Salmonella Typhi

Background: Salmonella enterica subsp. enterica serovar Typhi is a serovar of the O:9 (D1) serogroup. S. Typhi causes typhoid fever, a life-threatening disease that is characterized by sustained fever as high as 103° to 104° F (39° to 40° C). In developed countries, this serovar is considered rare; however, in developing countries, it is among the top ten Salmonella serovars that caused disease in humans. S. Typhi kills approx. 600,000 people annually. A number of projects have sequenced the genome of strains of S. Typhi; these studies have concluded that S. Typhi is a highly clonal serovar that emerged approx. 30,000-50,000 years ago. In addition, studies have found that horizontal gene transfer plays an important role in the evolution S. Typhi, this included the acquisition of plasmids encoding multiple antibiotic resistant genes in multidrug resistant strains.

Animal reservoir: S. Typhi is a human-restricted serovar.

Geographical distribution: S. Typhi is widely distributed; however, the prevalence of this serovar varies considerable. In developed countries (U.S., Canada, Europe), S. Typhi isolations correspond to less than 1% of all Salmonella serovars isolated from humans. In developing countries, S. Typhi isolations correspond to up to 30% of all Salmonella isolated in some countries in Latin America and Asia.

Outbreaks: Salmonella Typhi has caused multiple outbreaks in the U.S. and Europe. On large outbreak with 5,963 cases, was reported in Nepal. However, in developing countries, outbreaks are mostly undetected.

<table>
<thead>
<tr>
<th>Year</th>
<th>Location</th>
<th>Associated source</th>
<th>Number of cases</th>
</tr>
</thead>
<tbody>
<tr>
<td>2010</td>
<td>US-multistate</td>
<td>Frozen mamey fruit pulp</td>
<td>9</td>
</tr>
<tr>
<td>2002</td>
<td>Nepal</td>
<td>Drinking water</td>
<td>5963</td>
</tr>
<tr>
<td>2000</td>
<td>US-New York</td>
<td>Food handler</td>
<td>7</td>
</tr>
<tr>
<td>1999</td>
<td>US-Florida</td>
<td>Frozen mamey fruit pulp (imported)</td>
<td>16</td>
</tr>
<tr>
<td>1998</td>
<td>France</td>
<td>Chicken rice</td>
<td>27</td>
</tr>
<tr>
<td>1997</td>
<td>France</td>
<td>Pork, food handler</td>
<td>26</td>
</tr>
</tbody>
</table>

Relevant genetic characteristics: Whole genome sequences for 20 strains of S. Typhi have been deposited at GenBank as of October, 2013. Genomic characteristics of the sequenced S. Typhi include (i) a genome size ranging from 4.54 to 5.03 Mb, (ii) a mol G+C% of approx. 52, and (iii) 4,419 to 5,336 predicted genes. Plasmids and prophages have been identified in S. Typhi. For example, a resistant plasmid of 218 kb and seven prophages were detected in S. Typhi CT18. Up to 15 Salmonella pathogenicity islands (SPIs) have been detected in S. Typhi, these include SPI-1 to 7, 9, 11 to 13, and 15 to 18. Comparative genomics and phylogenetic analyses have shown that S. Typhi (i) had a monophyletic origin approx. 50,000 years ago (ii) has suffered reductive evolution (approx. 200 genes are functionally inactive), (iii) belongs to clade A, according to den Bakker et al. (2011) classification, and (iv) has 349 gene families unique to this serovar.

Genome sequences available:


Relevant links and references: