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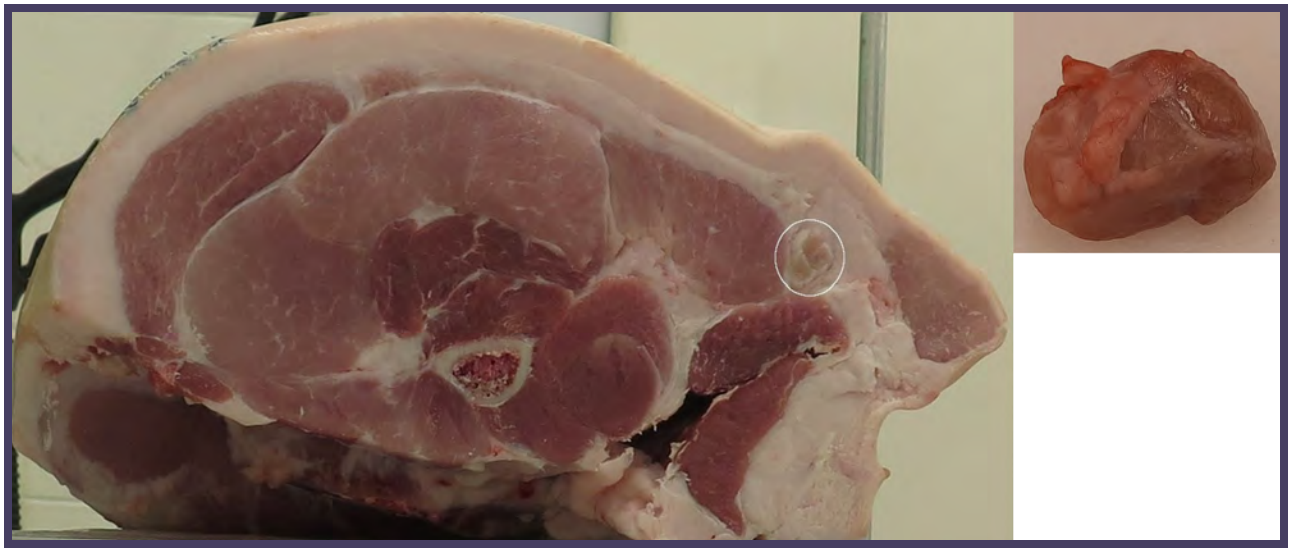

Salmonella Prevalence is Low in Deep Tissue Lymph Nodes of Hog Carcasses from a Pork Processing Plant in Alberta, Canada

ABSTRACT

Deep tissue lymph nodes (DTLNs) could be an important source of *Salmonella* in pork because carcass decontamination strategies have no effect on *Salmonella* cells that are deeply embedded and protected. The objective of this study was to determine the prevalence, concentration, and antimicrobial resistance of *Salmonella* in DTLNs in chilled hog carcasses as well as in ground pork. A total of 400 DTLNs were collected over a 10-month period from a commercial pork processing plant. *Salmonella* was detected in 2 (0.5%) of 400 DTLNs; *Salmonella* Uganda was detected in a DTLN from the belly and *Salmonella* Bovismorbificans in one DTLN from the shoulder. *Salmonella* Uganda was also detected in one ground pork sample. The three *Salmonella* isolates were susceptible to all antimicrobials tested, and no clinically significant antimicrobial resistance genes were detected in these genomes after sequencing. The prevalence of *Salmonella* in DTLNs in pork tissues intended for human consumption is very low and could be a minor source of contamination in the production of ground pork. These findings are important for the pork industry to assess the risks and benefits of removing DTLNs from pork cuts and trimmings.

