Protection against deleterious nitrogen compounds: role of $\sigma^S$-dependent small RNAs encoded adjacent to sdiA

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ABSTRACT

Here, we report the characterization of a set of small, regulatory RNAs (sRNAs) expressed from an Escherichia coli locus we have denoted sdsN located adjacent to the LuxR-homolog gene sdiA. Two longer sRNAs, SdsN137 and SdsN178 are transcribed from two $\sigma^S$-dependent promoters but share the same terminator. Low temperature, rich nitrogen sources and the Crl and NarP transcription factors differentially affect the levels of the SdsN transcripts. Whole genome expression analysis after pulse overexpression of SdsN137 and assays of lacZ fusions revealed that the SdsN137 directly represses the synthesis of the nitroreductase NfsA, which catalyzes the reduction of the nitrogroup (NO2) in nitroaromatic compounds and the flavohemoglobin HmpA, which has aerobic nitric oxide (NO) dioxygenase activity. Consistent with this regulation, SdsN137 confers resistance to nitrofurans. In addition, SdsN137 negatively regulates synthesis of NarP. Interestingly, SdsN178 is defective at regulating the above targets due to unusual binding to the Hfq protein, but cleavage leads to a shorter form, SdsN124, able to repress nfsA and hmpA.

INTRODUCTION

In order to survive in many different, constantly-changing environments, bacteria have intricate mechanisms to sense environmental cues and increase or decrease the levels of the appropriate proteins and enzymes at the transcriptional and/or post-transcriptional levels. Key post-transcriptional regulators are small RNAs (sRNAs), typically 50 to 300 nucleotides in length, that base pair with mRNAs encoded in trans at a distinct genomic location (1,2). By base pairing at or near the ribosome-binding site, the sRNAs can block translation. These sRNAs can also activate translation when base pairing results in a change in mRNA secondary structure that liberates a ribosome binding site. In addition, base pairing can lead to the recruitment of RNase E either in conjunction with or independent of effects on ribosome binding. Given the limited complementarity to their target mRNAs, the sRNAs in a number of bacteria including Escherichia coli require the RNA chaperone Hfq to stabilize the sRNAs and facilitate RNA–mRNA duplex formation (3,4).

Many base pairing sRNAs are induced in response to very specific environmental signals and then act to protect the cells and/or make maximal use of limited resources under these conditions. For example, RyhB, whose levels are induced by conditions of iron starvation, represses the synthesis of non-essential iron-storage and iron-utilization proteins (5). Similarly, FnrS RNA, whose levels are induced by oxygen limitation, represses the synthesis of proteins that are not needed under anaerobic conditions (6,7). Three $\sigma^E$-dependent sRNAs, RybB, MicA and MicL, that are all induced by cell envelope stress, repress the synthesis of all abundant outer membrane proteins thus allowing chaperones required for the insertion of new proteins to be redirected to misfolded cell envelope proteins (8).

Expression of a number of sRNAs is highest in stationary phase (9), conditions under which bacteria undergo substantial changes in morphology and physiology to conserve energy and become resistant to starvation and various environmental stresses. The key regulator in stationary phase is $\sigma^S$, encoded by the rpoS gene (10,11). This alternative sigma factor directs the expression of hundreds of genes when cells enter stationary phase or encounter other stresses, alone at some promoters and in conjunction with additional transcription factors at other promoters. The GadY, SraL and

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SdsR sRNAs have been shown to be σ8-dependent sRNAs (12–14). GadY, positively regulates the expression of GadX and GadW, two transcription factors controlling the acid response, by directing cleavage of the gadZW mRNA to give more stable products (13,15). SraL was found to down-regulate the expression of the hom gene, which encodes the chaperone Trigger Factor involved in protein folding (14). SdsR acts as a repressor by base pairing with the coding region of mutS encoding a component of the methyl-directed mismatch repair complex and the 5′UTR of tolC encoding an outer membrane porin in E. coli (16,17). In Salmonella, SdsR also represses synthesis of the major porin OmpD by basepairing with the coding region of the ompD mRNA (12).

Here, we report on another σ8-dependent sRNA in E. coli. SdsN, which is induced in stationary phase, particularly when cells are grown at low temperature or with preferred nitrogen sources, and regulates the levels of the nitrate- and nitrite-responsive NarP transcription factor as well as enzymes that metabolize oxidized nitrogen compounds.

