Supporting Information

Hammarlöf et al. 10.1073/pnas.1714718115

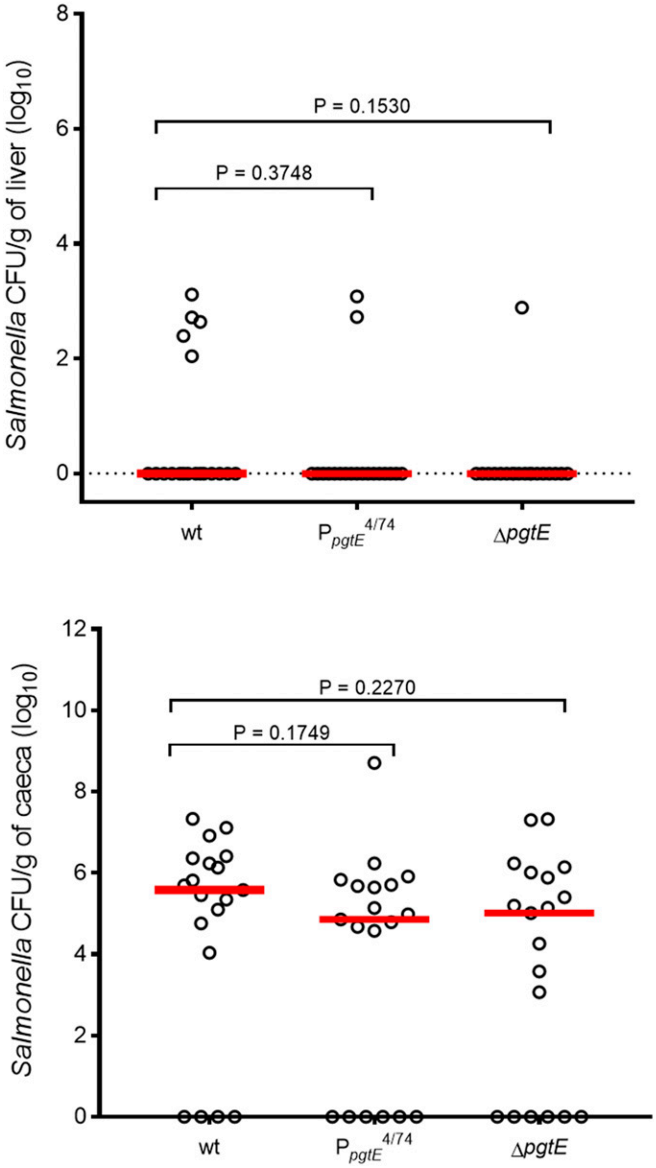

Fig. S1. The T^{D23580} SNP in the *pgtE* promoter of *Salmonella* Typhimurium does not affect colonization of the liver or caeca in the chicken infection model. Viable counts of *S.* Typhimurium D23580-derived strains as log CFU/g of liver and caeca at 3-d postoral infection (10^8 CFU) of 7-d-old Lohmann Brown Layers. Data based on 19 individually sampled birds for each group; combined data for two separately repeated experiments. Each symbol represents the value for an individual chicken and the bars represent the median value for each group.