INTRODUCTION

Salmonella, an important foodborne pathogen in Canada *(37)* and across the globe *(34)*, is frequently associated with pork *(38, 39)*. Decontamination strategies to remove bacteria on the surfaces of hog carcasses originating from the hide or other sources has led to a decrease in the prevalence of pathogens such as *Escherichia coli* O157 on carcasses and in ground pork *(39, 41)*. However, increasing attention is being paid to the presence of *Salmonella* in deep tissue lymph nodes (DTLNs), which are embedded in fat frequently used in the production of ground beef *(2, 7)* and ground pork *(11, 16, 19)*. Most or all of the lymph nodes located in fat tissues of beef and hog carcasses are not removed during fabrication and are ground with lean and fat trimmings to produce ground meat; thus, lymph nodes are a possible source of *Salmonella* contamination in ground meat *(24, 26)*.

A 2017 study reported that approximately 90% of hog carcasses were positive for *Salmonella* in two slaughter

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facilities (n = 100 per plant) in Alberta, Canada *(33)*. These researchers also noted that the percentage of *Salmonella*-positive carcasses was reduced to approximately 7% prior to blast chilling and that *Salmonella* was not detected on the surface of pork cuts (n = 100 per plant). Almost all carcasses in that study were positive for *Salmonella*; thus, it would be warranted to investigate the prevalence and concentration of *Salmonella* in nonvisceral DTLNs because these will not be eliminated during carcass processing. Several isolates in the study by Sanchez-Maldonado et al. *(33)* also displayed multidrug resistance, with five isolates resistant to five or more antibiotics, including those considered to be of very high importance in human medicine *(20, 33)*. Studies on the prevalence and concentration of *Salmonella* in DTLNs have not been reported in pork in Canada. The lymph nodes in hog carcasses have been mapped *(8)* because full removal of lymph nodes in specific pork cuts and trimmings can be required in certain markets. The objective of the study was to determine the prevalence, concentration, and antibiotic resistance profiles of *Salmonella* in ground pork and DTLNs from the belly, ham, shoulder, and salivary glands of hog carcasses at a pork processing plant over a 10-month period.

MATERIALS AND METHODS

Sample collection and processing

Samples were collected from belly, ham, shoulder, and salivary gland DTLNs (n = 100 each) from blast-chilled carcasses during fabrication at a pork processing plant in Alberta, Canada, from June 2016 through February 2017 (10 samples per tissue per visit). Ground pork samples were also collected during each visit (n = 100). At the time of sampling, the plant processed up to 8,500 hogs per day from multiple swine producers. The DTLNs were located and removed using the *Hog Carcass Lymph Node System Handbook* as a guide *(8)*. Grab samples of ground pork and individual DTLNs were aseptically placed into sterile sample bags and placed on ice for transport to the laboratory. Each DTLN was trimmed and surface sterilized by immersion in boiling water for 3 s, cooled on ice, weighed, minced into small pieces with a sterile scalpel, and placed into a sterile stomacher bag.

Minced DTLNs were stomached with 20 ml of sterile buffered peptone water (BPW) for 2 min and 8 ml of homogenate was incubated for 24 h at 35°C as a preenrichment step. The remaining 12 ml of the homogenate was stored at 4°C to allow samples that were positive for *Salmonella* to be enumerated by hydrophobic grid membrane filtration. To enhance detection of *Salmonella* among a large background microbiota in DTLNs, 1 ml of preenriched BPW was subjected to immunomagnetic separation (IMS) with a BeadRetriever (Invitrogen, Thermo Fisher Scientific, Waltham, MA) using anti-*Salmonella* magnetic beads (Invitrogen, Thermo Fisher Scientific) according to standard procedures prior to enrichment. For ground pork samples, a 25-g subsample was preenriched with 225 ml of BPW.

