Regulation of bistability in the std fimbrial operon of Salmonella enterica by DNA adenine methylation and transcription factors HdfR, StdE and StdF

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ABSTRACT
Bistable expression of the Salmonella enterica std operon is controlled by an AND logic gate involving three transcriptional activators: the LysR-type factor HdfR and the StdE and StdF regulators encoded by the std operon itself. StdE activates transcription of the hdfR gene, and StdF activates std transcription together with HdfR. Binding of HdfR upstream of the std promoter is hindered by methylation of GATC sites located within the upstream activating sequence (UAS). Epigenetic control by Dam methylation thus antagonizes formation of the StdE-StdF-HdfR loop and tilts the std switch toward the StdOFF state. In turn, HdfR binding hinders methylation of the UAS, permitting activation of the StdE-StdF-HdfR loop and concomitant formation of StdON cells. Bistability is thus the outcome of competition between DNA adenine methylation and the StdE-StdF-HdfR activator loop.

INTRODUCTION
Fimbriae (pili) are hair-like appendages that permit adhesion to biotic and abiotic surfaces. Such appendages are present in the surface of many Gram-negative bacteria, and have prominent roles in bacterial pathogenesis (1). A canonical fimbrial type includes morphologically diverse fimbriae assembled by the chaperone/usher secretion system (1,2). Pili assembled by this pathway are virulence factors that promote attachment of pathogenic bacteria to host cell surfaces. In addition, chaperone-usher fimbriae may modulate host cell signaling pathways, promote or inhibit bacterial invasion of host cells, and facilitate biofilm formation (1).

Chaperone-usher fimbriae encoded by the std operon of Salmonella enterica serovar Typhimurium bind a fucosylated receptor present in the mucus of the murine caecum (3). Like other fimbrial loci (4,5), std undergoes bistable expression with concomitant formation of StdON and StdOFF subpopulations. Under laboratory conditions, such populations have disparate sizes, >99% StdOFF cells and <1% StdON cells (6). The sizes of StdON and StdOFF subpopulations in the animal intestine remain unknown. However, the observation that mice infected with S. Typhimurium serotype A deliver the major fimbrial subunit of Std fimbriae (7), raises the possibility that the StdON lineage may become larger during animal colonization.

Expression of the std operon is derepressed in mutants lacking DNA adenine (Dam) methylation (8), and constitutive std expression attenuates S. Typhimurium virulence in a mouse model of acute infection (9). Virulence attenuation, however, is not caused by production of Std fimbriae but by downregulation of pathogenicity island (SPI-1) by two std-encoded proteins, StdE and StdF (10). Actually, SPI-1 downregulation is merely an example of the capacity of StdE and StdF to control gene expression: both proteins are transcriptional regulators that act either as repressors or as activators of numerous S. enterica genes (6). As a consequence, formation of fimbriae in the StdON subpopulation is accompanied by changes in motility, chemotaxis, virulence, biofilm formation and probably in additional phenotypic traits (6). This pleiotropic control is a unique feature among fimbrial operons, and may contribute to adaptation of StdON cells to the environment of the large intestine.

In this study, we describe cellular factors and mechanisms that govern bistable expression of the std operon. Formation of StdON cells requires positive feedback involving three transcriptional regulators (StdE, StdF, and HdfR). In turn, DNA adenine methylation prevents HdfR binding to the std UAS, thus permitting formation of StdOFF cells.
MATERIALS AND METHODS

Bacterial strains, bacteriophages and strain construction

*Salmonella enterica* strains listed in Supplementary Table S1 belong to serovar Typhimurium and derive from the mouse-virulent strain SL1344 (11). For simplicity, *S. enterica* serovar Typhimurium is often abbreviated as *S. enterica*. Escherichia coli BL21 [F− dcm ompT hsdS (rB− mB−) gal (mabB− K12) (A5)] (Stratagene, La Jolla, CA, USA) was used for protein purification. Targeted gene disruption was achieved using plasmids pKD3, pKD4 or pKD13 as templates to generate polymerase chain reaction (PCR) products for homologous recombination (12). Antibiotic resistance cassettes introduced during strain construction were excised by recombination with plasmid pCP20 (12). Primers used in strain construction are shown in Supplementary Table S2. Transductional crosses using phage P22 HT 105 were used for strain construction operations involving chromosomal markers. The transduction protocol has been previously described (14). To obtain phage-free isolates, transductants were purified by plating on green plates. Phage sensitivity was tested by cross-streaking with the clear-plaque mutant P22 H5.

Construction of strain SV9322 (PLtetO-stdEF stdA::gfp) was achieved by insertion of the PLtetO promoter upstream of stdE on the *Salmonella* chromosome. For this purpose, the PLtetO promoter (including a kanamycin resistance [KmR] cassette linked to the PLtetO promoter) was amplified from SV7553 (6), using the oligonucleotides PLtetOstdEF pStd UP and PLtetOstdEF pStd DO and the PCR product used for homologous recombination. For verification of correct chromosomal insertion, primers PLtetO sense and stdE 2E were used.

Strain SV8449 (PLtetOhdfR) harbors the PLtetO promoter upstream the hdfR coding sequence on the *S. enterica* chromosome. To construct this strain, the PLtetO promoter was amplified from SV7553 (6) with oligos PLtetOhdfR UP and PLtetOhdfR DO. The resulting PCR product was integrated into the chromosome of *S. enterica*. The KmR cassette introduced during construction was excised by recombination with plasmid pCP20 (12). For verification of correct chromosomal insertion, primers PLtetO sense and hdfR 2E were used.