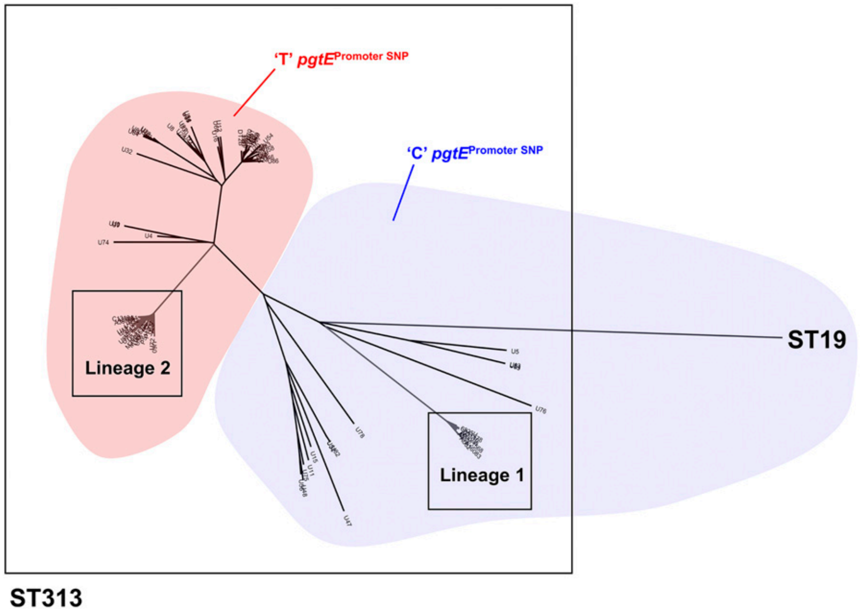

Fig. S2. Radial phylogeny illustrating the population structure of *S.* Typhimurium ST313 in the context of the *pgtE* promoter SNP. The phylogenetic tree is reproduced with permission (69). Red and blue colored areas represent the presence of the T^{D23580} or $C^{4/74}$ genotype, respectively. Black-outlined box indicates the isolates belonging to the 313 sequence type.

Table S1. Bacterial strains and plasmids

Bacterial strains or plasmids	Description*	Source
Bacteria		
S. Typhimurium ST19		
4/74 derivatives		
4/74	4/74 wild-type	(69)
JH3827	4/74 Δ*pgtE*::*frt* Δ*waaG*::Kan; Km^{R}	Present study
JH3915	4/74 P_{pgtE}^{D23580}	Present study
JH3919	4/74 Δ*waaG*::Kan; Km^{R}	Present study
JH4140	4/74 *pgtE*-FLAG-*frt*	Present study
JH4149	4/74 P_{pgtE}^{D23580}, *pgtE*-FLAG-*frt*	Present study
JH4158	4/74 Δ*pgtE*::*frt*	Present study
LT2 derivatives		
LT2	LT2 wild-type	(70)
JH4147	LT2 *pgtE*-FLAG-*frt*	Present study
14028s derivatives		
14028s	14028s wild-type	(71)
JH4148	14028s *pgtE*-FLAG-*frt*	Present study
S. Typhimurium ST313 lineage 1		
A130 derivatives		
A130	A130 wild-type	(5)
JH4150	A130 *pgtE*-FLAG-*frt*	Present study
D25248 derivatives		
D25248	D25248 wild-type	(5)
JH4151	D25248 *pgtE*-FLAG-*frt*	Present study
ST313 lineage 2		
D23580 derivatives		
D23580	D23580 wild-type	(5)
JH3812	D23580 $P_{pgtE}^{4/74}$	Present study
JH3813	D23580 Δ*pgtE*::*frt*	
JH3828	D23580 Δ*pgtE*::*frt*, Δ*waaG*::Kan; Km^{R}	
JH4154	D23580 *pgtE*-FLAG-*frt*	Present study
JH4156	D23580 $P_{pgtE}^{4/74}$, *pgtE*-FLAG-*frt*	Present study
D37712 derivatives		Present study
D37712	D37712 wild-type	(72)
JH4151	D37712 *pgtE*-FLAG-*frt*	Present study
Escherichia coli		
S17-1 λ*pir*	*pro thi hsdR recA* chromosome::RP4-2 Tc::Mu Km::Tn*7*/λ*pir*; Tp^{R}, Sm^{R}	(73)
Plasmids		
pCP20-TcR	FLP recombinase expression plasmid; Tc^{R}	(57)
pEMG	Suicide plasmid; Km^{R}	(60)
pKD3	*frt-cat-frt* cassette template plasmid; Cm^{R}	(53)
pKD4	*frt-aph-frt* cassette template plasmid; Km^{R}	(53)
pNAW41	pEMG carrying a 989 bp EcoRI/BamHI fragment corresponding to P_{pgtE}^{D23580} flanked by ∼500-bp regions of 4/74; Km^{R}	Present study
pSIM5-*tet*	λ *red* recombination plasmid, temperature-inducible; Tc^{R}	(55)
pSW-2	Plasmid for *m*-toluate–inducible expression of the I-SceI enzyme; Gm^{R}	(60)

*Relevant antibiotic resistances are indicated by^{R}: Gm, gentamicin; Km, kanamycin, Sm, streptomycin; Tc, tetracycline; Tp, trimethoprim. "$P_{pgtE}^{4/74}$" or "P_{pgtE}^{D23580}" indicate the corresponding allele of the *pgtE* promoter. The residual FLP recognition target sequence coming from plasmid pKD3 and pKD4 are indicated by *frt*. The term "Kan" denotes the presence of an *frt-aph-frt* module (Km^{R}) from pKD4. The natural resistances of ST313 strains (5) and derivatives are not indicated.