Detection, enumeration, isolation, and characterization of *Salmonella*

Samples from DTLNs and ground pork were enriched by transferring 1 ml of the preenriched BPW or pre-enriched BPW+IMS into 9 ml of tetrathionate broth (Oxoid, Nepean, ON, Canada). Simultaneously, 0.1 ml of the preenriched BPW was transferred into 10 ml of modified Rappaport Vassiliadis broth. Both inoculated broths were incubated at 42°C for 24 h. *Salmonella* isolates were recovered from presumptive positive enrichment broths according to Health Canada's *Compendium of Analytical Methods* (MFHPB-20) as described by Aslam et al. *(3)*. Briefly, 10 µl of presumptive positive enrichment broth was streaked onto bismuth sulphite agar (BD Difco, Fisher Scientific, Mississauga, ON, Canada), brilliant green sulfa agar (Oxoid), and xylose lysine desoxycholate agar (BD Difco) and incubated at 35°C for 48 h. Three agar plates with well-separated, presumptive *Salmonella* colonies from each sample were selected, and one colony from each was restreaked onto MacConkey agar (Oxoid) and incubated at 35°C for 24 h. Each presumptive *Salmonella* colony was screened biochemically on triple sugar iron, lysine iron, and urea agars (Oxoid) for 24 at 35°C. Final confirmation was carried out using PCR with primers targeting the internal transcribed spacer region *(13)* of *Salmonella*.

For enumeration of DTLN samples that were presumptive positive for *Salmonella* by enrichment, 250 µl of 0.2% Tween 80 (Sigma-Aldrich) was added to 12 ml of the original homogenate, mixed by inversion, and then incubated at room temperature for 5 min. A 10^{-2} dilution of the homogenate was then prepared in 0.1% peptone water, and the undiluted and 10^{-2} dilution were each filtered through hydrophobic grid membrane filter units (Neogen) according to standard procedures *(22)*. After they were incubated for 24 h at 35°C on xylose lysine desoxycholate agar plates, presumptive colonies were counted and confirmed.

Up to three *Salmonella* isolates from each original sample were selected and used for further characterization. Serotyping and phage typing were performed by the Reference Laboratory for Salmonellosis (Public Health Agency of Canada, Guelph, Ontario). Antimicrobial susceptibility testing using the Sensititre NARMS (National Antimicrobial Resistance Monitoring System) gram-negative CMV3AGPF plate (Trek Diagnostics, Independence, OH) and the detection of 15 different antibiotic resistance genes via PCR were carried out as described by Sanchez-Maldonado et al. *(33)*.

Whole genome sequencing of *Salmonella* isolates

Salmonella isolates were streaked from glycerol stocks onto bismuth sulphite agar and grown overnight at 35°C for 48 h. A black colony was selected, streaked onto MacConkey agar, and incubated for 24 h at 35°C; next, an off-white opaque colony was selected and inoculated into tryptic soy broth

and grown at 35°C for 24 h. DNA was then extracted from this culture using the DNeasy Blood and Tissue kit (Qiagen, Toronto, ON, Canada) as described by the manufacturer. The extracted DNA concentration was determined using the Qubit dsDNA HS assay kit (Thermo Fisher Scientific) as per manufacturer's instructions. The Illumina DNA Prep kit (Illumina Inc., San Diego, CA) was used for library preparation as per manufacturer's protocol with 500 ng of DNA used as input. Nextera DNA CD indexes (Illumina Inc.) were used to amplify and index the samples with a total of five PCR cycles. The average size of each library, after library cleanup, was determined to be approximately 600 bp using the Bioanalyzer High Sensitivity DNA Analysis kit (Agilent, Mississauga, ON, Canada), and the concentration of each library was assessed with the Qubit dsDNA HS assay kit. Each library was then diluted to 4 nM and pooled, as per manufacturer's instructions. Prior to loading, the pooled library was denatured and diluted to a final loading concentration of 10 pM according to the supplier's protocol, and denatured PhiX (1%) (Illumina Inc.) was added to the library. The libraries were sequenced on a MiSeq instrument using the MiSeq Reagent Kit v2 (300 cycles) (Illumina Inc.) as per manufacturer's instructions.