Media and growth conditions

Bertani’s lysogeny broth (LB) (15) was used as standard rich medium. Solid LB contained agar at 1.5% final concentration. Cultures were grown at 37°C. Aeration of liquid cultures was obtained by shaking at 200 rpm in an Infors Multitron shaker. 5-bromo-4-chloro-3-indolyl-β-D-galactopyranoside (X-gal, Sigma-Aldrich) was used as chromogenic indicator of β-galactosidase activity. Antibiotics were used at the final concentrations described elsewhere (16).

Genetic screen

Strain SV8188 (stdA::lacZ) was transduced with nine pools of a *S. enterica* pBR328 plasmid library (10). Each pool contained around 1000 independent clones. Transductants were selected on LB supplemented with ampicillin. Candidates that retained high β-galactosidase activity after re-transformation were further analyzed. The DNA fragments contained in the plasmids of selected candidates were sequenced using specific primers flanking the insertion site (Supplementary Table S2).

β-galactosidase assays

Levels of β-galactosidase activity were determined using the CHCl₃-sodium dodecyl sulfate permeabilization procedure (17). β-galactosidase activity data (Miller units) are averages and standard deviations from ≥3 independent experiments.

Flow cytometry analysis

Bacterial cultures were grown at 37°C in LB until stationary phase (OD₆₀₀ ≈ 2). Cells were then diluted in phosphate-buffered saline (PBS) to a final concentration of ~10⁷ cells/ml. Data acquisition was performed using a Cytomix FC500-MPL cytometer (Beckman Coulter, Brea, CA, USA). Data were collected for 100,000 events per sample and were analysed with CXP and FlowJo 8.7 softwares. Data are shown by dot plots representing forward scatter (cell size) in the y-axis versus fluorescence intensity in the x-axis.

In vivo visualization of std-expressing cells

For time-lapse microscopy, strains containing the stdA::gfp fusion in wild-type and PLtetOhdfR backgrounds (SV9597 and SV9292, respectively) were grown overnight at 37°C in LB and diluted 1:100 in fresh medium. Cultures were grown to the desired optical density and concentrated 10-fold by centrifugation at 8000 g for 5 min. Cells were placed on an agarose slab (0.8% agarose/1% LB) and warmed to 37°C.

Images were captured with a Zeiss Apotome fluorescence microscope equipped with a 100× Plan Apochromat objective and an incubation system that permits observation and cultivation of living cells. Pictures were taken at different times using an Axioscan 506 camera, and the images were analyzed using ImageJ software (Wayne Rasband, Research Services Branch, National Institute of Mental Health).

Purification of HdfR-His₆

The *S. Typhimurium* hdfR gene was PCR-amplified using primers hdfR-Nhel FOR and hdfR-EcoRI REV, and cloned onto the Nhel and EcoRI restriction sites of pET-21a[+] (Novagen). The GTG start codon of hdfR was replaced with the ATG start codon of the vector. The resulting plasmid, pLZ1803, allows expression of the hdfR gene from the T7 promoter, and the HdfR protein harbors a 6xHis tag at the C-terminus. For purification of HdfR-His₆, *E. coli* strain BL-21 was transformed with pLZ1803 and grown at 37°C in LB. Gene expression was induced with 1 mM IPTG, added when cells reached an OD₆₀₀ ≈ 0.5. After IPTG addition, cells were grown for 2 h. For lysis, bacteria were sonicated in lysis buffer (30 mM Tris HCl pH 7, 2 M NaCl). HdfR-His₆ protein was purified from the cell-free extract on HIS-Select® Nickel Affinity Gel (Sigma-Aldrich), treated with...
washing buffer (30 mM Tris–HCl pH 7, 2 M NaCl, 10 mM imidazole) and eluted with elution buffer (30 mM Tris–HCl pH 7, 2 M NaCl, 200 mM imidazole). At last, the protein was dialyzed using a dialysis tubing cellulose membrane, 10 × 6 mm (Sigma-Aldrich) in lysis buffer to eliminate imidazole.

Electrophoretic mobility shift assays (EMSA)

An std promoter probe labeled with 6-carboxyfluorescein (6-FAM) was prepared by PCR amplification of a 306 bp region containing the std promoter (−295 to +11), using 5’-labeled oligonucleotide std EMSA-6FAM FOR and non-labeled std EMSA REV. A ‘cold’ DNA probe was prepared using the same primers without 6-FAM label. For Electrophoretic mobility shift assays (EMSA) with methylated DNA, the 6-FAM labeled probe was methylated in vitro using Dam methylase (New England Biolabs), and digested with Mbol (New England Biolabs) to discard nonmethylated DNA. The undigested product was purified with the Wizard® SV Gel and PCR clean-up system (Promega). For a standard binding reaction, 50 ng of DNA probe, 1 µg of poly[d(I-C)] (Roche, Penzberg, Germany) and different amounts of purified HdfR-His₆ were mixed to yield 20 µl final volume. The binding buffer contained 50 mM KCl, 2 mM Tris–Cl (pH 8), 1 mM dithiothreitol, 10% glycerol and bovine serum albumin 150 µg/ml. The mixture was stored at 4°C for 20 min. As a negative control, a competition assay with excess of ‘cold’ DNA fragment was performed using 500 ng of purified HdfR-His₆ and 50 ng FAM-labeled stdA promoter probe. Increasing amounts of ‘cold’ stdA promoter probe from 0 to 1000 ng were tested. DNA–protein complexes were subjected to electrophoresis at 4°C in a 5% non-denaturing acrylamide/bisacrylamide (29:1) gel prepared in Tris-glycine buffer (25 mM trizma base, 190 mM glycine, 1 mM ethylenediaminetetraacetic acid (EDTA)). DNA fragments were visualized with a FLA-5100 Imaging system (Fujifilm, Tokyo, Japan).

