Ecology of Salmonella

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Salmonella evolution

• Evolved over the past 12—160 million years! (split between E. coli and Salmonella)

• Can infect >100 different species including mammals, birds, reptiles, and insects

• Complex nomenclature:
  • Two major species: S. enterica and S. bongori
  • Seven subspecies, including enterica (I) accounting for >99% of human infection
Salmonella evolution

MINIREVIEW

Evolution of Host Adaptation in Salmonella enterica

ANDREAS J. BAUMLER,1* RENÉE M. TSOLIS,2 THOMAS A. FICHIT,2 AND L. GARRY ADAMS2

Department of Medical Microbiology and Immunology, College of Medicine,1 and Department of Veterinary Pathobiology, College of Veterinary Medicine,2 Texas A&M University, College Station, Texas 77843-4467

REVIEW

A genomic overview of the population structure of Salmonella

Nabil-Fareed Alikhan, Zhemin Zhou, Martin J. Sergeant, Mark Achtman*

Warwick Medical School, University of Warwick, Coventry, United Kingdom
Salmonella evolution
Tradeoffs for host range versus host adaptation
Evolution of *Salmonella* within Hosts

Jennifer R. Tanner and Robert A. Kingsley

**Infection with a typical gastroenteritis strain of *Salmonella* Enteritidis**

**Invasion of epithelial cells (EC) of the intestinal mucosa initiates infection**

**Mutation in mutS results in hypermutator phenotype and diversification**

**Bloodstream**

**Dissemination to systemic sites due to deficient immune response**

**Hypermuation results in genome degradation and selection for beneficial mutations**

**Attenuated intestinal virulence**

**Adaptation to disseminated disease and occult bacteraemia**

**Loss of transmissibility**
Salmonella typing

- Kauffmann-White serotyping scheme give the serovars their names
  - LPS (O) antigen
  - H1 and H2 flagellar antigens
  - Capsular antigen
- O antigen divides into 6 serogroups: A, B, 1, C2, D, E
- >2,300 serovars
Factors involved in host range

• Colonization
  • SPI-3, SPI-4
  • Numerous fimbrial operons (agf, sef, pil, lpf, pef)

• Persistence
  • LPS

• Invasion
  • Exotoxins and enterotoxins
  • SPI-1, SPI-5

• Intracellular survival
  • SPI-2 through SPI-6
  • Virulence plasmid (spv)

• Phase variation in flagella expression
Plasmids

• Often ignored in outbreak investigations
• They provide critical hints about host source and host range
• They can encode for multidrug resistance
• They can encode for enhanced virulence
• They can enable enhanced fitness
Plasmids – virulence plasmid

The role of the *spv* genes in *Salmonella* pathogenesis

Donald G. Quiney* and Joshua Fierer†

*1 Department of Medicine, University of California San Diego School of Medicine, La Jolla, CA, USA
† Veterans Administration Medical Center, La Jolla, CA, USA
Salmonella Pathogenicity and Host Adaptation in Chicken-Associated Serovars

Steven L. Foley, Timothy J. Johnson, Steven C. Ricke, Rajesh Nayak, Jessica Danzeisen
Division of Microbiology, National Center for Toxicological Research, U.S. Food and Drug Administration, Jefferson, Arkansas, USA; Department of Veterinary and Biomedical Sciences, University of Minnesota, Saint Paul, Minnesota, USA; Center for Food Safety and Department of Food Science, University of Arkansas, Fayetteville, Arkansas, USA
Plasmids – IncX and Col plasmids

RESEARCH ARTICLE
Hotspot mutations and ColE1 plasmids contribute to the fitness of Salmonella Heidelberg in poultry litter

Adelumola Ogedeine1*, Kimberly Cook1*, Alex Oriek2*, Greg Zock1*, Kyler Herrington2, Nelson Cox3, Jodie Plumlee Lawrence1, Carolina Hall1*
Plasmids – ColV plasmid
Plasmids – ColV plasmid

Horizontal Gene Transfer of a ColV Plasmid Has Resulted in a Dominant Avian Clonal Type of Salmonella enterica Serovar Kentucky

Timothy J. Johnson¹, Jessica L. Thorsness¹, Cole P. Anderson¹, Aaron M. Lynne¹, Steven L. Foley³, Jing Han³, W. Florian Fricke⁵, Patrick F. McDermott⁶, David G. White⁷, Mahesh Khatri¹, Adam L. Stell¹, Cristian Flores¹, Randall S. Singer¹
Plasmids – IncA/C plasmid