MATERIALS AND METHODS

Bacterial strains and plasmids

The strains and plasmids used in this study are given in Supplementary Tables S1 and S2, respectively. E. coli K-12 MG1655 was employed as the wild-type (WT) strain. Phage λ Red-mediated recombineering was used to construct deletion alleles marked by KmR flanked by FRT (FLP recognition target) sites, which were amplified using pKD13 as template for PCR (18). After P1 transduction into MG1655, the Km cassette was removed by introduction of the FLP expression plasmid pCP20. Other alleles were transduced from previously published strains (19,20). The nfsA-lacZ, hmpA-lacZ and narP-lacZ translational fusions were created as described (21); the first nine codons of nfsA and hmpA, or the first 30 codons of narP as well as the entire 5′-UTR of each gene were PCR amplified and fused to lacZ driven by an arabinose-inducible pBAD promoter. SdsN derivatives were overexpressed from the PBPlac plasmid (22). The sdsN178, sdsN137 and sdsN124 fragments were PCR amplified from MG1655 chromosomal DNA, digested with EcoRI and AatII, and cloned into the corresponding sites of PBPlac. The mutant derivatives of the lacZ fusions and SdsN-overexpression plasmids were generated by overlapping PCR and introduced into the chromosome or PBPlac as described above. All plasmid and chromosomal constructs were verified by DNA sequencing. Primers used for PCR and sequencing are listed in Supplementary Table S3.

Growth conditions

Unless indicated otherwise, bacterial strains were grown overnight with shaking at 37°C in Luria Broth (LB) or M63 with 0.2% glucose media, both supplemented with standard concentrations of the appropriate antibiotics, and then diluted (OD600 ≈ 0.02–0.03) into the same medium. For the nitrofuranzone sensitivity assays, back-diluted cultures were grown to OD600 ≈ 0.3 in LB or for 14 h in M63 glucose. Half of each culture was challenged with 1 or 2 mM nitrofurazone (Sigma) or azomycin (Sigma) for 1 h after which 100 μl of 10−5-dilutions of the LB cultures and 10−6-dilutions of the M63 glucose cultures were plated on LB agar.

RNA extraction

Total RNA was isolated by extraction with hot acid phenol (23) or TRIzol Reagent (Ambion). For the hot acid phenol extraction, RNA was isolated from 750 μl of LB-grown cells or 10 ml of cells grown in M63 glucose, collected and resuspended in 700 μl of M63. For both types of samples, the cells were mixed with 500 μl of acid-phenol-chloroform (Ambion) and 102 μl of cell lysis solution (320 mM sodium acetate, 8% SDS and 16 mM EDTA) and incubated 15 min at 65°C. Supernatants were transferred to a new tube containing pre-heated 500 μl of acid-phenol-chloroform and incubated at 65°C for another 15 min. RNA was precipitated with 700 μl of 100% ethanol. For the TRIzol extraction, total cellular RNA was isolated from ≈5–10 OD600 of cells according to the manufacturer’s instructions. RNA was precipitated by combining the ≈0.6 ml of the top aqueous phase with 0.5 ml isopropyl alcohol. For both extraction methods, precipitated RNA pellets were washed with 70% ethanol and resuspended in nuclease-free water. Total RNA concentrations were determined using a NanoDrop (Thermo Scientific).

Northern analysis

Total RNA (10 μg) was separated on a 8% polyacrylamide-7M urea gel in 1X TBE (90 mM Tris-borate 2 mM EDTA). The RNA was transferred to a Zeta-Probe GT blotting membrane (Bio-Rad) at 20V for ~16 h at 4°C in 0.5X TBE. After transfer, membranes were allowed to dry, UV cross-linked on both sides, and incubated overnight at 45°C in UltraHyb (Ambion) hybridization buffer and oligonucleotide 5′-end-labeled with 32P-ATP with T4 polynucleotide kinase (New England Biolabs). Subsequently, membranes were washed once with 2X SSC (150 mM NaCl 15 mM sodium citrate) 0.1%SDS, incubated 10 min at 45°C in 2X SSC 0.1%SDS, and washed 5X with 0.2X SSC 0.1% SDS. After washing, air-dried membranes were exposed to HyBlot CL film (Denville Scientific) at −80°C.