Analysis of *Salmonella* genomes

Reads with a quality score of less than 15 over a 4-bp sliding window, and less than 100 bp in length, were removed with fastp v. 0.23.2 *(12)*. The quality-filtered reads were then assembled using SPAdes v. 3.15.4 *(4)*, contigs shorter than 500 bp were removed, and the completeness and contamination of each assembly was assessed using CheckM v. 1.2.0 *(31)*. Assembly statistics were determined using QUAST v. 5.0.2 *(18)*, and the genome assemblies were confirmed as *Salmonella enterica* with the GTDB-toolkit v. 2.1.0 *(10)*. To compare the *Salmonella* isolates from the current study with other *Salmonella* isolates of similar origin, all *Salmonella* genome assemblies in GenBank from porcine lymph nodes were retrieved (n = 66; *Supplemental Table S1*). Prokka v. 1.14.6 *(35)* was then used to annotate all *Salmonella* genome assemblies, and the core genes of these assemblies were identified using Roary v. 3.13.0 *(30)* and were aligned with MAFFT v. 7.505 *(23)*. A maximum likelihood phylogenomic tree was inferred from this alignment using RAxML v. 8.2.12 *(36)* and was visualized with iTol v. 6 *(25)*. The serovar of each genome assembly was determined using Seqsero2 v. 1.2.1 *(40)*. The *Salmonella* genomes were also screened for antimicrobial resistance genes using the resistance gene identifier v. 5.2.1 with the comprehensive antibiotic resistance database v. 3.1.4 *(1)*. The genome assemblies and raw sequences are available under BioProject accession PRJNA871292.

RESULTS AND DISCUSSION

Overall, *Salmonella* was detected in only 2 (0.5%) of 400 DTLNs following enrichment: *Salmonella* Uganda and *Salmonella* Bovismorbificans were isolated from a shoulder and belly DTLN, respectively. Each positive sample was recovered on a separate sampling occasion, and *Salmonella* concentrations were below the limit of detection (2 CFU per lymph node) by the hydrophobic grid membrane filter method. These results strongly indicate that *Salmonella* prevalence is far lower in DTLNs in chilled carcasses than in mesenteric and tracheobronchial lymph nodes (13.4 to 34.0%) *(5, 17)*. *Salmonella* Uganda was isolated from one ground pork sample taken from the processing facility, also on a different sampling period. *Salmonella* Uganda was occasionally detected from carcasses in our previous study *(33)*, whereas *Salmonella* Bovismorbificans was not. *Salmonella* Bovismorbificans has also been previously reported to be present in porcine lymph nodes and carcasses at low prevalence *(27, 29)*. However, foodborne outbreaks caused by *Salmonella* Bovismorbificans have been associated with ground pork *(16)* and ham *(6)*, and outbreaks of *Salmonella* Uganda have been linked to ready-to-eat pork *(21)*.

All *Salmonella*-positive samples were positive with and without the IMS step. Although IMS is an extra step that adds time and cost to the detection method, it would be prudent to include IMS in future studies until stronger data is available to support either the need for or elimination of this step, given the lack of information on the concentration of *Salmonella* in nonvisceral DTLNs *(41)*. The three *Salmonella* isolates were susceptible to all antimicrobials tested, and none of the 15 antimicrobial resistance genes screened were detected. These findings agree with Harvey et al. *(19)*, who reported that the majority (>90%) of *Salmonella* isolates obtained from nonvisceral DTLNs were pansusceptible or resistant to only one antimicrobial. However, multidrug-resistant *Salmonella* isolates have been detected in mesenteric as well as other DTLN lymph nodes in swine *(14, 19, 32)*, and multidrug resistance has been reported in *Salmonella* Bovismorbificans *(9, 15)*.

The three *Salmonella* isolates recovered here were also sequenced and compared against other publicly available *Salmonella* genomes from porcine lymph nodes (n = 66; *Supplemental Table S1*). The two *Salmonella* Uganda isolates (GP-100A-1A; LS-21-G) clustered with another *Salmonella* Uganda isolate collected from a pig lymph node in the United States. *Salmonella* Uganda genomes appeared to be most closely related to the serovars I -:l,v:1,6, Geraldton, and London *(Fig. 1)*. There were no publicly available *Salmonella* Bovismorbificans genomes from pork lymph nodes to compare to strain LB-002-A from the current study; however, this isolate was most closely related to lymph node isolates belonging to the serovars I -:i:1,2, I 4,[5],12:i:-, and Typhimurium. The 69 *Salmonella* genomes compared shared 3,206 genes from a pan-genome of 12,814 genes. The aminoglycoside resistance gene *aac*(6′)-Iy was detected in all three isolates and was the only notable antimicrobial