Chromatin immunoprecipitation followed by sequencing (ChIP-seq) and data analysis

Strain SV9287 (P₆₄::tetO-stdEF::3xFLAG) was used to perform ChIP-seq experiments, and the protocol was described elsewhere (6). ChIP DNA samples were sequenced at the Functional Genomics Core Facility of the Institute for Research in Biomedicine, Barcelona (Spain) using Illumina’s sequencing technology. BAM files were converted to FASTQ format with the BAM2FASTQ tool (http://www.hudsonalpha.org/gsl/software/software/bam2fastq). The quality of the sequence reads was examined using FASTQC (18). The adapters were trimmed with the FASTX_CLIPPER tool of the FASTX-Toolkit suite (http://hannonlab.cshl.edu/fastx-toolkit/). Reads shorter than 40 nt were discarded. NCBI GCA_000210855.2 genome assembly of S. enterica SL1344 was used as reference genome. Mapping was performed with Bowtie (19) allowing two-matches for only unique alignment. Peaks were called using CisGenome version 2.0 (20) using default parameters. The IGV browser (21) was used for data visualization. Genes closest to a ChIP peak were identified using the bedtools suite (22).

Chromatin immunoprecipitation coupled to quantitative PCR (ChIP-qPCR)

ChIP-qPCR assays were used to test StdE, StdF and HdfR binding to the std promoter region. The strains used were SV9324 (Δdam stdE-3xFLAG), SV9325 (Δdam stdEF-3xFLAG), SV9287 (P₆₄::tetOstdEF-3xFLAG), SV9766 (P₆₄::tetOstdEF-3xFLAG Δ35nt), SV8487 (Δdam hdfR-3xFLAG) and SV8504 (hdfR-3xFLAG). The chromatin immunoprecipitation (ChIP) protocol used was described previously (6). After DNA purification, quantitative PCR was performed in a Light Cycler 480 II apparatus (Roche). Each reaction was carried out on a 480-well optical reaction plate (Roche) in a total volume of 10 µl, containing 5 µl SYBR mix, 0.2 µl DYE II (Takara), 4 µl DNA and two gene-specific primers (0.2mM), named RT-promoter std FOR and RT-promoter std REV, listed in Supplementary Table S2, for amplification of the std promoter region in both IP sample and mock IP sample. Real-time cycling conditions were as follows: (i) 95°C for 10 min and (ii) 40 cycles at 95°C for 15 s, 60°C for 1 min. Triplicates were run for each reaction, and the Ct value is averaged from them. Absence of primer dimers was corroborated by running a dissociation curve at the end of each experiment to determine the melting temperature of the amplicon. Melting curve analysis verified that each reaction contained a single PCR product. For quantification, the efficiency of each primer pair was determined to be between 90%–110%, following the instructions for efficiency determination described in the ‘Guide to Performing Relative Quantification of Gene Expression Using Real-Time Quantitative PCR’ (Applied Biosystems). These efficiencies indicate that the amount of DNA is doubled in each PCR cycle, and allows for direct comparison between different genes. Relative RNA levels were determined using the ΔΔCt method as described in the above mentioned guide. Briefly, each gene Ct value is normalized to the Ct value for the internal control (rfaH), which gives the ΔCt value. This value is then related to a given gene in the reference strain (S. enterica, in this case) giving us the ΔΔCt value. Since the amount of DNA doubles in each PCR cycle, the relative amount of input cDNA can be determined by using the formula 2–ΔΔCt. Each ΔΔCt determination was performed at least in three different DNA samples (three biological replicates), and the results are representative example of such determinations.

Southern blotting

Genomic DNA was isolated by phenol extraction and ethanol precipitation from stationary cultures in LB (O.D.₆₀₀ ≈ 2). Forty µg of each DNA sample was digested with SspI (New England Biolabs), purified and divided into four fractions, three of which were subsequently digested with DpnI, Mbol or Sau3A1 (New England Biolabs). After digestion the samples were run in a denaturing 5% TBE (tris-borate-EDTA)-polyacrilamide (19:1), 8 M urea gel. Electrophoresis was carried out in a Hoefer SE400 (Hoefer Scientific Instruments) apparatus subjected to an electric field of 35 mV for 60 min. After electrophoresis, DNA was transferred to an Amersham Hybond-N+ membrane (GE Healthcare, Wauwatosa, WI, USA), using a semidry
Electroblotting system (Thermo Scientific) (400mA, 5V, 3 h). The DNA in the membrane was immobilized by UV crosslinking. A radioactive probe was prepared by PCR using $\alpha^{32}$P labeled dCTP (Perkin Elmer) and oligonucleotides std PLtetO UP and std southern DO. After the PCR reaction, non-incorporated nucleotides were removed using a Sephadex G-25 column (Illustra MicroSpin G-25 columns, GE Healthcare) following manufacturer's instructions. Prior to hybridization the double-stranded DNA probe was denatured by heating at 95°C for 3 min, followed by incubation on ice. Hybridization with the probe was performed overnight at 52°C in hybridization buffer (0.5 M sodium phosphate pH 7.2, 10 mM EDTA, 7% sodium dodecyl sulphate (SDS)). Excess probe was removed with washing buffer (40 mM sodium phosphate pH 7.2, 1% SDS) at 48°C (three washes, 30 min each). The membrane was developed using a FLA-5100 Scanner (Fujifilm).