Primer extension analysis

Primer extension assays were carried out as previously described (24). Briefly, RNA samples (5 μg of total RNA) were incubated with 2 pmol of 5′-32P-end-labeled primer at 80°C and then slow-cooled to 42°C. After the addition of dNTPs (1 mM each) and AMV reverse transcriptase (10 U, Life Sciences Advanced Technologies Inc.), the reactions were incubated in a 10 μl reaction volume at 42°C for 1 h. Reactions were terminated by adding 10 μl of Gel Loading Buffer II (Ambion). The DNA sequencing ladder was generated using Thermo SequenaseTM Dye Primer Manual Cycle Sequencing Kit (Affymetrix) and an sdsN or sdiA PCR fragment. The cDNA products and sequencing ladder were fractionated on an 8% polyacrylamide urea sequencing gel containing 8 M urea in 1X TBE buffer at 70 W for 70 min.
The gel was dried and imaged using a STORM 840 (Ameri-
sham Biosciences).

**Terminator-5’-phosphate-dependent exonuclease (TDE) di-
genesis**

Total RNA (7 μg) extracted from MG1655 cells grown to
OD$_{600}$ ≈ 5 at 25°C in LB or 20 h at 37°C in M63 glucose
were placed in two RNa-se-free 1.5 ml tubes; the sample
in one was treated with TDE (Epitome) while the second
sample was incubated with buffer as described (8).

**In vitro RNA synthesis**

The narP, hmpA, SdsN$_{137}$ and SdsN$_{178}$ RNAs were syn-
thesized using Megascript T7 kit (Ambion). SdsN$_{137}$
and SdsN$_{178}$ RNA were 5’-end-labeled with $^{32}$P by treating
the RNA with alkaline phosphatase (New England Bi-
olabs) and then T4 polynucleotide kinase. $^{32}$P-labeled
RNAs were purified from 8% polyacrylamide-7M urea
gels by excising and crushing the bands in RNA elution
buffer (0.1 M sodium acetate, 0.1% SDS and 10 mM
EDTA). The elution was extracted with an equal volume of
phenol:chloroform:IAA (Invitrogen). The RNA was then
ethanol precipitated, re-suspended in nuclease free dH$_2$O
and quantified using the NanoDrop.

**In vitro RNA structure probing**

$^{32}$P-labeled SdsN$_{137}$ or SdsN$_{178}$ (~2 nM) was incubated
with purified Hfq (or equal volume of buffer) and 1 μg of
yeast RNA (Ambion) in 1X RNA structure buffer (Ambi-
on) in a total volume of 8 μl at 37°C for 15 min. Samples
were mixed with RNase T1 (0.02 U, Ambion) or an
equal volume of buffer and incubated at 37°C for 6
min. Inactivation/Precipitation Buffer (20 μl, Ambion) was
added, and samples were placed at −80°C for ∼30 min.
RNA pellets were collected by centrifugation, washed with
100 μl of 70% ethanol, air-dried and dissolved in 7 μl Gel
Loading Buffer II. For the hydroxide (OH) ladder, 1 μl of
$^{32}$P-labeled SdsN$_{137}$ or SdsN$_{178}$ in 9 μl Alkaline Hydro-
lysis Buffer (Ambion) was incubated 5 min at 90°C. For the
RNase T1 ladder, 1 μl of $^{32}$P-labeled SdsN$_{137}$ or SdsN$_{178}$ in 9 μl Sequencing Buffer (Ambion) was denatured by incu-
bating at 95°C for 1 min followed by cooling to 37°C. RNase
T1 (0.1 U) was added, and the sample was incubated for 5
min at 37°C. For both ladders, the reactions were stopped
by adding 12 μl of Gel Loading Buffer II. Samples (2 μl)
were run on a 8% polyacrylamide-7M urea sequencing gel
in 1X TBE. The gel was transferred onto Whatman filter
paper, dried at 80° for 1 h, and imaged using the STORM
840.

**Electrophoretic mobility shift assays (EMSA)**

$^{32}$P-labeled SdsN$_{137}$ or SdsN$_{178}$ RNA (4 nM) was incubated
at 37°C for 15 min with purified Hfq and 1 μg of yeast RNA
in 1X RNA Structure Buffer in a total volume of 10 μl. For
some samples, 1 μl 1X RNA Structure Buffer or unlabel-
ed hmpA or narP RNA diluted in 1X RNA Structure Buffer
was added and samples were incubated at room temperature
for an additional 1 h. After the indicated incubation, 2.5 μl
of non-denaturing RNA loading buffer (100 mM NH$_4$Cl,
50 mM NaCl, 50 mM KCl, 20 mM Tris-HCl, pH 8 and 50%
glycerol) was added to each sample. Samples were then sep-
ated at 100 V on a native 6% polyacrylamide gel (37.5:1
Bis-Acrylamide, National Diagnostics) at 4°C in pre-chilled
0.5X TBE. Gels were imaged using the STORM 840.