Comparative Sequence Analysis of Multidrug-Resistant IncA/C Plasmids from Salmonella enterica

Marta Hoffmann1,2, James B. Pettengill1, Nacio Gonzalez-Escalona2, John Miller1,3, Sherry L. Ayers1, Shachua Zhao1, Marc W. Alfar1, Patrick F. McDermott1, Eric W. Brown1 and Steven R. Mount1
## Plasmids – IncA/C plasmid

<table>
<thead>
<tr>
<th></th>
<th><strong>S. Kentucky</strong></th>
<th><strong>S. Newport</strong></th>
<th><strong>S. Typhimurium</strong></th>
<th><strong>S. Agona</strong></th>
<th><strong>S. Heidelberg</strong></th>
<th><strong>S. Infantis</strong></th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Resistance Phenotype</strong></td>
<td>AMC, AMP, FOX, AXO, CHL, GEN, KAN, STR, FIS, TET, TIO</td>
<td>AMC, AMP, FOX, AXO, CEP, CHL, STR, FIS, TET, TIO</td>
<td>AMC, AMP, FOX, AXO, CEP, CHL, KAN, NAL, STR, FIS, TET, TIO</td>
<td>AMC, AMP, FOX, AXO, CHL, STR, FIS, TET, TIO</td>
<td>AMC, AMP, FOX, AXO, CHL, GEN, KAN, STR, FIS, TET, TIO</td>
<td>AMC, AMP, FOX, AXO, CHL, GEN, KAN, STR, FIS, TET, TIO</td>
</tr>
<tr>
<td><strong>Beta-Lactams</strong></td>
<td>bla&lt;sub&gt;emy&lt;/sub&gt;–2, bla&lt;sub&gt;tem&lt;/sub&gt;–1</td>
<td>bla&lt;sub&gt;emy&lt;/sub&gt;–2&lt;sup&gt;*&lt;/sup&gt;</td>
<td>bla&lt;sub&gt;emy&lt;/sub&gt;–2&lt;sup&gt;*&lt;/sup&gt;</td>
<td>bla&lt;sub&gt;emy&lt;/sub&gt;–2</td>
<td>bla&lt;sub&gt;emy&lt;/sub&gt;–2&lt;sup&gt;*&lt;/sup&gt;, bla&lt;sub&gt;tem&lt;/sub&gt;–1&lt;sup&gt;†&lt;/sup&gt;</td>
<td>bla&lt;sub&gt;emy&lt;/sub&gt;–2&lt;sup&gt;*&lt;/sup&gt;, bla&lt;sub&gt;tem&lt;/sub&gt;–1&lt;sup&gt;†&lt;/sup&gt;</td>
</tr>
<tr>
<td><strong>Aminoglycosides</strong></td>
<td>strA, strB, aadB&lt;sup&gt;a&lt;/sup&gt;, aph(3)&lt;sup&gt;−&lt;/sup&gt;–la</td>
<td>strA, strB, aadB</td>
<td>strA, strB, aadB&lt;sup&gt;a&lt;/sup&gt;</td>
<td>strA, strB</td>
<td>strA, strB, aadA1, aadB, aac(3)&lt;sup&gt;−&lt;/sup&gt;–VI, aac(3)&lt;sup&gt;−&lt;/sup&gt;–la&lt;sup&gt;a&lt;/sup&gt;</td>
<td>strA, strB, aadA1, aac(3)&lt;sup&gt;−&lt;/sup&gt;–VI</td>
</tr>
<tr>
<td><strong>Tetracyclines</strong></td>
<td>tetR(A), tetA</td>
<td>tetR(A), tetA</td>
<td>tetR(A), tetA&lt;sup&gt;a&lt;/sup&gt;</td>
<td>tetR(A), tetA</td>
<td>tetR(A), tetA</td>
<td>tetR(A), tetA</td>
</tr>
<tr>
<td><strong>Chloramphenicols</strong></td>
<td>floR, cmA&lt;sup&gt;a&lt;/sup&gt;</td>
<td>floR</td>
