621| 742  | 863  | 2,247| 1,821| 3,042| 3,755| 5,164| 34,160 |

*L* lineage; PFGE, pulsed-field gel electrophoresis; *SL*, sublineage.
**Appendix Figure.** Genetic maps of plasmids pR16.0676-90k (A) and pR16.0676-34k (B) in *Salmonella enterica* serovar Anatum strain R16.0676 and pConj125k, pConj83k and pConj58k (C) from transconjugants.