**Microarray analysis**

MG1655 cells harboring pBR, pBR-SdsN$_{137}$ or pBR-
SdsN$_{178}$ were grown to OD$_{600}$ ≈ 0.4 in LB at 37°C,
then cells were induced with 100 μM isopropyl β-D-
thiogalactopyranoside (IPTG) for 5 min. Cells were har-
vested and total RNA was isolated by hot-phenol method.
Chromosomal DNA was removed with DNase I treatment
before cDNA synthesis and hybridization of cDNA to the
Affymetrix E. coli Genome2.0 array was carried according
to the instructions in Affymetrix manual.

**Immunoblot analysis**

Cells collected from 1 ml of culture were resuspended in 80
μl/ OD$_{600}$ 1X SDS PAGE loading buffer containing 5% β-
mercaptoethanol, heated for 20 min at 95°C and then
loaded onto a 4–15% Tris-Glycine gel (BioRad). Proteins
were transferred onto a nitrocellulose membrane (Invitro-
gen) at 100 V for 1 h at 4°C in 1X Tris-glycine-SDS run-
ning buffer (KD Medical) with 20% methanol. Membranes
were blocked 1 h at room temperature in 1X PBST (phos-
phate buffer saline with Tween20, Corning) with 5% milk
and then probed with a 1:4000 dilution of α-RpoS anto-
body (provided by Susan Gottesman, NCI) for ∼16 h at 4°C.
After three washes in 1X PBST, membranes were incubated
with a 1:5000 dilution of HRP-anti-rabbit IgG (Sigma) for
1 h at room temperature. After three additional washes,
membranes were developed using SuperSignal® West Pico
Chemiluminescent Substrate (Thermo Scientific) and ex-
plored by HyBlot CL film.

**β-galactosidase assays**

Three or four individual colonies from the indicated lacZ
translational fusions transformed with pBR plasmids were
grown overnight at 37°C in LB media containing 100 μg/ml
ampicillin, diluted to an OD$_{600}$ = 0.03 into fresh LB media
with 100 μg/ml of ampicillin and 0.2% arabinose (to induce
lacZ expression). IPTG (100 μM or 1 mM) was simultane-
ously added to some of the samples to induce expression
from the pBR plasmids. Cells were grown to OD$_{600}$ ≈ 0.5 or
1.0 and then lysed in 700 μl of Z buffer containing 0.002%
SDS and 30 μl chloroform. β-galactosidase activity levels
were assayed as described before (6).

**RESULTS**

**Multiple sRNA species are transcribed from the sdiA-tcyN
intergenic region**

Microarray analysis of RNAs that co-immunoprecipitate
with Hfq in E. coli suggested an sRNA bound by Hfq was
encoded in the intergenic region between sdiA, the gene
for a LuxR-family transcription regulator that serves as a ‘suppressor of the cell division inhibitor’, and tcyN (formerly yecC), the gene for the ATP binding subunit of an L-cystine/L-cysteine ABC transporter (Figure 1A), but no signal was detected by northern analysis under the conditions examined (25). Recent deep sequence analysis of the E. coli transcriptome again showed a small transcript is encoded in the sdiA-tcyN intergenic region (26,27). To obtain further information about the expression of this putative sRNA, we probed the total RNA isolated from E. coli MG1655 grown to different stages in LB rich medium and M63 glucose minimal medium at 37°C (Figure 1B). We now detected multiple transcripts, particularly in stationary phase. The two most prominent bands were ~140 nt (SdsN178) and ~180 nt (SdsN137), with the highest levels at OD600 ≈ 5 in LB medium and after 20 h of growth in M63 glucose medium. A number of additional bands were also observed for both samples. Probing with a downstream oligonucleotide showed that the longest transcripts prevalent early in growth are 3′ extensions of the major transcripts (Supplementary Figure S1A). In contrast, the shorter transcripts of ~120 nt (SdsN124) lack the 5′ end. These smaller RNAs accumulate in late stationary phase, especially in M63 glucose medium.

The 5′ ends of the ~140 and ~180 nt transcripts were mapped by primer extension analysis (Supplementary Figure S1B) and examination of transcriptional promoter mapping data (27). While multiple 5′ ends were detected by both approaches, the promoter mapping data indicate the prominent bands correspond to transcripts of 137 and 178 nt that share the same Rho-independent terminator (Figure 2A). Both forms were not fully digested by terminase exonuclease from RNA extracted from cells grown in LB and M63 glucose media (Supplementary Figure S1C), unlike the complete digestion observed for the processed derivative of SdsR. Thus, SdsN178 and SdsN137 likely have 5′-triphosphates consistent with transcription from two distinct promoters. The 5′ end of the ~120 nt transcript was also mapped by primer extension analysis, which showed that one form is 124 nt (Supplementary Figure S1B). This band is no longer detected upon terminase exonuclease treatment indicating it is derived by processing (Supplementary Figure S1C).