<td>floR, cmA</td>
<td>floR</td>
<td>floR, cmA</td>
<td>floR</td>
</tr>
<tr>
<td><strong>Folate synthesis inhibitors</strong></td>
<td>sul1, sul2&lt;sup&gt;a&lt;/sup&gt;</td>
<td>sul1, sul2&lt;sup&gt;a&lt;/sup&gt;</td>
<td>sul1, sul2&lt;sup&gt;a&lt;/sup&gt;</td>
<td>sul1&lt;sup&gt;a&lt;/sup&gt;, sul2</td>
<td>sul1&lt;sup&gt;a&lt;/sup&gt;, sul2&lt;sup&gt;a&lt;/sup&gt;</td>
<td>sul1&lt;sup&gt;a&lt;/sup&gt;, sul2</td>
</tr>
<tr>
<td><strong>Quaternary ammonium compounds</strong></td>
<td>quacE, sugE&lt;sup&gt;a&lt;/sup&gt;</td>
<td>quacE, sugE&lt;sup&gt;a&lt;/sup&gt;</td>
<td>quacE, sugE&lt;sup&gt;a&lt;/sup&gt;</td>
<td>sugE</td>
<td>quacE&lt;sup&gt;a&lt;/sup&gt;, sugE&lt;sup&gt;a&lt;/sup&gt;</td>
<td>quacE&lt;sup&gt;a&lt;/sup&gt;, sugE&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
<tr>
<td><strong>Mercury ions</strong></td>
<td>merA&lt;sup&gt;a&lt;/sup&gt;, merB&lt;sup&gt;a&lt;/sup&gt;, merC&lt;sup&gt;a&lt;/sup&gt;, merD&lt;sup&gt;a&lt;/sup&gt;, merE&lt;sup&gt;a&lt;/sup&gt;, merP, merT, merR&lt;sup&gt;a&lt;/sup&gt;</td>
<td>merA&lt;sup&gt;a&lt;/sup&gt;, merB&lt;sup&gt;a&lt;/sup&gt;, merC&lt;sup&gt;a&lt;/sup&gt;, merD&lt;sup&gt;a&lt;/sup&gt;, merE&lt;sup&gt;a&lt;/sup&gt;, merP&lt;sup&gt;a&lt;/sup&gt;, merT&lt;sup&gt;a&lt;/sup&gt;, merR&lt;sup&gt;a&lt;/sup&gt;</td>
<td>merA&lt;sup&gt;a&lt;/sup&gt;, merB&lt;sup&gt;a&lt;/sup&gt;, merC&lt;sup&gt;a&lt;/sup&gt;, merD&lt;sup&gt;a&lt;/sup&gt;, merE&lt;sup&gt;a&lt;/sup&gt;, merP&lt;sup&gt;a&lt;/sup&gt;, merT&lt;sup&gt;a&lt;/sup&gt;, merR&lt;sup&gt;a&lt;/sup&gt;</td>
<td>merA&lt;sup&gt;a&lt;/sup&gt;, merB&lt;sup&gt;a&lt;/sup&gt;, merC&lt;sup&gt;a&lt;/sup&gt;, merD&lt;sup&gt;a&lt;/sup&gt;, merE&lt;sup&gt;a&lt;/sup&gt;, merP&lt;sup&gt;a&lt;/sup&gt;, merT&lt;sup&gt;a&lt;/sup&gt;, merR&lt;sup&gt;a&lt;/sup&gt;</td>
<td>merA&lt;sup&gt;a&lt;/sup&gt;, merB&lt;sup&gt;a&lt;/sup&gt;, merC&lt;sup&gt;a&lt;/sup&gt;, merD&lt;sup&gt;a&lt;/sup&gt;, merE&lt;sup&gt;a&lt;/sup&gt;, merP&lt;sup&gt;a&lt;/sup&gt;, merT&lt;sup&gt;a&lt;/sup&gt;, merR&lt;sup&gt;a&lt;/sup&gt;</td>
<td>merA&lt;sup&gt;a&lt;/sup&gt;, merB&lt;sup&gt;a&lt;/sup&gt;, merC&lt;sup&gt;a&lt;/sup&gt;, merD&lt;sup&gt;a&lt;/sup&gt;, merE&lt;sup&gt;a&lt;/sup&gt;, merP&lt;sup&gt;a&lt;/sup&gt;, merT&lt;sup&gt;a&lt;/sup&gt;, merR&lt;sup&gt;a&lt;/sup&gt;</td>
</tr>
</tbody>
</table>