Site-directed mutagenesis

Mutation of the three GATC sites contained in the promoter region of the std promoter was achieved using the QuikChange® Site-Directed Mutagenesis Kit (Stratagene). Briefly, a 1 Kb fragment of the std promoter region containing the three GATC sites was cloned into the pGEMT plasmid using the oligonucleotides Std-promoter-XbaI and Std-promoter-SacI. Mutations in every GATC were then introduced using oligonucleotides harboring GATC changes (labeled as mut For and mut Rev). Resulting plasmids containing fragments with changes in the GATC sites were then digested with XbaI and SacI, cloned onto the suicide plasmid pMDS197. Plasmids derived from pMDS197 were transformed into E. coli CC118 lambda pir. Plasmids derived from pMDS197 were transformed into E. coli S17–1 lambda pir. The resulting strains were used as donors in matings with Salmonella cells harboring a CmR cassette in place of the three GATC sites (constructed using oligonucleotides Mut std promoter P1 and Mut std promoter P2) as recipients. TeR transconjugants were selected on E plates supplemented with tetracycline. Several TeR transconjugants were grown in nutrient broth (without NaCl) containing 5% sucrose. Individual tetracycline-sensitive segregants were then screened for clorampenicol sensitivity and examined for the incorporation of the mutant allele by Sau3AI digestion and DNA sequencing using external oligonucleotides.

Dam methylation protection assay

A 306 bp DNA fragment was PCR-amplified from genomic DNA of strain SV6024 (containing a CATT sequence instead of GATC-1 at the std UAS). HdfR-His$_6$ was prepared to std DNA by incubation at 4°C for 20 min. Dam methylase (8 U) and S-adenosyl-methione (160 mM) prepared in 20 µl Dam methylase buffer were added. The DNA methylation reaction was allowed to proceed at 37°C for 2 h. To determine the extent of DNA binding, 10 µl was removed and run as an EMSA. The remainder of the reaction was incubated at 65°C for 20 min to dissociate bound HdfR-His$_6$ from the DNA and to inactivate Dam methylase. The DNA was finally digested with DpnI at 37°C for 1 h, and digestion products were resolved on an agarose 2% gel.

Magnetic activated cell sorting (MACS)

A 500 ml aliquot from a stationary culture (OD$_{600}$>2) of strain SV9602 (PLtetO-hdfR stdA:3xFLAG) was collected by centrifugation. The pellet was washed with 10 ml of TE buffer and fixed by adding the same volume of cold 70% ethanol. Ethanol-fixed cells were washed three times with PBS containing 0.05% of Tween (PBS-T). The pellet was resuspended in 5 ml of lysozyme solution (2 mg/ml lysozyme, 25 mM Tris–HCl pH 8.0, 50 mM glucose and 10 mM EDTA) and incubated at room temperature for 10 min. Cells were then washed three times with PBS-T and incubated for 30 min in 10 ml of 2% BSA in PBS-T. Cells were centrifuged and incubated 1 h at RT with anti-flag-PE antibody (Miltenyi). After incubation, cells were washed with PBS-T. Cells were then incubated overnight at 4°C with anti-PE microbeads (Miltenyi) and washed with PBS-T. Separation of labeled and unlabeled cells was performed using an autoMACS Pro Separator (Miltenyi).

Analysis of GATC methylation by PCR

Genomic DNA was isolated by phenol extraction and ethanol precipitation from StdOFF and StdON magnetic-activated sorted cells of strain SV9602. A total of 70 ng of each DNA sample were digested with the endonucleases DpnI and MboI (New England Biolabs). After digestion, RT-PCR was performed using the samples as templates. EMSA std and std southern DO oligonucleotides were used (Supplementary Table S2).

RESULTS

Genetic screen for activators of std expression

To search for factors that might activate expression of the std operon, a genetic screen was performed using a pBR328-based library containing 7–11 kb segments of the S. enterica genome (10). A strain carrying a stdA::lacZ translational fusion (SV8188) was used as reporter. This strain is Lac$^-$ on X-gal agar as a consequence of the small size of the StdON subpopulation (6). Strain SV8188 was transduced with nine pools of the plasmid library, each containing around 1000 independent clones. Forty-five colonies with increased β-galactosidase activity (blue) were chosen, and 22 independent candidates that retained high β-galactosidase activity after re-transformation of their plasmid were further analyzed. The DNA fragments contained in 15 candidate plasmids were sequenced using primers flanking the insertion site (Supplementary Table S1). Somehow surprisingly, 14 plasmids turned out to carry the std gene cluster as well as heterogeneous assortments of neighbouring genes. One such plasmid (pBR328 std) was propagated as pZZ2318. These observations indicated that activators of the std operon are contained within the operon itself (Figure 1A).

