

SUPPLEMENTARY DATA

Differences in Host Cell Invasion and SPI-1 Expression between *Salmonella enterica* serovar Paratyphi A and the Non-Typhoidal Serovar Typhimurium

Table S1. Bacterial strains and plasmids used in the study.

Strain or plasmid	Genotype and description	Reference or source
<i>S. Typhimurium</i> LT2		SGSC
<i>S. Typhimurium</i> 14028s		SGSC
<i>S. Typhimurium</i> SL1344	wild type Sm ^r <i>xyl hisG rpsL</i>	SGSC
<i>S. Typhimurium</i> SL1344 <i>invA</i>	$\Delta invA$	(1)
<i>S. Typhimurium</i> SL1344 <i>invG</i>	$\Delta invG$	(1)
<i>S. Typhimurium</i> 73727	Clinical isolate 2002	Human stool
<i>S. Typhimurium</i> 74701	Clinical isolate 2002	Human stool
<i>S. Typhimurium</i> 80609	Clinical isolate 2002	Human stool
<i>S. Typhimurium</i> 82788	Clinical isolate 2003	Human stool
<i>S. Typhimurium</i> 88359	Clinical isolate 2003	Human stool
<i>S. Typhimurium</i> 88894	Clinical isolate 2004	Human stool
<i>S. Typhimurium</i> 92273	Clinical isolate 2004	Human stool
<i>S. Typhimurium</i> 92280	Clinical isolate 2004	Human stool
<i>S. Typhimurium</i> 92576	Clinical isolate 2004	Human stool
<i>S. Typhimurium</i> 98666	Clinical isolate 2006	Human blood
<i>S. Typhimurium</i> 103259	Clinical isolate 2006	Human blood
<i>S. Typhimurium</i> 116449	Clinical isolate 2008	Human blood
<i>S. Typhimurium</i> 125904	Clinical isolate 2009	Human stool
<i>S. Paratyphi</i> A 45147	Outbreak strain	(2)
<i>S. Paratyphi</i> A 45147 <i>invA</i>	$\Delta invA$	(1)
<i>S. Paratyphi</i> A 45147 <i>invG</i>	$\Delta invG$	(1)
<i>S. Paratyphi</i> A 118239	Clinical isolate 2008	Traveler from India
<i>S. Paratyphi</i> A 9150		SGSC
<i>S. Paratyphi</i> A AKU 1260		SGSC
<i>S. Paratyphi</i> A 83698	Clinical isolate 2003	Traveler from India

<i>S. Paratyphi</i> A 83753	Clinical isolate 2003	Traveler from India
<i>S. Paratyphi</i> A 93223	Clinical isolate 2004	Traveler from Romania
<i>S. Paratyphi</i> A 108003	Clinical isolate 2007	Traveler from India
<i>S. Paratyphi</i> A 108599	Clinical isolate 2007	Traveler from India
<i>S. Paratyphi</i> A 124597	Clinical isolate 2009	Traveler from India
<i>S. Paratyphi</i> A 119989	Clinical isolate 2008	Traveler from Thailand & India
<i>S. Paratyphi</i> A 113498	Clinical isolate 2008	Traveler from Sri Lanka
<i>S. Paratyphi</i> A 105493	Clinical isolate 2006	Traveler from Thailand & Nepal
<i>S. Paratyphi</i> A 51190	Clinical isolate 2009	Traveler from Nepal
<i>S. Paratyphi</i> A 36056/7	Clinical isolate 2007	Traveler from Nepal
<i>S. Paratyphi</i> A 45842/7	Clinical isolate 2007	Traveler from Nepal
Plasmids		
pKD4		(3)
pKD46		(3)
pCP20		(3)
pWSK29		(4)
pACYC184		(4)
pBAD18		(5)
pDE-hilA _{STM}	<i>S. Typhimurium</i> SL1344 <i>hilA</i> fused to arabinose promoter cloned into pBAD18	This study
pDE-sptP::2HA _{STM}	<i>S. Typhimurium</i> SL1344 <i>sptP</i> fused to 2HA tag cloned into pACYC184	This study
pDE-sptP::2HA _{SPA}	<i>S. Paratyphi</i> A 45157 <i>sptP</i> fused to 2HA tag cloned into pACYC184	This study
pDE-steA::2HA _{STM}	<i>S. Typhimurium</i> SL1344 <i>steA</i> fused to 2HA tag cloned into pWSK29	This study
pDE-steA::2HA _{SPA}	<i>S. Paratyphi</i> A 45157 <i>steA</i> fused to 2HA tag cloned into pWSK29	This study
pDE-sipB::2HA _{STM}	<i>S. Typhimurium</i> SL1344 <i>sipB</i> fused to 2HA tag cloned into pWSK29	(6)