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**Comparative Sequence Analysis of Multidrug-Resistant IncA/C Plasmids from Salmonella enterica**  
Marie Hoffmann<sup>1,2</sup>, James B. Pettingill<sup>3</sup>, Necol Gonzalez-Escalona<sup>4</sup>, John Miller<sup>1,2</sup>, Sherry L. Ayers<sup>5</sup>, Shaohua Zhao<sup>6</sup>, Marc W. Allard<sup>1</sup>, Patrick F. McDermott<sup>1</sup>, Eric W. Brown<sup>1</sup> and Shawn R. Munday<sup>1</sup>
Restricted versus non-restricted host range

- Those dominating human infection tend to have broad host range
  - Typhimurium, Enteritidis, Newport, Heidelberg
- Others have restricted host range
  - Typhi, Paratyphi, Gallinarum, Pullorum, Choleraesuis, Dublin
- When spillover of restricted serovars occurs, they tend to be more invasive
- Most of the host-adapted serovars have tendency to accumulate pseudogenes
<table>
<thead>
<tr>
<th>Host species</th>
<th>Disease</th>
<th>S. enterica subspecies I serotype(s) most frequently encountered</th>
<th>Most susceptible age groups</th>
<th>Typical symptoms or sign(s) of disease</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>Humans</td>
<td>Salmonella enteritis</td>
<td>Typhimurium, Enteritidis</td>
<td>Children (&lt;4 yr)</td>
<td>Diarrhea, dysentery, fever</td>
<td>78</td>
</tr>
<tr>
<td></td>
<td>Typhoid fever</td>
<td>Typhi&lt;sup&gt;c&lt;/sup&gt;</td>
<td>Children and adults</td>
<td>Septicemia, fever&lt;sup&gt;a&lt;/sup&gt;</td>
<td>78</td>
</tr>
<tr>
<td></td>
<td>Paratyphoid fever</td>
<td>Sendai; Paratyphi A, B, and C&lt;sup&gt;c&lt;/sup&gt;</td>
<td>Children and adults</td>
<td>Septicemia, fever&lt;sup&gt;a&lt;/sup&gt;</td>
<td>78</td>
</tr>
<tr>
<td>Cattle</td>
<td>Salmonellosis</td>
<td>Typhimurium</td>
<td>Calves (&lt;8 wk)</td>
<td>Diarrhea, dysentery, septicemia, fever</td>
<td>104</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Dublin</td>
<td>Calves and adult cattle</td>
<td>Diarrhea, dysentery, septicemia, abortion, fever</td>
<td>99, 104</td>
</tr>
<tr>
<td>Poultry</td>
<td>Pullorum disease</td>
<td>Pullorum&lt;sup&gt;e,d&lt;/sup&gt;</td>
<td>Growing stock and adults</td>
<td>Diarrhea, septicemia</td>
<td>27</td>
</tr>
<tr>
<td></td>
<td>Fowl typhoid</td>
<td>Gallinarum&lt;sup&gt;e,d&lt;/sup&gt;</td>
<td>Growing stock and adults</td>
<td>Diarrhea, comb discoloration, septicemia</td>
<td>27</td>
</tr>
<tr>
<td></td>
<td>Avian paratyphoid</td>
<td>Enteritidis, Typhimurium</td>
<td>Newly hatched birds</td>
<td>Diarrhea, septicemia</td>
<td>27</td>
</tr>
<tr>
<td>Sheep</td>
<td>Salmonellosis</td>
<td>Abortusovis&lt;sup&gt;c&lt;/sup&gt;</td>
<td>Adult sheep</td>
<td>Septicemia, abortion, vaginal discharge</td>
<td>90</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td>Lambs</td>
<td>Diarrhea, dysentery, septicemia</td>
<td>90</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Typhimurium</td>
<td>Lambs</td>
<td>Diarrhea, dysentery, septicemia</td>
<td>90</td>
</tr>
<tr>
<td>Pigs</td>
<td>Pig paratyphoid</td>
<td>Choleraesuis&lt;sup&gt;e&lt;/sup&gt;</td>
<td>Weaned and adult pigs</td>
<td>Skin discoloration, septicemia, fever&lt;sup&gt;b&lt;/sup&gt;</td>
<td>106</td>
</tr>
<tr>
<td></td>
<td>Salmonellosis</td>
<td>Typhimurium</td>
<td>Weaned pigs (&lt;4 mo)</td>
<td>Diarrhea</td>
<td>106</td>
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<td></td>
<td>Chronic paratyphoid</td>
<td>Typhisuis</td>
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<td>Intermittent diarrhea</td>
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<tr>
<td>Horses</td>
<td>Salmonellosis</td>
<td>Abortusequii&lt;sup&gt;c&lt;/sup&gt;</td>
<td>Adult horses</td>
<td>Septicemia, abortion</td>
<td>110</td>
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<tr>
<td></td>
<td></td>
<td>Typhimurium</td>
<td>Foals</td>
<td>Diarrhea, septicemia</td>
<td>110</td>
</tr>
<tr>
<td>Wild rodents</td>
<td>Murine typhoid</td>
<td>Typhimurium, Enteritidis</td>
<td>Foals</td>
<td>Diarrhea, septicemia</td>
<td>110</td>
</tr>
</tbody>
</table>