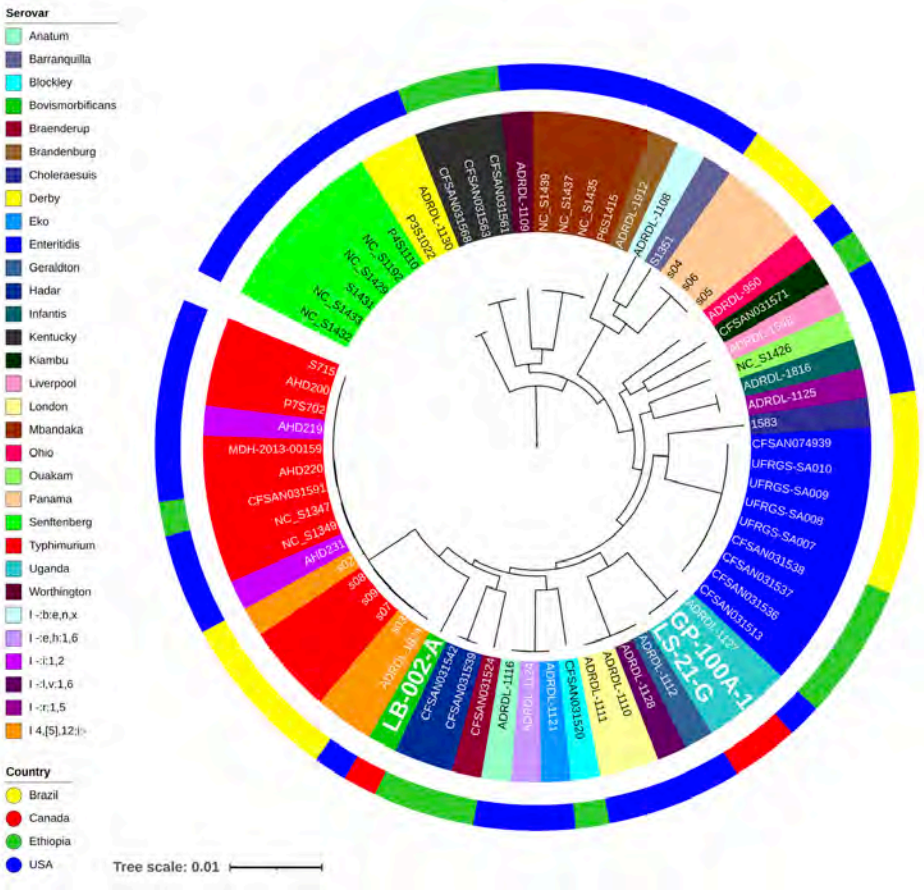

Figure 1. Phylogenomic tree of three *Salmonella* isolates (bold type) from the current study and all publicly available *Salmonella* genomes from pork lymph nodes (n = 66). Isolates are colored by serovar in the inner ring and by country of origin on the outer ring. Phylogeny was inferred from the alignment of 3,206 core genes using RAxML. Scale bar represents substitutions per nucleotide.

resistance gene found. However, this antimicrobial resistance gene is usually inactive in *Salmonella* strains because an upstream deletion is required for its activation *(28)*; this explains the phenotypic susceptibility to gentamicin and streptomycin observed here. Among the publicly available porcine lymph node isolates, 41 (62%) of 66 carried genes conferring resistance to two or more classes of antimicrobials.

The findings of this study suggest that the prevalence of *Salmonella* in DTLNs in porcine tissues intended for human consumption is very low and could be a minor source of contamination in the production of ground pork in Alberta. These findings are in agreement with Zhang et al. *(41)*, who used a quantitative microbial risk assessment to assess the contribution of DTLNs to the risk of salmonellosis from ground pork. Zhang et al. *(41)* indicated that the labor-intensive and time-consuming practice of complete removal of DTLNs during pork processing would be negligible in reducing foodborne illness compared to consumer behavior and other carcass decontamination measures during hog carcass processing. These findings are important for the pork industry to assess the costs and benefits of removing DTLN from hog carcasses and trimmings and for international trading partners.

