Supplementary Tables S1–S4

Miller et al. 2020. Emergence of a novel *Salmonella enterica* serotype Reading clonal group is linked to its expansion in commercial turkey production, resulting in unanticipated human illness in North America. mSphere 5:e00056-20. https://doi.org/10.1128/mSphere.00056-20.

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Table S1. Comparison of mean core SNP differences between unique core SNP profiles within and between phylogenetic clades.

	SNP difference		
Clade comparison	**Mean ± SD**	**Minimum**	**Maximum**
All profiles[a]			
Overall	1,903.08 ± 3,288.69	1	9,287
Clade 1	7.72 ± 5.61	1	71
Clade 2	59.23 ± 44.10	1	208
Clade 3	32.87 ± 16.84	1	63
Clade 1 vs. Clade 2	1,638.72 ± 8.49	1,625	1,711
Clade 1 vs. Clade 3	8,165.04 ± 10.91	8,147	8,227
Clade 2 vs. Clade 3	9,246.30 ± 12.72	9,223	9,287
Random profile subset[b]			
Overall	4,282.82 ± 4,047.42	1	9,287
Clade 1	8.52 ± 6.15	2	30
Clade 2	59.23 ± 44.10	1	208
Clade 3	32.64 ± 16.43	1	63
Clade 1 vs. Clade 2	1,639.30 ± 8.72	1,626	1,682
Clade 1 vs. Clade 3	8,165.14 ± 11.30	8,148	8,198
Clade 2 vs. Clade 3	9,245.77 ± 12.95	9,223	9,287

[a]The number of unique core SNP profiles were as follows: n = 430 for clade 1, n = 37 for clade 2, and n = 62 for clade 3.
[b]For the random profile subset, there were 37 unique core SNP profiles from each clade.

Table S2. Results from 2x2 Fisher's exact tests for the pairwise comparisons of the IncQ1 replicon and antimicrobial resistance genes *sul2*, *tet*(A), and *strAB*.

Comparison	Odds ratio	95% CI	*P*-value	Adjusted *P*-value[a]
sul2 vs. *tet*(A)	1,912.24	637.17 – Inf	1.56E-118	3.89E-118
sul2 vs. *strA*	1,187.48	343.01 – Inf	3.37E-106	5.61E-106
sul2 vs. *strB*	587.26	227.47 – Inf	3.34E-102	4.18E-102
sul2 vs. IncQ1	14,888.05	1,877.26 – Inf	8.76E-128	4.38E-127
tet(A) vs. *strA*	306.87	143.15 – Inf	1.88E-96	2.09E-96
tet(A) vs. *strB*	236.06	117.94 – Inf	3.03E-93	3.03E-93
tet(A) vs. IncQ1	9,194.06	1,252.19 – Inf	1.32E-123	4.39E-123
strA vs. *strB*	Inf	4,311.58 – Inf	5.71E-143	5.71E-142
strA vs. IncQ1	Inf	692.35 – Inf	6.36E-109	1.27E-108
strB vs. IncQ1	1,121.38	324.72 – Inf	3.73E-104	5.33E-104
$bla_{\text{TEM-1C}}$ vs. Col440II-like	4.50E+15	4,311.58 – Inf	5.68E-152	1.71E-151
$bla_{\text{TEM-1C}}$ vs. ColRNAI-like	Inf	303.19 – Inf	5.00E-96	5.00E-96
Col440II-like vs. ColRNAI-like	Inf	303.19 – Inf	5.00E-96	5.00E-96

[a]*P*-values adjusted using the Benjamini-Hochberg procedure.

Table S3. Results from the 2x2 Fisher's exact tests reporting which plasmid replicon markers were significantly associated with either the contemporary subclade (*n* = 201) or historical subclade (*n* = 65).

Comparison	Odds ratio	*P*-value	Adjusted *P*-value[a]
Col440II-like	0	1.19E-01	2.52E-01
ColRNAI-like	8.26	3.22E-11	5.48E-10
Col156	0	1.56E-02	3.79E-02
Col(BS512)	0	1.00E+00	1.00E+00
Col(MG828)	0	1.00E+00	1.00E+00
ColpVC	0	4.03E-05	2.28E-04
ColRNAI	0	3.41E-01	4.83E-01
IncFIB(K)	0	1.70E-03	4.81E-03
IncFIB(S)	0	1.00E+00	1.00E+00
IncFII	0	1.00E+00	1.00E+00
IncHI2	Inf	2.44E-01	3.89E-01
IncHI2A	Inf	2.44E-01	3.89E-01
IncI1-alpha	7.06	4.39E-04	1.49E-03
IncI2	3.14	2.51E-01	3.89E-01
IncQ1	0	5.14E-06	4.36E-05
IncX1	Inf	1.78E-04	7.55E-04
IncX4(FN543504)	0	1.00E+00	1.00E+00

[a]*P*-values adjusted using the Benjamini-Hochberg procedure.

Table S4. Results from the 2x2 Fisher's exact tests reporting which plasmid replicon markers were significantly associated with either the emergent subclade (*n* = 295) or contemporary subclade (*n* = 201).

Comparison	Odds ratio	*P*-value	Adjusted *P*-value[a]
Col440II-like	33.63	3.99E-43	6.78E-42
ColRNAI-like	12.29	2.01E-32	1.70E-31
Col156	0.66	2.79E-01	5.93E-01
Col8282	Inf	1.00E+00	1.00E+00
Col(BS512)	0	1.64E-01	3.98E-01
Col(MG828)	0	4.05E-01	6.26E-01
ColpVC	0	1.00E+00	1.00E+00
ColRNAI	1.26	8.03E-01	1.00E+00
IncFIB(K)	0	4.31E-10	2.44E-09
IncFIB(S)	0	4.05E-01	6.26E-01
IncFII	0	4.05E-01	6.26E-01
IncI1-alpha	0	1.06E-02	3.61E-02
IncI2	0	1.64E-01	3.98E-01
IncI2-delta	Inf	1.00E+00	1.00E+00
IncQ1	1.94	2.19E-03	9.29E-03
IncX1	Inf	1.00E+00	1.00E+00
IncX4(FN543504)	0.34	5.69E-01	8.06E-01

[a]*P*-values adjusted using the Benjamini-Hochberg procedure