**MINIREVIEW**

Evolution of Host Adaptation in *Salmonella enterica*

ANDREAS J. BAUMLER,<sup>1</sup> RENÉE M. TSOLIS,<sup>2</sup> THOMAS A. FICHT,<sup>1</sup> AND L. GARRY ADAMS<sup>2</sup>

<sup>1</sup>Department of Medical Microbiology and Immunology, College of Medicine, and Department of Veterinary Pathobiology, College of Veterinary Medicine, Texas A&M University, College Station, Texas 77843-4467
Pseudogene formation in *Salmonella*

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**Pseudogene accumulation in the evolutionary histories of Salmonella enterica serovars Paratyphi A and Typhi**

Kathryn E Hoh llii, Nicholas R Thomson, John Wein, Gemma C Leighton, Runina Hasan, Zulficar A Bhatta, Michael A Goad, Halina Noberczak, Danielle Walker, Mark Simmonds, Brian White, Nathalie Boson, Karen Mungall, Gordon Dougan and Julian Parkhill
### Pseudogene formation in *Salmonella*

<table>
<thead>
<tr>
<th>Strain</th>
<th>Number of protein-coding genes</th>
<th>Genome-wide $K_a / K_s$ ratio</th>
<th>Number of pseudogenes classified by the number of inactivating mutations</th>
</tr>
</thead>
<tbody>
<tr>
<td>Gallinarum</td>
<td>3,965</td>
<td>0.100</td>
<td>141, 4, 2</td>
</tr>
<tr>
<td>Enteritidis</td>
<td>4,206</td>
<td>0.098</td>
<td>21, –, –</td>
</tr>
<tr>
<td>Choleraesuis</td>
<td>4,413</td>
<td>0.102</td>
<td>81, 9, 3</td>
</tr>
<tr>
<td>Typhimurium</td>
<td>4,423</td>
<td>0.097</td>
<td>13, –, –</td>
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<tr>
<td>Typhi</td>
<td>4,395</td>
<td>0.100</td>
<td>90, 8, 6</td>
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<tr>
<td>S. enterica subsp. arizonae</td>
<td>4,498</td>
<td>–</td>
<td>–, –, –</td>
</tr>
</tbody>
</table>

The Extinction Dynamics of Bacterial Pseudogenes

Chih-Horng Kuo*, Howard Ochman*

*Department of Ecology and Evolutionary Biology, University of Arizona, Tucson, Arizona, United States of America*
MICROBIOLOGY AND FOOD SAFETY
Population dynamics and antimicrobial resistance of the most prevalent poultry-associated Salmonella serotypes

Deveshria H. Shah, Narayan C. Paul, William C. Siecho, Rocio Crespo, and Jean Guard

*Department of Veterinary Microbiology and Pathology, †Department of Veterinary Clinical Sciences, Washington State University, Pullman, WA 99164-3510, and ‡Egg Quality and Safety Research Unit, United States Department of Agriculture, Athens, GA 30605, USA
MICROBIOLOGY AND FOOD SAFETY
Population dynamics and antimicrobial resistance of the most prevalent poultry-associated Salmonella serotypes

Decina H. Shah,*† Nazaryan C. Paul,* William C. Sischo,† Rocio Crespo,* and Jean Guard‡

*Department of Veterinary Microbiology and Pathology; †Department of Veterinary Clinical Sciences, Washington State University, Pullman, WA 99164-7070; and ‡Egg Quality and Safety Research Unit, United States Department of Agriculture, Athens, GA 30605, USA
Niche replacement

- Principle of competitive exclusion applies to Salmonella
- Example: *Salmonella* Gallinarum, Pullorum, and Enteritidis
  - All are O9 antigen
  - Gallinarum and Pullorum were deadly to poultry and were eradicated
  - Enteritidis now occupies that niche
  - Enteritidis has tropism for the reproductive tract of the chicken
  - Spillover into table eggs occurs more frequently than pre-eradication of Gallinarum/Pullorum
Whole genome sequencing is here!

