Supporting Online Material

σ^{E} -dependent sRNAs of *Salmonella* respond to membrane stress by accelerating global *omp* mRNA decay

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Supplementary Materials and Methods

Sample preparation for microarray experiments

3 OD aliquotes were removed, treated with 0.2 vol of stop solution (95% EtOH; 5% water saturated Phenol), snap-frozen in liquid nitrogen and stored at -80°C. For RNA extraction the cells were thawed on ice and pelleted by centrifugation (10 min, 4000 rpm, 4°C). RNA was isolated using the Promega SV total RNA purification kit as described at www.ifr.ac.uk/safety/microarrays/protocols.html. RNA concentration was determined on a Nanodrop machine (NanoDrop Technologies), and RNA quality was assessed using the RNA Laboratory-on-a-Chip (Agilent Technologies, Palo Alto, CA) as directed by the manufacturers. Experiments were performed in triplicates.

Microarray data generation

The microarrays used in this study include PCR products of all the genes present in the sequenced S. typhimurium strain LT2. In addition, we added 229 genes specific to S. typhimurium strain SL1344. Details of all the amplicons can be found at http://www.ifr.ac.uk/Safety/MolMicro/pubs.html. Our experimental design involves the use of Salmonella enterica serovar Typhimurium genomic DNA as the co-hybridized control for one channel on all microarrays. This method has the advantage of allowing the direct comparison of multiple samples. Total RNA and chromosomal DNA were labelled by random priming according to the protocols described at http://www.ifr.bbsrc.ac.uk/safety/microarrays/protocols.html. Briefly, 16 µg RNA were reverse transcribed and labelled with Cy3-conjugated dCTP (Pharmacia) using 200U of Stratascript (Stratagene) and random octamers (Invitrogen). Chromosomal DNA (400 ng) was labelled with Cy5dCTP using the Klenow fragment. After labelling, each Cy3-labelled cDNA sample was combined with Cy5-labelled chromosomal DNA and hybridised to a microarray overnight at 65°C. After hybridisation, slides were washed and scanned using a GenePix 4000A scanner (Axon Instruments, Inc.). Fluorescent spots and the local background intensities were identified and quantified using Bluefuse software (BlueGnome, Oxford). To compensate for unequal dye incorporation, data centring to zero was performed for each block (one block being defined as the group of spots printed by the same pin). We considered genes to be differentially expressed if they displayed \geq 3-fold changes in all replicates and were statistically significantly different using Significance Analysis of Microarrays (Tusher et al. 2001). The final list included a number of genes whose gene expression is highly sensitive to small changes in growth conditions (data not shown). The consequence is that those genes have a higher probability to be false positives. Quantitative RT-PCR on independent RNA samples confirmed that the gene expression level of those genes (cydA, napC, narK, nirB) was not dependent on RybB (data not shown). Those genes were therefore excluded from further analysis. Data visualisation and data mining was performed using GeneSpring 7.3 (Agilent).

Supplementary Tables & Figures

Name	Sequence in $5' \rightarrow 3'$ direction			
JVO-0019	AAATAAACTGAACTCTTTGTTCCGGGGCGAGTCTGAGTATATGAAAGACGTGTAGGCTGGAGCTGCTTC			
JVO-0020	GGCGGATACCGAGCCGTTTGCCGCGTGGCTTGCAAAACACGCCTGACCCAGGTCCATATGAATATCCTCCTTAG			
JVO-0021	GTTTTTCTCGAGCAGATCAAACACGGTGATT			
JVO-0023	GTTTTTCTAGAGCCGCTGGAGATTTTACA			
JVO-0236	GAAAGACGCGCATTTGT			
JVO-0266	GTTTTTTTTAATACGACTCACTATAGGGAGGCACGGAGTGGCCAAA			
JVO-0279	GTTTGCCTTTAAGTGAAAAAATTTTGCCAATAGGTCGAACTTTTCGTTAAGGTCCATATGAATATCCTCCTTAG			
JVO-0280	CGTTGGGCAACAAAAAACCCAACCTTGAACCGAAATGGCGGGGTTGAGTGTAGGCTGGAGCTGCTTC			
JVO-0281	GTTTTCCCGAGCGGCGATGGAAATCAT			
JVO-0282	GTTTTTCTAGACGCCGGAGTGTCAAT			
JVO-0322	CTACGGCGTTTCACTTCTGAGTTC			
JVO-0397	CGGTAGAGTAACTATTGAGCAGAT			
JVO-0398	GTTTTTTTTAATACGACTCACTATAGGGAGGCCTAACCAGTCGTAGC			
JVO-0430	GTTTTTATGCATAGACACATAAAGACACCAAACTC			
JVO-0717	GTTTTGCTAGCTGGTACCAGGAGGG			
JVO-0719	GTTTATGCATGCCGACTGGTTAATGAG			
JVO-0900	GGAGAAACAGTAGAGAGTTGC			
JVO-0901	TTITTTCTAGATTAAATCAGAACGCAGA			
JVO-0906	5P-GCCACTGCTTTCTTTGA			
JVO-0932				
JVO-0933				
JVO-1057				
JVO-1038				
JVO-1074	TATECTICATAGCTCAGGCCATCCAGGCCCCCGTAAGGCGATGCCATACGTGTAGGCTGGAGCTGCTTC			
JVO-1076	GATAAGACCTGTCTACAACATGA			
JVO-1077	TAACTCTCCCAGGTTTTCTG			
JVO-1090	CTTCATTCACAATGATGGCCC			
JVO-1091	TCGTAGCCCATTTCAAAGCC			
JVO-1092	CCTACGGCGCTGACAACTTTA			
JVO-1093	TAACGCGAAGTCCAGACCATC			
JVO-1094	ACGTTCTGCCAGAGTTTGGTG			
JVO-1095	CCAGGCCAAAGAAGTCAGTGTT			
JVO-1117	TCAGCCATTTTGTGCGCTT			
JVO-1118	TTCAGGATCGACAACGCCTT			
JVO-1186	TTTTCCGAGTTAATAGGACTCACTATAGGCCATTGACAAACG			
JVO-1187	GACACCGTGAATCGCA			
JVO-1188	GTTTTTTTTTAATACGACTCACTATAGGGAGGCAGTGATGCCGTAGT			
JVO-1195				
JVO-1196				
JVO-1197				
JVO-1198				
JVO-1200	GTTTTTTATACGACTCACTATAGGAGGTCGAGTTGTTGCC			
JVO-1202	GTITITITAATACGACTCACTATAGGGAGGCTTTACCGTACAGATCCAG			
JVO-1203	GCCACTGGTCTGATTTCTA			
JVO-1204	GTTTGTTTAATACGACTCACTATAGGGAGGGCCAGAGGAAGAAAAT			
JVO-1205	GTTGATGGGCTCCACAA			
JVO-1230	GTTTTGACGTCGCAGATCAAACACGGT			
JVO-1231	GTTTTGCTAGCGTCTTTCATATACTCAGAC			
JVO-1232	GTTTTGACGTCGCGCAGTAATATTCCA			
JVO-1233	GTTTTGCTAGCAGTGGCAATAGGTATG			
JVO-1234	AGGTTTGGCATTGTCGCCT			
JVO-1235	CTTTTTCGAGCATCGGTGC			
JVO-1236	ACTATTGAGTCCCTCCCGGAAG			
JVO-1237	ACCGGACAATCCATGATAGCC			
JVO-1242	GTTTTTTTAATACGACTCACTATAGGCCACTGCTTTTCTTTGA			
JVO-1243	AACCCAACCTTGAA			
JVO-1244	GTTTTTTTAATACGACTCACTATAGGATGCCTTTGATTCAA			
JVO-1245	GTTGCCGTCTTTGTTATAAAT			