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Supplemental TABLE S1. Publicly available *Salmonella* genomes from pork lymph nodes that were compared with the three *Salmonella* isolates from this study

Isolate ID	Serotype	Antimicrobial resistance genes	GenBank accession	BioProject
ADRDL-1116	Anatum	*aac(6′)-Iy*	GCA_007098425.1	PRJNA280335
S1351	Barranquilla	*aac(6′)-Iy*	GCA_005584275.1	PRJNA293224
CFSAN031520	Blockley	*aac(6′)-Iy, tet(A), aph(6)-Id, aph(3″)-Ib, aph(3′)-Ia, blaTEM-1*	GCA_010542145.1	PRJNA275961
CFSAN031524	Braenderup	*sul1, aac(6′)-Iaa, aadA, sul2, aph(6)-Id, aph(3″)-Ib, blaTEM-1*	GCA_010765935.1	PRJNA275961
ADRDL-1912	Brandenburg	*sul1, aac(6′)-Iaa, aadA, aac(3)-VIa, sul2, tet(A), aph(6)-Id, aph(3″)-Ib*	GCA_005678815.1	PRJNA280335
1583	Choleraesuis	*tet(B), aac(6′)-Iaa, sul2, aph(6)-Id, aph(3″)-Ib, aac(3)-IV, aph(4)-Ia, blaTEM-1*	GCA_018359665.1	PRJNA280335
P3S1022	Derby	*aac(6′)-Iy, sul1, tet(A), ant(3″)-IIa*	GCA_005903325.1	PRJNA293224
ADRDL-1130	Derby	*aac(6′)-Iy, tet(C)*	GCA_007098345.1	PRJNA280335
ADRDL-1121	Eko	*aac(6′)-Iy*	GCA_007098465.1	PRJNA280335
CFSAN031513	Enteritidis	*aac(6′)-Iy*	GCA_007763755.1	PRJNA275961
CFSAN031536	Enteritidis	*aac(6′)-Iy*	GCA_008913785.1	PRJNA275961
CFSAN031537	Enteritidis	*aac(6′)-Iy*	GCA_008913245.1	PRJNA275961
CFSAN031538	Enteritidis	*aac(6′)-Iy*	GCA_008914205.1	PRJNA275961
CFSAN074939	Enteritidis	*aac(6′)-Iy*	GCA_006076935.1	PRJNA275961
UFRGS-SA007	Enteritidis	*aac(6′)-Iy*	GCA_006001745.1	PRJNA183850
UFRGS-SA008	Enteritidis	*aac(6′)-Iy*	GCA_006144495.1	PRJNA183850
UFRGS-SA009	Enteritidis	*aac(6′)-Iy, aph(6)-Id, aph(3″)-Ib, aac(3)-IV, aph(4)-Ia*	GCA_006076895.1	PRJNA183850

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Supplemental TABLE S1. Publicly available *Salmonella* genomes from pork lymph nodes that were compared with the three *Salmonella* isolates from this study (cont.)