We also monitored the induction of the sdsN promoter by integrating the lacZ reporter gene downstream of both the sdsN178 and sdsN137 promoters. Expression of this P<sub>sdsN</sub>-lacZ fusion was low in exponential phase and increased in stationary phase, particularly in cells grown at lower temperatures (Supplementary Figure S2A).

**Stationary phase induction of SdsN is dependent on σ<sup>S</sup>**

The stationary phase induction of SdsN suggested regulation by σ<sup>S</sup>. To investigate this possibility, we examined the SdsN levels in an rpoS deletion strain. Northern analysis showed that the levels of all SdsN transcripts are significantly lower in an ΔrpoS mutant strain in both LB (Supplementary Figure S2B) and M63 glucose medium (Figure 2B), indicating SdsN is indeed a σ<sup>S</sup>-dependent sRNA. Consistent with the northern analysis, expression from the P<sub>sdsN</sub>-lacZ fusion also was decreased in the rpoS mutant strain (Supplementary Figure S2A).

We also compared the levels of SdsN with the levels of the other known σ<sup>S</sup>-dependent sRNAs (12–14). Interestingly, the expression patterns are not identical, and do not necessarily correlate with the highest levels of σ<sup>S</sup> (Figure 1B). In LB, the levels of SdsN, GadY and SraL begin to increase at OD600 ≈ 3 and are highest at OD600 ≈ 5, while the levels of SdsR increase and peak at later time points. In M63 glucose medium, the peak of GadY expression is much earlier than...
Figure 2. SdsN expression is dependent on σ^S. (A) Sequence of sdsN and sdsN-sdiA promoter region. The sequence that is common to SdsN178 and SdsN137 is shaded in dark grey, while the sequence specific to SdsN178 is shaded in light grey. The mapped transcription start sites of SdsN178 and SdsN137 are indicated with arrows that show the direction of transcription; the corresponding −10 sequences are boxed. Two transcription start sites for the sdiA gene are also indicated with arrows that show the direction of transcription. The −10 elements for both sdiA transcription start sites are denoted with brackets. The 5′ end of SdsN124 is also indicated with a vertical bracket. The sdiA start and tcyN stop codons are italicized, and the sequences corresponding to the stem of the SdsN terminator are underlined. (B) Levels of SdsN in WT, Δcrl, ΔrpoS, and ΔrpoS Δcrl cells. Total RNA was isolated from WT MG1655 and the isogenic Δcrl::kan (GSO760), ΔrpoS::Tn10 (GSO108) and Δcrl::kan ΔrpoS::Tn10 (GSO761) mutants grown 20 h in M63 glucose media (to OD600 ≈ 2.39, 2.40, 2.48 and 2.45, respectively) and analyzed as in Figure 1. (C) Effect of non-preferred and preferred nitrogen sources on SdsN levels. WT MG1655 and ΔnarP mutant (GSO763) cells were grown 20 h in M63 glucose with preferred ammonium (15 mM) or non-preferred arginine (0.2%) as the sole nitrogen source (to OD600 ≈ 3.61 and 2.36, respectively for wild-type cells and OD600 ≈ 3.62 and 2.76 for the ΔnarP mutant cells). RNA was processed for northern analysis as in Figure 1.

the peaks for SdsN, SraL and SdsR. Furthermore, there is limited sequence similarity among the sdsN, gadY, sdsR and sraL promoters (Supplementary Figure S2C). These observations suggest additional factors may modulate the transcription of SdsN as well as the other σ^S-dependent sRNAs or σ^S is acting indirectly, possibly by modulating sRNA stability.

σ^S-dependent induction of SdsN is impacted by nitrogen availability

Given the partial match to the consensus σ^S promoter (Supplementary Figure S2C) and sdsN-lacZ induction at low temperature (Supplementary Figure S2A), we considered the possibility that expression might be influenced by the Crl assembly factor, which stimulates σ^S binding to RNA polymerase and thus enhances expression from σ^S-dependent promoters when Crl levels are elevated under conditions such as low temperature (28–30). Consistent with an influence of Crl, the levels of SdsN178 and SdsN137 are somewhat lower in a crl deletion strain grown in both LB (Supplementary Figure S2B) and M63 glucose (Figure 2B) medium.