Table S1: Oligodeoxynucleotides used in this study.

JVO-1246	GTTTTTTTAATACGACTCACTATAGGCCGACTGGTTAATGAG
JVO-1247	GGTCTAATTTGTTGCCGT
JVO-1328	CGCAAACGCAGCAGAAATT
JVO-1329	TTTTACTATCGCCGGTCGTTG
JVO-1330	GTCTGAACTTCGCGTTGCAAT
JVO-1331	CACCGTTAGCGTTCTTCACGT
JVO-1332	CCTGTACGGCAAAGTTGATGG
JVO-1333	CGTTAATCTGCGTTTCGCCT
JVO-1334	ATTCCAGCAGCAAAGTGCGT
JVO-1335	GGACAGCCCGGCATTTTTA
JVO-1393	CGAACGTCCATTTTGTCGC
JVO-1394	CCGGCGTATGTGTCGTTAAAC
PBADFW	ATGCCATAGCATTTTTATCC
PBADREV	TTATCAGACCGCTTCTGC

Table S2: Microarray results (provided as an separate EXCEL file).

Table S3: Probes for Northern detection and hybridization conditions.

gene	probe	hybridization
		temperature (°C) / buffer
micA	Riboprobe generated from PCR product amplified with primers JVO-0236/ JVO-0266	42 / RAPIDhyb
rybB	oligo JVO-1205	45 / RAPIDhyb
ompA	dsDNA; PCR product amplified with primers JVO-0397 / JVO-0398	65 / RAPIDhyb
ompC	dsDNA, PCR product amplified with primers JVO-717 / JVO-719	65 / RAPIDhyb
ompD	Riboprobe generated from PCR product amplified with primers JVO-1057 / JVO-1058	70 / RAPIDhyb
ompF	dsDNA; PCR product amplified with primers JVO-0430 / JVO-1202	68 / RAPIDhyb
ompN	Riboprobe generated from PCR product amplified with primers JVO-1195 / JVO-1196	68 / RAPIDhyb
ompS	Riboprobe generated from PCR product amplified with primers JVO-1199 / JVO-1200	68 / RAPIDhyb
ompW	Riboprobe generated from PCR product amplified with primers JVO-1197 / JVO-1198	68 / RAPIDhyb
ompX	dsDNA; PCR product amplified with primers JVO-1187 / JVO-1188	68 / RAPIDhyb
fadL	Riboprobe generated from PCR product amplified with primers JVO-1203 / JVO-1204	68 / RAPIDhyb
sodB	dsDNA; PCR product amplified with JVO-0932 / JVO-0933	68 / RAPIDhyb
5S rRNA	oligo JVO-0322	45 / RotiQuick

Legend for Supplementary Figure S1: Northern blot showing that polymyxin B-induced downregulation of *ompD* mRNA in wild-type *Salmonella* is dependent on σ^{E} activation. RNA samples were taken from polymyxin B-treated wild-type and $\Delta rpoE$ cells in late exponential phase (OD₆₀₀ of 1). Total RNA was prepared prior to (0 min) and after 5 and 10 min of polymyxin B addition.

Supplementary References

Tusher, V.G., R. Tibshirani, and G. Chu. 2001. Significance analysis of microarrays applied to the ionizing radiation response. *Proc Natl Acad Sci U S A* 98: 5116-21.

Figure S1 Papenfort *et al.*, 2006