A candidate that formed faint blue colonies turned out to contain an incomplete std fimbrial operon lacking the downstream 21 nt of the stdE coding sequence and the entire stdF gene (pBR328 stdA21stdDE-stdF, propagated as pZZ2319) (Figure 1A). β-galactosidase analysis confirmed that stdA::lacZ expression decreased when stdE contained
a downstream deletion and the stdF gene was absent (Figure 1A). These observations suggested that StdE and StdF, previously shown to act as global regulators of gene transcription (6), might also be involved in autogenous control of std transcription. This hypothesis was confirmed upon constitutive expression of StdE and StdF, using a strain (SV9322) that harbors an stdA::gfp transcriptional fusion and stdEF expression driven by the heterologous constitutive promoter P_{LtetO} (24,25), placed upstream of stdEF. Single cell analysis of stdA::gfp expression was monitored by flow cytometry, and a representative experiment is shown in Figure 1B. Constitutive transcription of stdEF increased the size of the StdON subpopulation, and deletion of stdEF resulted in loss of StdON cells. Hence, formation of the StdON lineage does require transcriptional activation by StdE and/or StdF.

Transcriptional activation of std by StdF

ChIP followed by sequencing (ChIP-seq) revealed the existence of an StdF binding site upstream of the stdA promoter (Figure 2A). The existence of this site was further tested using ChIP coupled with quantitative PCR (ChIP-qPCR). Because Dam methylation represses std transcription (9), the trial was performed in a Dam- strain. A chromatin fragment containing the std promoter immunoprecipitated with StdF-3xFLAG was found to be enriched 6 times compared with the mock immunoprecipitated sample (Figure 2B), confirming that StdF binds upstream of the std promoter in vivo. No binding was observed for StdE. In turn, StdF failed to bind when a strain containing a deletion upstream of the std promoter (from −338 to −303) was subjected to ChIP-qPCR (Figure 2C), thus confirming the existence of the StdF binding site identified by ChIP-seq. These observations, together with the existence of autogenous positive control (Figure 1), provide evidence that StdF directly activates std transcription.

Transcriptional activation of hdfR by StdE

In a previous study, the hdfR gene was found to be upregulated upon constitutive expression of stdEF (6), suggesting that StdE and/or StdF might activate hdfR transcription. β-galactosidase analysis using a translational hdfR::lacZ fusion (strain SV7889) provided evidence that StdE alone is sufficient to activate hdfR transcription (Figure 3A). Furthermore, ChIP-seq analysis identified an StdE binding site upstream of the hdfR gene (Figure 3B). StdF binding was not detected, thus providing further evidence that the transcriptional activator of hdfR is StdE only.

Because HdfR is a LysR-type transcriptional regulator and LysR-like factors often repress their own expression (26), we cloned a 260 bp DNA fragment that contained the putative hdfR promoter as well as upstream and downstream regions (from −160 to +100) on the promoter-probe vector pIC552 (27). The resulting plasmid (pIZ2320) thus harbored a P_{hdfR}::lacZ Y transcriptional fusion. The activity of the fusion was monitored in HdfR+ and HdfR− strains, and decreased activity in the HdfR+ background provided evidence that HdfR undergoes autogenous transcriptional repression (Figure 3C).

Transcriptional activation of std by HdfR

Because a previous study had identified HdfR as an activator of the std operon (9), we examined whether formation of the StdON lineage was HdfR dependent. For this purpose, we placed hdfR under the control of the heterologous, constitutive promoter P_{LtetO} (24,25). In the construct, the native hdfR promoter was removed, thus avoiding autogenous control (strain SV8449). Transcription of the std operon was then examined using stdA::lacZ and stdA::gfp fusions (strains SV8477 and SV9292, respectively). Analysis of β-galactosidase activity and flow cytometry assessment of stdA::gfp expression showed that constitutive hdfR transcription upregulates stdA::lacZ expression (Figure 4A) and increases the size of the StdON subpopulation (Figure 4B, upper panel). The latter observation was made not only by flow cytometry but also on X-gal plates, where Lac+ (StdON) and Lac− (StdOF) colonies were observed in strain SV8477 (P_{LtetO}hdfR stdA::lacZ) but not in SV8188 (stdA::lacZ) (Figure 4C). Formation of the StdON subpopulation thus requires both StdEF and HdfR (Figure 4B, lower panel), suggesting the existence of a network of posi-
Figure 2. Binding of StdF to the std promoter. (A) ChIP-seq analysis of StdE and StdF binding to the std UAS. StdE-C and StdF-C are mock immunoprecipitated samples. (B) In vivo analysis of StdE and StdF binding to the std UAS by ChIP coupled with quantitative PCR. The experiment was performed in a Dam− background. (C) In vivo analysis of StdF binding to wild-type and deleted versions of std UAS by ChIP coupled with quantitative PCR. The strain carrying the P}_{\text{LtoO}}stdEF-3xFLAG Δ35nt construct lacks the Std binding site. In B and C, data are averages and standard deviations from three independent experiments.

Figure 3. Regulation of hdfR transcription by StdE. (A) β-galactosidase activity of a hdfR::lacZ transcriptional fusion in the presence and in the absence of StdE. (B) ChIP-seq analysis of StdE and StdF binding upstream of the hdfR gene. StdE-C and StdF-C are mock immunoprecipitated samples. (C) β-galactosidase driven by the hdfR promoter in the presence and in the absence of HdfR.