pDE-sipB::2HA _{SPA}	<i>S. Paratyphi</i> A 45157 <i>sipB</i> fused to 2HA tag cloned into pWSK29 (6)
pDE-sopE2::2HA _{STM}	<i>S. Typhimurium</i> SL1344 <i>sopE2</i> fused to 2HA tag cloned into pWSK29 This study
pDE-sopE2::2HA _{SPA}	<i>S. Paratyphi</i> A 45157 <i>sopE2</i> fused to 2HA tag cloned into pWSK29 This study
pDE-sopB::2HA _{STM}	<i>S. Typhimurium</i> SL1344 <i>sopB</i> fused to 2HA tag cloned into pWSK29 (6)
pDE-sopB::2HA _{SPA}	<i>S. Paratyphi</i> A 45157 <i>sopB</i> fused to 2HA tag cloned into pWSK29 (6)
pDE-prgJ::2HA _{STM}	<i>S. Typhimurium</i> SL1344 <i>prgJ</i> fused to 2HA tag cloned into pACYC184 (6)
pDE-prgJ::2HA _{SPA}	<i>S. Paratyphi</i> A 45157 <i>prgJ</i> fused to 2HA tag cloned into pACYC184 (6)

SGSC – *Salmonella* genetic Stock Center the University of Calgary.

Table S2. Primers used in the study.

Primer	Sequence 5'-3'
steA 2HA STM/SPA SacI F	TTTTGAGCTCTAGTCTGTGTTTTTCATTACG
steA 2HA STM XbaI R	TTTTTCTAGAATAATTGTCCAAATAGTTATG
steA 2HA SPA XbaI R	TTTTTCTAGAATACTTGTCTAAATAGTTATG
sopE2 2HA STM/SPA SacI F	TTTTGAGCTCTTCCATTTGTTAACCTATTG
sopE2 2HA STM/SPA XbaI R	TTTTTCTAGAGGAGGCATTCTGAAGATAC
sptP 2HA STM/SPA SalI F	TTTTGTCGACAGTCTTGAGTCCAGGGTGTAG
sptP 2HA STM/SPA BglII R	TTTTAGATCTGCTTGCCGTCGTCATAAGC
SDhilA F STM EcorI	TTTTGAATTTCGAATACACTATTATCATGC
SDhilA R STM XbaI	TTTTTCTAGATTACCGTAATTTAATCAAGC
rpoD RT-PCR F	GGTCTGACCATCGAACAGGTG
rpoD RT-PCR R	ATCAGACCGATGTTGCCTTC
invF RT-PCR F	TGTCGCACCAGTATCAGGAG
invF RT-PCR R	ACTCGCAGCGTTTACGATC
invA RT-PCR F	TCCACGAATATGCTCCACAAG
invA RT-PCR R	CAGACATGCCACGGTACAAC
sipB RT-PCR F	GTGGGC AAAAATACGGAAG
sipB RT-PCR R	CCCGATACATCCCATAAATGC
sopB RT-PCR F	GAAAATCGGCGCAAAAAGATATC
sopB RT-PCR R	TCATGATAGGGGGAAAGCAC

sptP RT-PCR F	CTGAAGCCATCTCCTGGAAG
sptP RT-PCR R	GTCATAAAAGGCGGCGATAC
steA RT-PCR F	GCTTTCTGATGGTCGGATG
steA RT-PCR R	AAAGCCCTCTTCCAGTCTC
sopE2 RT-PCR F	CCGACTACCCATTTTCATCG
sopE2 RT-PCR R	GCTTCGCATGTCTGACGAGC

Fig. S1. *S. Paratyphi* A and *S. Typhimurium* show more similar SPI-1 expression pattern under microaerobiosis than under aerobic conditions. (A) The mean fold change in the expression of 41 SPI-1 genes in *S. Paratyphi* A relative to *S. Typhimurium* is shown for cultures grown to the late logarithmic phase under aerobic conditions and for cultures grown to the stationary phase under microaerobic conditions. Results are based on two independent RNA extractions and the RNA-seq values presented in Table 1. Two-tailed t-test was used to determined statistical significance. (B) RNA was extracted from *S. Paratyphi* A 45157 and *S. Typhimurium* SL1344 grown to the late logarithmic phase aerobically and to the stationary phase under microaerobic growth conditions. qRT-PCR was performed to determine the relative expression of *invA*, *invF*, *sipB*, *sopB* and *sopE2* in *S. Paratyphi* A relative to *S. Typhimurium*. The indicated values present the mean and the SEM of at least three independent RT-PCR experiments.

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