Since Crl levels are modulated by nitrogen, with reduced Crl synthesis under conditions of nitrogen limitation (30), we examined SdsN expression in cells grown in M63 glucose medium with rich and poor nitrogen sources. Growth on the preferred nitrogen source ammonium was associated with higher SdsN levels than growth on the poor nitrogen source arginine (Figure 2C). There are a number of transcription factors that regulate gene expression in response to nitrogen availability. One of these is NarP, the response regulator of the NarP-NarQ two-component system, which mediates the nitrate/nitrite responsive transcriptional regulation of anaerobic respiration (31). Since we found narP to be a target of SdsN (see below), we considered the possibility of a feedback loop and examined SdsN levels in a ΔnarP background (Figure 2C). We did not observe a significant difference between the two strains grown with ammonium,
but interestingly, the levels of SdsN\textsubscript{178} and SdsN\textsubscript{137} were elevated, and the level of SdsN\textsubscript{124} was reduced in the ΔnarP strain grown with arginine.

Given the proximity between sdsN and sdiA and reports of SdiA autoregulation (32), we also wondered whether the LuxR-type SdiA transcription factor impacts SdsN levels. Primer extension analysis (Supplementary Figure S3A) and dRNA-seq data (27) revealed two sdiA transcription start sites. These are both absent in an ΔsdiA mutant but differ from the previously reported starts (33), which we still detect in the ΔsdiA mutant and thus are likely to be artifacts (Supplementary Figure S3B). Both of the corresponding promoters overlap the sdsN promoters (Figure 2A). We examined the levels of SdsN in two ΔsdiA backgrounds but did not find a significant difference in SdsN expression under the conditions tested (Supplementary Figure S3C).

**SdsN\textsubscript{137} and SdsN\textsubscript{178} bind the RNA chaperone Hfq with different affinities**

Energetically favorable secondary structures of SdsN\textsubscript{137} (Figure 3A) and SdsN\textsubscript{178} (Supplementary Figure S4) were predicted using mfold (34). These predictions are supported by in vitro RNase T1 cleavage (Figure 3B). SdsN\textsubscript{137} and SdsN\textsubscript{178} contain the same two stem-loop structures, with the 3′ stem-loop forming the Rho-independent terminator. The 5′ AU-rich region present only on SdsN\textsubscript{178} appears to be largely single stranded.

While one report suggested the RNA encoded in the sdiA-tcyN intergenic region was bound by Hfq (25), another report showed the transcript was not stabilized by Hfq (26). To resolve this discrepancy, we subjected extracts from stationary phase cells to immunoprecipitation with either Hfq antibody or preimmune serum. Total RNA from WT and hfq mutant cells as well as immunoprecipitated RNA were probed for SdsN. The different forms of SdsN were detected by immunoprecipitation with Hfq. However, we observed stronger enrichment for SdsN\textsubscript{178} than for SdsN\textsubscript{137} or SdsN\textsubscript{124} (Figure 3C). The enhanced Hfq binding to SdsN\textsubscript{178} relative to SdsN\textsubscript{137} in vivo was also observed in an EMSA in vitro binding assay in which increasing amounts of purified Hfq were added to radiolabeled SdsN\textsubscript{137} or SdsN\textsubscript{178} in the presence of an excess of competitor RNA (Figure 3D). The addition of Hfq to both sRNAs resulted in two shifts in mobility (complex I and II), similar to what is observed upon Hfq binding to other sRNAs (35). The dissociation constant (K\textsubscript{d}) for RNA bound to Hfq in complex I, was calculated to be ∼80 nM for SdsN\textsubscript{137} and ∼28 nM for SdsN\textsubscript{178}, comparable to the 25 nM K\textsubscript{d} observed for DsrA and RprA using the same assay (35). Together these results show Hfq binds SdsN\textsubscript{178} with higher affinity than SdsN\textsubscript{137} in vivo and in vitro. Structure probing carried out after incubating SdsN\textsubscript{138} and SdsN\textsubscript{178} with Hfq (Figure 3B), showed one region of protection (G96 G97 G99) for SdsN\textsubscript{137}, a region between two stem-loops and another in the 5′ extension.