Role of positive StdE-StdF-HdfR feedback in the stability of the StdON state

The observation that constitutive transcription of hdfR yields Lac+ and Lac− colonies on X-gal plates raised the possibility that activation of StdE-StdF-HdfR feedback above a critical threshold might increase the stability of the StdON state making it heritable. Note that a previous study using the same stdA::lacZ fusion had failed to detect Lac+ (StdON) colonies on X-gal plates, and had explained the absence of Lac+ colonies as a consequence of the instability (and concomitant small size) of the StdON subpopulation (6). The effect of StdE-StdF-HdfR feedback activation on the stability of StdON state was examined by time lapse experiments, monitoring expression of an stdA::gfp fusion in a wild-type background (strain SV9597) and in a strain that carried an P}_{\text{LtoO}}hdfR construct (SV9292). The results of these experiments were clear-cut: (i) cells expressing a native level of HdfR failed to transmit the StdON state to daughter cells (Figure 5A); (ii) in contrast, among cells with increased HdfR level, a fraction was found to transmit the StdON state to the progeny (Figure 5B). Hence, the small size of the StdON population in a wild-type background (6) appears to be caused indeed by quick return to the StdOFF state upon cell division. This view was confirmed by fluorescence microscopy: StdON cells did not produce StdON progeny (Figure 5C) unless HdfR expression increased (Figure 5D). The latter observation is in agreement with the
Figure 4. Role of HdfR in std transcription. (A) β-galactosidase activity of an std::lacZ transcriptional fusion in the wild-type and in a strain that constitutively expresses hdfR (P<sub>LtetO</sub>hdfR). (B) Flow cytometry analysis of expression of an stdA::gfp transcriptional fusion in the wild-type and upon constitutive expression of either HdfR or StdEF. (C) Formation of Lac<sup>-</sup> colonies on X-gal plates by the wild-type (left panel). Formation of Lac<sup>+</sup> and Lac<sup>-</sup> colonies by a strain carrying an stdA::lacZ transcriptional fusion in a P<sub>LtetO</sub>hdfR background (right panel).

Figure 5. Heritability of the Std<sup>ON</sup> state. (A) Time lapse (120 min) microscopy observation of Salmonella enterica cells carrying an stdA::gfp transcriptional fusion. The upper panel shows the bright field merged with the gfp channel while the bottom panel shows the gfp channel only. (B) Time lapse (120 min) microscopy observation of S. enterica cells carrying an stdA::gfp transcriptional fusion in a P<sub>LtetO</sub>hdfR background. Panels are as above. (C) Absence of fluorescent microcolonies due to instability of the Std<sup>ON</sup> state. (D) Inheritance of the Std<sup>ON</sup> state and formation of a fluorescent microcolony.
formation of Lac⁺ colonies upon constitutive synthesis of HdfR (Figure 4C).

Binding of HdfR to the std upstream activating sequence (UAS)

The finding that HdfR activates std transcription prompted the examination of HdfR binding to the std promoter region in vitro. For this purpose, we used a 306 bp DNA fragment containing std DNA from −295 to +11. The fragment included the std promoter and the transcription start site (9). Binding of HdfR to the fragment was assayed using purified HdfR-His₆ protein. Complementation of an hdfR mutation by HdfR-His₆ indicated that this protein is functional (Supplementary Figure S1). Electrophoretic mobility shift assays (EMSA) showed that 500 ng of HdfR-His₆ was able to retard 50 ng of stdA FAM-labeled probe (Figure 6A). HdfR binding to the std UAS was thus confirmed.

The std UAS contains three GATC sites in a 25 bp interval, at positions −242 (GATC-1), −229 (GATC-2) and −220 (GATC-3) (9). Because std transcription is repressed in Dam⁻ strains (8,9), we considered the possibility that the interaction between HdfR and the std promoter might be dependent on the DNA methylation state of the UAS. For this purpose, EMSA was performed using a methylated version of the FAM-labeled probe described above. HdfR-His₆ failed to bind the methylated std probe in vitro (Figure 6A). Binding of HdfR-His₆ was reduced when ‘cold’ competitor DNA was added to the binding reaction (Figure 6B).

The effect of DNA adenine methylation on HdfR binding to the std UAS was also investigated in vivo, using ChIP coupled with quantitative PCR. Strains SV8504 (hdfR-3xFLAG) and SV8487 (∆dam hdfR-3xFLAG) were used. In the Dam⁻ strain, a chromatin fragment containing the std promoter was 13-fold enriched in the immunoprecipitated (IP) sample compared with the mock IP sample (Figure 6C). However no enrichment was detected in the Dam⁺ strain (Figure 6C). In vitro and in vivo analyses thus confirm that HdfR binding to the std UAS is hindered by DNA adenine methylation, and explain why derepression of the std operon is observed in a Dam⁺ background (8,9).

Site-directed mutagenesis of the std UAS

To investigate whether the GATC-1, GATC-2 and GATC-3 sites were located in the region bound by HdfR in the std UAS, individual GATC sites were subjected to site-directed mutagenesis. Two types of nucleotide substitutions were introduced: GATC → GTTC, and GATC → GATG. A strain that lacked all three GATC sites was also constructed. The effect of nucleotide substitutions on std expression was monitored by quantitative RT-PCR. Because the operon is repressed in the wild-type, the experiments were performed in a Dam⁺ background. The results can be summarized as follows:

(i) Site-directed mutagenesis of GATC-1 permitted std expression, irrespective of the nucleotide substitution introduced (GATC → GTTC or GATC → GATG). This observation suggests that GATC-1 may not be part of the HdfR binding site, thus making unlikely that GATC-1 methylation may participate in std repression.
(ii) Site-directed mutagenesis of either GATC-2 or GATC-3 abolished std expression in a Dam⁻ background (Figure 7). A tentative explanation may be that GATC-2 and GATC-3 are both part of the HdfR binding site, which is destroyed by GATC → GTTC and GATC → GATG nucleotide substitutions. If this view is correct, it is not surprising that site-directed mutagenesis of all three GATC sites, converting them to either GTTC or GATG, abolished std expression in a Dam⁺ background (Figure 7A.).