Isolate ID	Serotype	Antimicrobial resistance genes	GenBank accession	BioProject
UFRGS-SA010	Enteritidis	*aac(6′)-Iy, aph(6)-Id, aph(3″)-Ib, aac(3)-IV, aph(4)-Ia, blaCARB-3, aadA3, ant(3″)-IIa*	GCA_006001805.1	PRJNA183850
ADRDL-1112	Geraldton	*aac(6′)-Iaa, tet(C)*	GCA_007098435.1	PRJNA280335
CFSAN031539	Hadar	*aac(6′)-Iy, tet(A), aph(6)-Id, aph(3″)-Ib*	GCA_010412175.1	PRJNA275961
CFSAN031542	Hadar	*aac(6′)-Iy, tet(A), aph(6)-Id, aph(3″)-Ib*	GCA_010734435.1	PRJNA275961
ADRDL-1108	I -:b:e,n,x	*aac(6′)-Iy*	GCA_007098385.1	PRJNA280335
ADRDL-1124	I -:e,h:1,6	*aac(6′)-Iy*	GCA_007093645.1	PRJNA280335
AHD231	I -:i:1,2	*sul1, aac(6′)-Iaa, aadA, tet(A), aph(6)-Id, aph(3″)-Ib*	GCA_006000465.1	PRJNA280335
AHD219	I -:i:1,2	*sul1, aac(6′)-Iaa, tet(D), floR*	GCA_006075515.1	PRJNA280335
ADRDL-1128	I -:l,v:1,6	*aac(6′)-Iaa*	GCA_007098025.1	PRJNA280335
ADRDL-1125	I -:r:1,5	*aac(6′)-Iy*	GCA_007093705.1	PRJNA280335
s02	I 4,[5],12:i:-	*aadA2, tet(B), aac(6′)-Iaa, aadA, sul2, aph(6)-Id, aph(3″)-Ib, cmlA1, blaTEM-1, sul3*	GCA_012971885.1	PRJNA527724
s03	I 4,[5],12:i:-	*sul1, aac(6′)-Iaa, aadA, tet(A), aph(6)-Id, aph(3″)-Ib, blaTEM-1, aac(3)-IIe*	GCA_012971825.1	PRJNA527724
ADRDL-1824	I 4,[5],12:i:-	*tet(B), aac(6′)-Iaa, sul2, aph(6)-Id, aph(3″)-Ib, blaTEM-1*	GCA_010584285.1	PRJNA280335
ADRDL-1816	Infantis	*aac(6′)-Iy, tet(B)*	GCA_011133275.1	PRJNA280335
CFSAN031568	Kentucky	*sul1, aac(6′)-Iaa, tet(A), aac(3)-Id, aadA7, blaTEM-82*	GCA_011103755.1	PRJNA275961
CFSAN031561	Kentucky	*sul1, aac(6′)-Iaa, tet(A), aph(6)-Id, aph(3″)-Ib, blaTEM-1, aac(3)-Id, aadA7*	GCA_011542475.1	PRJNA275961
CFSAN031563	Kentucky	*sul1, aac(6′)-Iaa, tet(A), aph(6)-Id, aph(3″)-Ib, blaTEM-1, aac(3)-Id, aadA7*	GCA_011564425.1	PRJNA275961
CFSAN031571	Kiambu	*aac(6′)-Iy. sul2, tet(A), aph(6)-Id, aph(3″)-Ib, blaTEM-1*	GCA_011421095.1	PRJNA275961
ADRDL-1548	Liverpool	*aac(6′)-Iy*	GCA_010505995.1	PRJNA280335
ADRDL-1110	London	*aac(6′)-Iaa*	GCA_007098405.1	PRJNA280335
ADRDL-1111	London	*aac(6′)-Iaa*	GCA_007099305.1	PRJNA280335
NC_S1435	Mbandaka	*sul1, aadA2, aac(6′)-Iaa, tet(A)*	GCA_009477885.1	PRJNA293224
NC_S1437	Mbandaka	*sul1, aadA2, aac(6′)-Iaa, tet(A)*	GCA_009499735.1	PRJNA293224
NC_S1439	Mbandaka	*sul1, aadA2, aac(6′)-Iaa, tet(A)*	GCA_009499695.1	PRJNA293224
P6S1415	Mbandaka	*sul1, aadA2, aac(6′)-Iaa, tet(A)*	GCA_005904185.1	PRJNA293224
ADRDL-950	Ohio	*aac(6′)-Iy*	GCA_007098005.1	PRJNA280335
NC_S1426	Ouakam	*aac(6′)-Iy*	GCA_010652565.1	PRJNA293224
s04	Panama	*tet(B), aac(6′)-Iaa, floR, aadA, sul2, blaTEM-1, sat-2*	GCA_012912065.1	PRJNA527724
s05	Panama	*tet(B), aac(6′)-Iaa, floR, aadA, sul2, blaTEM-1, sat-2*	GCA_012912085.1	PRJNA527724
s06	Panama	*tet(B), aac(6′)-Iaa, floR, aadA, sul2, blaTEM-1, sat-2*	GCA_012912035.1	PRJNA527724

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Supplemental TABLE S1. Publicly available *Salmonella* genomes from pork lymph nodes that were compared with the three *Salmonella* isolates from this study (cont.)