**SdsN\textsubscript{137} targets mRNAs encoding proteins involved in the metabolism of and response to nitrogen compounds**

Given SdsN\textsubscript{137} and SdsN\textsubscript{178} association with Hfq, we postulated the sRNAs were acting to modulate expression by basepairing with target mRNAs. To identify possible targets, we examined the genome-wide changes in RNA levels upon short-term overproduction of either SdsN\textsubscript{137} or SdsN\textsubscript{178}. Exponentially-growing MG1655 cells carrying the pBR vector control, pBR-SdsN\textsubscript{137} or pBR-SdsN\textsubscript{178} were induced with 100 μM IPTG for 5 min after which total RNA was isolated and analyzed on microarrays (Supplementary Table S4). Table 1 lists genes showing greater than two-fold changes upon SdsN\textsubscript{137} overexpression in the two independent experiments.

**SdsN\textsubscript{137} overexpression led to the repression of three mRNAs encoding proteins associated with the metabolism of and response to nitrogen compounds.**

*SdsN\textsubscript{137} overproduction did not fall into a single category (cyaY, uraA, inaA and rhuA were down-regulated and fliC and ymT were up-regulated). We generated lacZ fusions to cyaY, uraA and inaA as described for nfsA, hmpA and narP**

### Table 1. Transcripts changed more than 2-fold upon SdsN\textsubscript{137} overexpression

<table>
<thead>
<tr>
<th>Gene</th>
<th>Function</th>
<th>Array 1</th>
<th>Array 2</th>
</tr>
</thead>
<tbody>
<tr>
<td>*nfsA</td>
<td>Oxygen-insensitive nitroreductase</td>
<td>7.7↓</td>
<td>2.7↓</td>
</tr>
<tr>
<td>*ybJC</td>
<td>Predicted oxidase co-transcribed with nfsA</td>
<td>2.4↓</td>
<td>2.6↓</td>
</tr>
<tr>
<td>*hmpA</td>
<td>NO dioxygenase, flavohemoglobin</td>
<td>2.9↓</td>
<td>2.3↓</td>
</tr>
<tr>
<td>*narP</td>
<td>Nitrate/nitrite response regulator</td>
<td>2.6↓</td>
<td>2.7↓</td>
</tr>
<tr>
<td>cyaY</td>
<td>Frataxin homolog with role in iron-sulfur cluster assembly</td>
<td>2.5↓</td>
<td>2.6↓</td>
</tr>
<tr>
<td>*uraA</td>
<td>High-affinity uracil/protein syrump system</td>
<td>2.6↓</td>
<td>2.2↓</td>
</tr>
<tr>
<td>*inaA</td>
<td>Induced by low pH</td>
<td>2.1↓</td>
<td>2.2↓</td>
</tr>
<tr>
<td>rhuA</td>
<td>23S rRNA and tRNA pseudouridine synthase</td>
<td>2.0↓</td>
<td>2.0↓</td>
</tr>
<tr>
<td>fliC</td>
<td>Flagellin</td>
<td>2.1†</td>
<td>2.6†</td>
</tr>
<tr>
<td>ymT</td>
<td>Predicted DNA-binding transcription regulator, e14 phage</td>
<td>2.5†</td>
<td>3.2†</td>
</tr>
</tbody>
</table>

Arrows indicate genes repressed (↓) or induced (↑) upon SdsN\textsubscript{137} overexpression. mRNAs for genes marked with an asterisk (*) are bound by Hfq (20). Annotation of function is from Ecocyc.org (52).
Figure 3. Both SdsN\textsubscript{137} and SdsN\textsubscript{178} bind Hfq. (A) Structure of SdsN\textsubscript{137} predicted by the mfold algorithm \cite{34}. Sites of RNase T1 cleavage as determined from Figure 3B are indicated by solid black dots with the size of the dots proportional to the amount of cleavage. Arrows indicate enhanced (↑) or repressed (↓) cleavage when RNA is pre-mixed with the indicated amounts of purified Hfq hexamer. The 5′ end of SdsN\textsubscript{124} is indicated with a vertical bracket. Regions involved in base pairing with narP at 5′ end and with nfsA and hmpA between two stem-loops are shaded. (B) Probing of SdsN\textsubscript{137} and SdsN\textsubscript{178} structures. Purified \textsuperscript{32}P end-labeled SdsN\textsubscript{137} and SdsN\textsubscript{178} were incubated with RNase T1 (Ambion) and, for indicated samples, 100 or 200 nM purified Hfq protein and run on an 8% polyacrylamide-7M urea sequencing gel. RNase T1 and OH ladders are shown. Sites of RNase T1 cleavage are indicated as in Figure 3A. (C) SdsN co-immunoprecipitation with Hfq. Cell extracts were prepared from WT MG1655 grown in LB to early stationary phase (OD\textsubscript{600} ≈ 5) and subject to immunoprecipitation with \textit{ ΔHfq} \textit{Hfq} or preimmune serum. Northern analysis was carried out on the immunoprecipitated samples (1 \textmu g RNA loaded) as well as on total RNA (10 \textmu g RNA loaded) isolated from WT MG1655 and the isogenic \textit{ΔHfq:cat-sacB} mutant (GSO748). (D) SdsN\textsubscript{137} and SdsN\textsubscript{178} both bind Hfq \textit{in vitro}. Purified \textsuperscript{32}P end-labeled SdsN\textsubscript{137} and SdsN\textsubscript{178} (4 nM) were incubated with the indicated amounts of purified Hfq hexamer for 15 min at 37° C. Samples were run on a native 6% polyacrylamide gel. Unbound, complex I and complex II are indicated by U, I and II, respectively. The intensities for the bands in each lane were determined using Multi Gauge Imaging Software V3.0. \textit{K}_d values were computed by plotting the appearance of protein–RNA complexes as a function of Hfq concentration using the saturation-binding feature of GraphPad Software.
below. However, we did not detect expression from the *inaA* fusion, and the *cyaY* and *uraA* fusions showed no regulation by SdsN137 (data not shown).