The above conclusions were supported by EMSA analysis of HdfR binding to FAM-labeled std fragments lacking specific GATC sites. A GATC → GATG mutation in GATC-1 did not prevent HdfR binding, while the same mutation in either GATC-2 or GATC-3 completely abolished binding (Figure 7B).

Dam methylation protection by HdfR

Binding of proteins to DNA containing GATC sites can result in methylation hindrance, thus yielding undermethylated DNA (28). To determine whether binding of HdfR to the std UAS can prevent DNA methylase activity in vitro, we examined whether the Dam enzyme was able to methylate GATC-2 and GATC-3 after HdfR binding. GATC methylation was tested by restriction analysis with DpnI, which cuts methylated DNA only. To simplify restriction analysis, the ‘uninteresting’ GATC-1 was excluded from the trial. A 306 bp DNA fragment was PCR amplified from genomic DNA of strain SV6024 (carrying a CATC sequence instead of GATC-1). HdfR-His₆ was bound to std DNA, and in vitro methylation by Dam methylase was tested. The conclusion from these experiments was unambiguous: HdfR did protect GATC-2 and GATC-3 from Dam methylation in vitro (Figure 8).

Methylation state of the std UAS in vivo

If the conclusion that HdfR is unable to bind a methylated std UAS is correct, one may predict that the GATC sites located within the HdfR binding site must be methylated in StdOFF cells and nonmethylated in StdON cells. This prediction was first tested in the wild-type, where StdOFF cells represent >99% of the population (6). A control was simultaneously performed using genomic DNA from a Dam⁻ strain (SV5367). The methylation state of individual GATC sites was inferred from Southern blot analysis using enzymes that cut GATC sequences depending on their methylation state (MboI, DpnI and SstI). All three GATC sites within the std UAS were found to be methylated in the wild-type (Figure 9A).

Because Southern blot analysis cannot be applied to the StdON cell lineage due to small size (6), StdON and StdOFF cell lineages were separated by magnetic activated cell sorting (MACS) using a strain that expressed hdfR under the control of the Ptet promoter (SV9602). Genomic DNAs were digested with MboI, which cuts nonmethylated DNA and DpnI, which cuts methylated DNA. The methylation
Figure 6. Binding of HdfR to the std promoter in vitro and in vivo. (A) Electrophoretic mobility shift assay performed with increasing amounts of purified HdfR-His6 and methylated and nonmethylated versions of a FAM-labeled stdA promoter probe. (B) Competition assay with excess of ‘cold’ DNA fragment. (C) In vivo analysis of HdfR binding to the std UAS by ChIP coupled with quantitative PCR. The experiment was performed in Dam+ and Dam− backgrounds. Data are averages and standard deviations from three independent experiments.

Figure 7. Role of individual GATC sites within the std UAS in transcriptional control. GATC-1 is the promoter-distal site, GATC-2 is the central site and GATC-3 is the promoter-proximal site. (A) Relative amounts of std mRNA transcribed from the stdA promoter in strains harboring one or more mutations in the GATC sites of the std UAS. Absolute data obtained with quantitative real-time PCR were normalized to the RNA content of the Dam− strain. Data are averages and standard deviations from five independent experiments. (B) EMSA analysis performed without HdfR (−) or with 500 ng of purified HdfR-His6 (+). Binding assays employed FAM-labeled std promoter probes carrying mutations in GATC-1, GATC-2 and GATC-3. A FAM-labeled std fragment containing the wild-type sequence was included as a positive control.

The state of the std UAS was determined by quantitative PCR. A delay in amplification compared with non-digested DNA indicated digestion. Results were as follows:

(i) DNA from StdOFF cells (Figure 9B, upper panel) showed delayed amplification of DpnI-treated DNA while MboI-treated DNA behaved as the control. Hence, we infer that the std UAS is methylated in StdOFF cells, in agreement with the evidence presented in Figure 9A.

(ii) DNA from StdON cells (Figure 9B, bottom panel) showed delayed amplification of both MboI- and DpnI-treated DNAs, suggesting that methylated and nonmethylated GATC sites are present. Because GATC-1 appears to lie outside the HdfR binding site (Figure 7), a tentative conclusion may be that GATC-1 may be methylated and that either GATC-2 and GATC-3 or both GATC-2 and GATC-3 may be nonmethylated in StdON cells.

DISCUSSION

The existence of epigenetic switches under DNA methylation control has been known for several decades, and a paradigm is the pap operon of uropathogenic E. coli (29,30). Additional examples include the agn43 and sci1 loci in E. coli (31–35) and the gtr and opvAB operons in S. enterica (36–38). In all these examples, formation of OFF and ON subpopulations is a consequence of bistable transcription, reversible (‘phase-variable’) or not. Another trait shared by those loci is formation of non-methylated GATC sites in regions that control transcription initiation (28,39). Non-methylation is in turn caused by GATC site occlusion and DNA methylation hindrance upon binding of transcriptional regulators to cognate regulatory regions (39,28).
Even though complex from a mechanistic point of view, the epigenetic switches that control bistability of the above loci are simple if compared with std. One complication comes from the fact that the std operon encodes pleiotropic regulators of transcription that activate or repress numerous genes (6). As a consequence, transition to the stdON state triggers not only cell fimbriation but additional phenotypic changes whose physiological significance remains to be fully understood (6). The speculation that these phenotypic differences may contribute to adapt stdOFF and stdON subpopulations to distinct host environments may be however reasonable (6).