A genomic overview of the population structure of *Salmonella*

Nabil-Fareed Alikhan, Zhemin Zhou, Martin J. Sergeant, Mark Achtman *

Warwick Medical School, University of Warwick, Coventry, United Kingdom
### Table 1. *Salmonella* MLST genotyping schemes offered by Enterobase (1 November, 2017).

<table>
<thead>
<tr>
<th>Legacy MLST</th>
<th>rMLST</th>
<th>cgMLST</th>
<th>wgMLST</th>
</tr>
</thead>
<tbody>
<tr>
<td>7 Loci</td>
<td>51 Loci</td>
<td>3,002 Loci</td>
<td>21,065 Loci</td>
</tr>
<tr>
<td>Conserved housekeeping genes</td>
<td>Ribosomal genes</td>
<td>A soft subset of core genes from wgMLST</td>
<td>All pan-genomic coding sequences from 537 completed/representative genomes</td>
</tr>
<tr>
<td>Conserved low resolution</td>
<td>Highly conserved medium resolution</td>
<td>Variable high resolution</td>
<td>Ultravariability extreme resolution</td>
</tr>
<tr>
<td>Different scheme for each species</td>
<td>Single scheme across tree of life</td>
<td>Different scheme for each genus</td>
<td>Different scheme for each genus</td>
</tr>
<tr>
<td>STs: 3,929</td>
<td>rSTs: 5,454</td>
<td>cgSTs: 96,108</td>
<td>wgSTs: 112,409</td>
</tr>
<tr>
<td>eBGs: 360</td>
<td>reBGs: 337</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

#### Review

A genomic overview of the population structure of *Salmonella*

Nabil-Fareed Alikhan, Zhemin Zhou, Martin J. Sergeant, Mark Achtman*

Warwick Medical School, University of Warwick, Coventry, United Kingdom
Outbreak of Multidrug-Resistant *Salmonella* Infections Linked to Raw Turkey Products

Latest Outbreak Information

- Ninety people infected with the outbreak strain of *Salmonella* Reading have been reported from 26 states.
  - Forty people have been hospitalized, and no deaths have been reported.
- **Epidemiologic and laboratory evidence** indicates that raw turkey products from a variety of sources are contaminated with *Salmonella* Reading and are making people sick.
- In interviews, ill people report eating different types and brands of turkey products purchased from many different locations. Two ill people lived in a household where raw turkey pet food was fed to pets.
- The outbreak strain has been identified in samples taken from raw turkey pet food, raw turkey products, and live turkeys.
- A single, common supplier of raw turkey products or of live turkeys has not been identified.
- The outbreak strain of *Salmonella* Reading is present in live turkeys and in many types of raw turkey products, indicating it might be widespread in the turkey industry. CDC and USDA-FSIS have shared this information with representatives from the turkey industry and asked about steps that they may be taking to reduce *Salmonella* contamination.

At A Glance

- **Reported Cases**: 90
- **States**: 26
- **Hospitalizations**: 40
- **Deaths**: 0
People infected with the outbreak strain of *Salmonella* Reading, by state of residence, as of July 11, 2018 (n=90)
People infected with the outbreak strain of *Salmonella* Reading, by date of illness onset*

*n=90 for whom information was reported as of July 11, 2018. Some illness onset dates have been estimated from other reported information.*
People infected with the outbreak strains of *Salmonella Typhimurium*, by date of illness onset*

*n=265 for whom information was reported as of April 4, 2018. Some illness onset dates have been estimated from other reported information.*
What I learned about the outbreak *Salmonella* Reading without any sampling of my own

- A new strain has emerged in the last two years
- The abundance of this strain is higher in turkey products than previous Reading strains
- It harbors a mobile DNA encoding drug resistance (ampicillin and tetracycline)
- Does not seem more virulent; however it has occupied a niche in turkeys
Salmonella 4,[5],12:i:- emergence in Europe and dissemination to USA
Salmonella 4,[5],12:i:- emergence in Europe and dissemination to USA
Take-home:

• *Salmonella* adapt and evolve to their surroundings
• Host adaptation versus host range are ongoing evolutionary forces
• Plasmids play a major role in adaptation
• Niche displacement occurs at both serovar and strain level