Table S2. ssDNA oligonucleotides used in this study

Oligo name	Sequence (5′ → 3′)*	Comments
DH90	AATCTGGAGAGGTGATGAAGTTTTCATCTTGTCAAATCGTCGGACAAGAGTACATTTATTA	$T^{D23580} \rightarrow C^{4/74}$ substitution in −10 *pgtE* promoter of D23580 by λ *red* recombination
DH40	GGGAGCTGGTTTATGATACC	Used for diagnostic PCR of the *pgtE* allele
DH41	AATTGAACGATCGGTCCAGC	
DH54	CGAACACTACATGCGCAAAC	Used for qRT-PCR of the *pgtE* transcript
DH55	ACCGCCCTTACCTTCTTCAT	
DH93	ACGGTTACCGCGGGGTTGCAGTATCGCTTCGACTACAAGGACGACGATGACAAGTAACATATGAATATCCTCCTTAG	Used for *pgtE*-FLAG strain construction by λ *red* recombination
DH94	CGGTTATGACCGATGACATCCCGATGTGGTGTGTAGGCTGGAGCTGCTTC	
DH95	TCTCCAGATTACATCTGAATATGAGGACAAGAGAACATATGAATATCCTCCTTA	Used for *pgtE* inactivation by λ *red* recombination
DH96	TCGGCCGGTTATGACCGATGACATCCCGATGTGGTGTGTAGGCTGGAGCT	
DH97	GACTGGGTAAATGCGCATGA	Used for the sequencing check of the *pgtE*-FLAG strains
DH98	GCATAACCTTTCGAGCGGTT	
del_waaG_F	AAATGCTGCCGCATGAGGCACGCACCATAGATTTGGACAGCCTGCTATGAGTGTAGGCTGGAGCTGCTTC	Used for *waaG* inactivation by λ *red* recombination
del_waaG_R	TTAACGGCGCTTTCAGCTCAACCATCTAAATCACCTGTAATAATATCCGCCATATGAATATCCTCCTTA	
NW_122	ACGT*GAATTC*CTGGCCAAGCAATGTGCGC (EcoRI)	Construction of the pNAW41 suicide plasmid used for $C^{4/74} \rightarrow T^{D23580}$ substitution in the *pgtE* promoter of 4/74 by allelic exchange
NW_123	ATCTTATCAAATCGTCGGACAAGAGTAC	
NW_124	GTCCGACGATTTGATAAGATGAAAACTTCATCACCTCTCC	
NW_125	ACGT*GGATCC*TGCAATAACCAACCTTTCAC (BamHI)	
NW_155	GACCGGATGATATCGAGCCG	Used for the sequencing check of the *pgtE* promoter allele
NW_156	TGCAATATCACCGGACATGC	
qPCR_hns_f	TCTGAACAACATCCGTACTCTTC	Used for qRT-PCR of the *hns* transcript
qPCR_hns_r	TTCTTCTTCACGACGCTCATTA	

*Relevant restriction sites are indicated in italics and specific mutated nucleotides are underlined.

Dataset S1. All TSS identified in D23580, and comparison with strain 4/74

Dataset S1

1. Kröger C, et al. (2012) The transcriptional landscape and small RNAs of *Salmonella enterica* serovar Typhimurium. *Proc Natl Acad Sci USA* 109:E1277–E1286.

Dataset S2. SNPs and indels in the D23580 genome compared with the 4/74 genome

Dataset S2

Dataset S3. All SNPs within the −40 bp region of identified primary TSS in D23580 and PUV values for the respective TSS in D23580 and 4/74

Dataset S3

Dataset S4. Accession numbers, phylogenetic designation, and *pgtE* TSS −40 sequence of all genomes sequences used in this study

Dataset S4