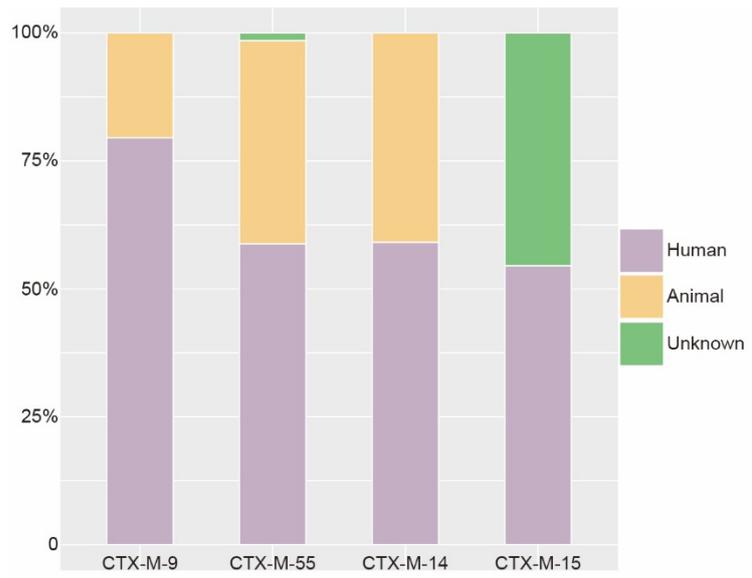


**Table S1.** The detection rate of 154 virulence genes in 330 *bla*<sub>CTX-M</sub>-positive *S. Typhimurium* isolates.

Virulence Gene	Rate	Virulence Gene	Rate	Virulence Gene	Rate	Virulence Gene	Rate
<i>csgA</i>	100.0%	<i>sscA</i>	100.0%	<i>sifB</i>	99.4%	<i>iucD</i>	3.0%
<i>csgB</i>	100.0%	<i>sscB</i>	100.0%	<i>sipB</i>	99.4%	<i>iutA</i>	3.0%
<i>csgC</i>	100.0%	<i>sseA</i>	100.0%	<i>sopA</i>	99.4%	<i>iroB</i>	1.8%
<i>csgF</i>	100.0%	<i>sseF</i>	100.0%	<i>sopE2</i>	99.4%	<i>iroC</i>	1.8%
<i>csgG</i>	100.0%	<i>sseG</i>	100.0%	<i>sptP</i>	99.4%	<i>iroD</i>	1.8%
<i>fepG</i>	100.0%	<i>steA</i>	100.0%	<i>csgD</i>	99.1%	<i>iroE</i>	1.8%
<i>fimC</i>	100.0%	<i>csgE</i>	99.7%	<i>lpfA</i>	99.1%	<i>iroN</i>	1.8%
<i>fimD</i>	100.0%	<i>entA</i>	99.7%	<i>lpfD</i>	99.1%	<i>cdtB</i>	0.6%
<i>invA</i>	100.0%	<i>fimF</i>	99.7%	<i>sinH</i>	99.1%	<i>faeD</i>	0.6%
<i>invB</i>	100.0%	<i>invI</i>	99.7%	<i>ssaD</i>	99.1%	<i>faeE</i>	0.6%
<i>invC</i>	100.0%	<i>invJ</i>	99.7%	<i>sseJ</i>	99.1%	<i>sspH1</i>	0.6%
<i>invE</i>	100.0%	<i>misL</i>	99.7%	<i>steC</i>	99.1%	<i>ybtP</i>	0.6%
<i>invF</i>	100.0%	<i>orgC</i>	99.7%	<i>ssaV</i>	98.8%	<i>ybtQ</i>	0.6%
<i>invG</i>	100.0%	<i>pipB</i>	99.7%	<i>sseC</i>	98.8%	<i>ybtS</i>	0.6%
<i>invH</i>	100.0%	<i>prgH</i>	99.7%	<i>ratB</i>	98.5%	<i>ybtX</i>	0.6%
<i>mgtB</i>	100.0%	<i>sifA</i>	99.7%	<i>slrP</i>	98.5%	<i>entE</i>	0.3%
<i>mgtC</i>	100.0%	<i>sipC</i>	99.7%	<i>entB</i>	98.2%	<i>faeC</i>	0.3%
<i>ompA</i>	100.0%	<i>sipD</i>	99.7%	<i>sodCI</i>	98.2%	<i>fyuA</i>	0.3%
<i>orgA</i>	100.0%	<i>sopB</i>	99.7%	<i>sseL</i>	98.2%	<i>irp1</i>	0.3%
<i>orgB</i>	100.0%	<i>sopD</i>	99.7%	<i>sopD2</i>	97.9%	<i>irp2</i>	0.3%
<i>prgI</i>	100.0%	<i>spaO</i>	99.7%	<i>mig-14</i>	97.6%	<i>senB</i>	0.3%
<i>prgJ</i>	100.0%	<i>spaR</i>	99.7%	<i>sseK2</i>	96.7%	<i>tviB</i>	0.3%
<i>prgK</i>	100.0%	<i>ssaC</i>	99.7%	<i>sseK1</i>	96.1%	<i>tviC</i>	0.3%
<i>sicA</i>	100.0%	<i>ssaM</i>	99.7%	<i>gogB</i>	91.8%	<i>tviD</i>	0.3%
<i>sicP</i>	100.0%	<i>ssaN</i>	99.7%	<i>pipB2</i>	89.4%	<i>tviE</i>	0.3%
<i>sipA</i>	100.0%	<i>ssaP</i>	99.7%	<i>sspH2</i>	83.0%	<i>vexA</i>	0.3%
<i>spaP</i>	100.0%	<i>ssaQ</i>	99.7%	<i>sseI</i>	79.7%	<i>vexB</i>	0.3%
<i>spaQ</i>	100.0%	<i>ssaR</i>	99.7%	<i>grvA</i>	31.8%	<i>vexC</i>	0.3%
<i>spaS</i>	100.0%	<i>ssaT</i>	99.7%	<i>spvB</i>	27.0%	<i>vexD</i>	0.3%
<i>spiC</i>	100.0%	<i>sseB</i>	99.7%	<i>spvC</i>	27.0%	<i>vexE</i>	0.3%
<i>ssaE</i>	100.0%	<i>sseD</i>	99.7%	<i>spvR</i>	27.0%	<i>ybtA</i>	0.3%
<i>ssaG</i>	100.0%	<i>sseE</i>	99.7%	<i>pefA</i>	26.7%	<i>ybtE</i>	0.3%
<i>ssaH</i>	100.0%	<i>steB</i>	99.7%	<i>pefB</i>	26.7%	<i>ybtI</i>	0.3%
<i>ssaI</i>	100.0%	<i>avrA</i>	99.4%	<i>pefC</i>	26.7%	<i>ybtU</i>	0.3%
<i>ssaJ</i>	100.0%	<i>fepC</i>	99.4%	<i>pefD</i>	26.7%		
<i>ssaK</i>	100.0%	<i>fimH</i>	99.4%	<i>rck</i>	26.4%		
<i>ssaL</i>	100.0%	<i>fimI</i>	99.4%	<i>shdA</i>	9.1%		
<i>ssaO</i>	100.0%	<i>lpfB</i>	99.4%	<i>iucA</i>	3.0%		
<i>ssaS</i>	100.0%	<i>lpfC</i>	99.4%	<i>iucB</i>	3.0%		
<i>ssaU</i>	100.0%	<i>lpfE</i>	99.4%	<i>iucC</i>	3.0%		



**Figure S1.** The analysis of hosts carrying the most common CTX-M allelic variants.