Another difference between std and other bistable loci under DNA methylation control is the sheer complexity of the mechanisms that control std bistability. Switching of scil, agr43, gtr and opvAB is under the control of one main regulator (Fur or OxyR) while switching of pap is controlled by two main regulators, Lrp and PapI (40,29–30). In contrast, bistable expression of std is controlled by a network of regulators that includes StdE and StdF, two transcription factors encoded on the std operon itself, and HdfR, a LysR-type factor encoded outside the std operon. Transcription of hdfR is activated by StdE (Figure 3) and transcription of std is activated by StdF and by HdfR (Figures 2 and 4), thereby creating a complex feedback loop: StdE is necessary for HdfR synthesis and HdfR is necessary for StdE and StdF synthesis. In addition, StdF is an autogenous activator of std transcription.

The StdE-StdF-HdfR circuit of std activation is subjected to negative control by DNA adenine methylation, a trait shared with other Dam-dependent bistable switches (40). Binding of HdfR to the std UAS in vitro is hindered if GATC sites embedded in the region are methylated (Figure 6), and the std UAS is methylated in the stdOFF cell lineage (Figure 9). In turn, the UAS of stdON cells may harbor methylated and non methylated GATC sites (Figure 9), a feature reminiscent of the regulatory patterns found in other Dam-dependent switches (28–29,39). HdfR prevents methylation of GATC-2 and GATC-3 in vitro (Figure 8), suggesting that formation of nonmethylated GATC sites in vivo may be a consequence of HdfR binding, in a fashion analogous to Dam methylation hindrance caused by other transcription factors (39).

In the model presented in Figure 10, we tentatively propose that methylation of the two promoter-proximal GATC sites (GATC-2 and GATC-3) hinders HdfR binding, thus preventing activation of the StdE-StdF-HdfR feedback loop. Because the upstream GATC site (GATC-1) appears to be dispensable for HdfR-mediated transcriptional control (Figure 7), its methylation state may not be relevant. However, this feature of the model must be considered hypothetical.

The molecular mechanisms that trigger std switching to the ON state remain speculative at this stage. However, a combination of experimental evidence and analogy with other Dam methylation-dependent switches may suggest the following chain of events:

(i) Low, noisy expression of the std operon may produce cell-to-cell variations in the amounts of StdE and StdF. In certain cells, StdE and StdF may reach a critical threshold. Above the threshold, StdE may activate hdfR transcription.

(ii) Activation of hdfR transcription by StdE may disrupt the negative feedback loop generated by autogenous repression of transcription by HdfR. As a consequence, the level of HdfR will increase, and binding of both StdF and HdfR to the UAS will activate std transcription. The mechanism by which HdfR overrides methylation of the std UAS remains unknown. However, analogy with models proposed for other Dam-dependent switches (41,42) supports the speculation that HdfR binding to the std UAS may occur upon UAS hemimethylation after DNA replication.

(iii) Ordinary intracellular concentration of HdfR may be sufficient to activate std transcription in rare cells but not to propagate the stdON state to the progeny (Figure 5, panel A). Inheritance of the stdON state is however observed upon increasing the HdfR concentration (Figure 5B). Because the intracellular concentration of HdfR is in turn dependent on StdE, the strength of the StdE-StdF-HdfR feedback loop may determine whether the stdON state is heritable or not.

The mechanism(s) that foster return from the stdON to the stdOFF state remain unknown. Any signal or condition that disrupts StdE-StdF-HdfR positive feedback may be able to trigger transition to OFF, and a drop in the con-
Figure 9. In vivo assessment of the methylation state of the GATC sites within the std UAS in Std\textsuperscript{ON} and Std\textsuperscript{OFF} subpopulations. (A) Southern blot of genomic DNA obtained from wild-type and non-methylated cultures, used as a control (Dam\textsuperscript{−}), digested with Spl (control, NC) and DpnI, MboI or Sau3AI (Bottom). (B) Methylation state of Std\textsuperscript{ON} and Std\textsuperscript{OFF} subpopulations inferred from quantitative PCR analysis after digestion with enzymes that cut GATC sequences depending on their methylation state (MboI and DpnI).

Figure 10. Model for formation of Std\textsuperscript{OFF} and Std\textsuperscript{ON} bacterial cell lineages. Methylated GATC sites are shown as black boxes and nonmethylated GATC sites as white boxes. The dashed line indicates that StdE-mediated disruption of autogenous hfdR control is hypothetical.
centration of HdfR can be expected to be crucial as it may permit methylation of the UAS.

Transcriptional control by more than one regulator can often be described by Boolean-type functions such as AND and OR logic gates (43). The regulatory mechanisms described in this study may be therefore be considered a complex AND logic gate involving three regulators and an epigenetic checkpoint. Positive StdE-StdF-HdfR feedback may imbalance the system toward the StdON state, while DNA adenine methylation may provide an explosion-preventing mechanism found in many bistable switches (44). In fact, lack of DNA adenine methylation locks the std switch in the ON state (9).

DATA AVAILABILITY

The NCBI genome assembly of S. enterica SL1344 was used as reference genome (NCBI GCA_000210855.2). Raw and processed data from ChIP-seq analysis have been deposited at the Gene Expression Omnibus (GEO) database (http://www.ncbi.nlm.nih.gov/geo/), with accession number GSE113562.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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