Isolate ID	Serotype	Antimicrobial resistance genes	GenBank accession	BioProject
NC_S1192	Senftenberg	*aac(6′)-Iy*	GCA_009471365.1	PRJNA293224
NC_S1429	Senftenberg	*aac(6′)-Iy*	GCA_009499945.1	PRJNA293224
P4S1110	Senftenberg	*aac(6′)-Iy*	GCA_005903165.1	PRJNA293224
NC_S1432	Senftenberg	*aac(6′)-Iy, sul1, aadA2, ant(2″)-Ia, mcr-9.1, tet(B)*	GCA_007765435.1	PRJNA293224
NC_S1433	Senftenberg	*aac(6′)-Iy, sul1, aadA2, ant(2″)-Ia, mcr-9.1, tet(B)*	GCA_007819265.1	PRJNA293224
S1431	Senftenberg	*aac(6′)-Iy, sul1, aadA2, ant(2″)-Ia, mcr-9.1, tet(B)*	GCA_005490325.1	PRJNA293224
s09	Typhimurium	*aac(6′)-Iaa, aadA3, tet(A), aadA9, aph(3′)-Ia, aadA15, cmlA1*	GCA_010119515.1	PRJNA527724
s08	Typhimurium	*aac(6′)-Iaa, tet(A), aadA9, aph(3′)-Ia, aadA15, cmlA1, aadA12*	GCA_010119595.1	PRJNA527724
s07	Typhimurium	*aac(6′)-Iaa, tet(A), aph(3″)-Ib*	GCA_010119535.1	PRJNA527724
NC_S1347	Typhimurium	*sul1, aac(6′)-Iaa, aadA, tet(A), aph(6)-Id, aph(3″)-Ib*	GCA_010628185.1	PRJNA293224
NC_S1349	Typhimurium	*sul1, aac(6′)-Iaa, aadA, tet(A), aph(6)-Id, aph(3″)-Ib*	GCA_010402085.1	PRJNA293224
CFSAN031591	Typhimurium	*sul1, aac(6′)-Iaa, tet(D), floR, blaCARB-3, aadA3*	GCA_008865065.1	PRJNA275961
S715	Typhimurium	*sul1, aac(6′)-Iaa, tet(D), floR, blaCARB-3, aadA3*	GCA_005660255.1	PRJNA293224
AHD200	Typhimurium	*sul1, aac(6′)-Iaa, tet(D), floR, blaCARB-3, aadA3, ant(3″)-IIa*	GCA_005999685.1	PRJNA280335
AHD220	Typhimurium	*sul1, aac(6′)-Iaa, tet(D), floR, blaCARB-3, aadA3, ant(3″)-IIa*	GCA_006144515.1	PRJNA280335
P7S702	Typhimurium	*sul1, aac(6′)-Iaa, tet(D), floR, blaCARB-3, aadA3, ant(3″)-IIa*	GCA_005904065.1	PRJNA293224
MDH-2013-00159	Typhimurium	*sul1, aac(6′)-Iaa, tet(D), floR, blaCARB-3, aadA3, tet(A), ant(3″)-IIa, aph(3′)-Ia, aac(6′)-Ib7, tet(M)*	GCA_011083885.1	PRJNA215333
ADRDL-1127	Uganda	*aac(6′)-Iy*	GCA_007098205.1	PRJNA280335
ADRDL-1109	Worthington	*aac(6′)-Iaa*	GCA_007099475.1	PRJNA280335