Salmonella Typhimurium

**Background:** Salmonella enterica subsp. enterica serovar Typhimurium (antigenic formula 4,5,12:i:1,2) is a serovar of the O:4 (B) serogroup. S. Typhimurium is a widely distributed serovar, which represent the second most common serovar isolated from humans in the United States and Europe. There is one variant named S. Typhimurium var. Copenhagen, which lacks the factor 5 in the O antigen (4,12:i:1,2). This serovar was named Typhimurium because it produces "Typhi like symptoms in the murine model. S. Typhimurium has been used as model to understand the pathogenicity of Salmonella. Serovar Typhimurium can cause disease in a wide range of hosts and invasive strains have been reported in some countries in Africa. This serovar is classified according to the susceptibility to typing phages, in definite phage types (DT); one common DT (DT104) has been found to have resistance to ampicillin, chloramphenicol, streptomycin, sulphonamide and tetracycline (ACSSuT resistance type). In England, two outbreaks caused by a multidrug resistant (MDR) strain (ASSuTTm resistant type) of S. Typhimurium DT120 occurred in 2011.

**Animal reservoir:** Serovar Typhimurium is found in multiple animal species, including cattle, poultry, swine, wild animals and insects.

**Geographical distribution:** Serovar Typhimurium is globally distributed. In multiple locations (i.e., U.S., Europe, Africa and Latin America), it is reported as the second most common Salmonella serovar in humans. In Australia, it is the most common serovar in humans. In Asia, it is among the ten most common serovars in humans.

**Outbreaks:** Numerous outbreaks have been associated with S. Typhimurium. Outbreaks have been linked to a number of foods and to contact with animals (chicks, ducklings, and other live baby poultry). Here we mention some of the latest outbreaks caused by this serovar.

<table>
<thead>
<tr>
<th>Year</th>
<th>Location</th>
<th>Associated source</th>
<th>Number of cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>2018</td>
<td>US-multistate</td>
<td>Chicken salad</td>
<td>265</td>
</tr>
<tr>
<td>2018</td>
<td>US-multistate</td>
<td>Dried Coconut</td>
<td>14</td>
</tr>
<tr>
<td>2013</td>
<td>US-multistate</td>
<td>Live poultry</td>
<td>37</td>
</tr>
<tr>
<td>2013</td>
<td>US-multistate</td>
<td>Ground beef</td>
<td>22</td>
</tr>
<tr>
<td>2012</td>
<td>Canada</td>
<td>Ground beef</td>
<td>50</td>
</tr>
<tr>
<td>2012</td>
<td>US-multistate</td>
<td>Pet Hedgehogs</td>
<td>26</td>
</tr>
<tr>
<td>2012</td>
<td>US-multistate</td>
<td>Cantaloupe</td>
<td>261</td>
</tr>
<tr>
<td>2011</td>
<td>US-multistate</td>
<td>Ground beef</td>
<td>20</td>
</tr>
<tr>
<td>2011</td>
<td>US-multistate</td>
<td>African Dwarf Frogs</td>
<td>241</td>
</tr>
<tr>
<td>2011</td>
<td>England</td>
<td>Pork</td>
<td>51</td>
</tr>
<tr>
<td>2011</td>
<td>Ireland</td>
<td>Duck eggs</td>
<td>34</td>
</tr>
<tr>
<td>2010</td>
<td>US-multistate</td>
<td>Contact with water frogs</td>
<td>85</td>
</tr>
<tr>
<td>2009</td>
<td>England</td>
<td>unknown</td>
<td>14</td>
</tr>
</tbody>
</table>

**Border Rejections and Recalls:**

<table>
<thead>
<tr>
<th>Year</th>
<th>Exporting Country (if applicable)</th>
<th>Country Issuing Recall/Rejection</th>
<th>Food</th>
</tr>
</thead>
<tbody>
<tr>
<td>2019</td>
<td>Poland</td>
<td>Poland</td>
<td>Turkey</td>
</tr>
<tr>
<td>2019</td>
<td>Belgium</td>
<td>Germany</td>
<td>Frozen Pig Intestines</td>
</tr>
</tbody>
</table>

**Relevant genetic characteristics:** Whole genome sequences for 27 strains of S. Typhimurium have been deposited at GenBank as of October, 2013. Genomic characteristics of the sequenced S. Typhimurium strains include (i) a genome size ranging from 4.82-5.09 Mb, (ii) a mol G+C% of approx. 52.2, and (iii) 4,556 to 5,619 predicted genes. Most of the strains of S. Typhimurium contain a plasmid of approx. 90 kb that carry virulence genes (Salmonella virulence plasmid (SVP)). Large resistant plasmids of approx. 200 kb that represented different incompatibility types (e.g., IncHI1), have also been identified in S. Typhimurium. Prophages and genomic islands are important genomic components of serovar Typhimurium; for example, S. Typhimurium str. LT2 has four prophages (Fels-1, Fels-2, Gifsy-1, and Gifsy-2). Pathogenicity islands (SPIs) are found in all S. Typhimurium sequenced to date, this include SPIs-1 to 6, 9, 11 to 14, and 16; being SPI-14 specific to S. Typhimurium. In addition, some genomic islands are strain-specific; for example, S. Typhimurium MDR strain ST1660/06 has three strain-specific genomic islands that encode putative virulence and resistance genes. Genomic islands that encode antibiotic resistance appear to be a common feature of a number of S. Typhimurium MDR strains, these genomic islands include, e.g., Salmonella genomic island 1 (SGI1) described in S. Typhimurium DT104 and genomic island GI-DT12 in S. Typhimurium T000240. The latest genomic island (GI-DT12) contains antibiotic resistance genes (i.e., bla(oxa-30), aadA1, qacE1, and sul1, cat, and tetA) and virulence genes (i.e., the aerobactin iron-acquisition siderophore system (lutA and lucABC), and an iron transporter (sitABCD)).

In Sub-Sahara regions of Africa, invasive strains of S. Typhimurium emerged, single nucleotide polymorphism (SNP)-based phylogeny of these invasive strains and strains from other regions, showed two lineages of invasive strains that clustered together. According to den Bakker et al. (2011) classification, Salmonella Typhimurium belongs to clade A.
Genome sequences available:


Relevant links and references:

2. http://www.nature.com/nature/journal/v413/n6858/full/413852a0.html
11. http://analytics.foodtrack.net/cgi-bin/read?rid=MjAxOTAyMjExMzQ0Rk9PRFRSQ0tCVUXzAyMjExOUw0MjY=&style=html&sour ce=email