Interestingly, SdsN178 overproduction did not affect any of the genes modulated by SdsN137 (data not shown). In fact, only one mRNA, *casA* encoding a subunit of CRISPR-associated complex, showed a 2-fold increase in levels upon SdsN178 overproduction in the two experiments.

SdsN137 base pairs directly with *nfsA*, *hmpA* and *narP* mRNAs

The *ybjC-nfsA*, *hmpA* and *narP* mRNAs all co-immunoprecipitate with Hfq (20) and are predicted to have complementarity with SdsN137 (Figure 4A, C and E) by the IntARNA base pairing prediction program (38,39). For *nfsA* and *hmpA*, the predicted pairing is with the internal region of SdsN137 shown to be single stranded by structure probing of SdsN137 (Figure 3A and B). For *narP*, the predicted pairing is at the base of the 5′ stem, though this region is likely to be partially single stranded, as is the case for the FnRS 5′ stem (6). To test whether SdsN137 directly base pairs with these targets, we constructed chromosomal lacZ fusions with the 5′ UTR as well as first nine codons of *nfsA* and *hmpA* and the first 30 codons of *narP* fused to the tenth codon of lacZ, all transcribed from the heterologous arabinose-inducible P<sub>BAD</sub> promoter (21). As shown in Figure 4, all of the target-lacZ fusions were repressed 1.6- to 3-fold by SdsN137 overexpression compared to the vector control. Mutations were introduced into the two regions of SdsN137 predicted to pair with the *nfsA*, *hmpA* and *narP* mRNAs. Consistent with the predictions, the *nfsA-lacZ* and *hmpA-lacZ* fusions were not repressed by SdsN137-2 (Figure 4B and D), while *narP-lacZ* was not repressed by SdsN137-1 (Figure 4F) but was repressed by SdsN137-2 (data not shown). However, repression was regained for fusions carrying compensatory mutations, *nfsA-2-lacZ*, *hmpA-2-lacZ* and *narP-1-lacZ*, that restore base pairing with the SdsN137 mutants (Figure 4B, D and F). These results confirm direct base pairing between SdsN137 and the *hmpA*, *nfsA* and *narP* mRNAs, and show that SdsN137 utilizes at least two different regions to regulate targets.

SdsN137 protects against nitrofurans

Previous studies have shown that the NfsA nitroreductase sensitizes *E. coli* cells to nitrofurans, nitrogen compounds that contain one or more nitrogen groups on a nitroaromatic backbone, and that cells lacking NfsA are resistant to these antibiotics (40,41). To test whether SdsN regulation of *nfsA* affects the sensitivity to these compounds, we treated LB-grown cells with 1 mM of the nitrofurans nitrofurazone or azomycin for 1 h. Overexpression of SdsN137 led to more resistance to these antibiotics than the vector control, SdsN178 or SdsN137-2, the mutant unable to regulate *nfsA-lacZ* (Figure 5A and Supplementary Figure S5A). SdsN137 did not confer further resistance to nitrofurazone in a Δ*nfsA* background (Supplementary Figure S5B).

We also examined the sensitivity of WT and ΔsdsN mutant cells grown 14 h in M63 glucose medium, when SdsN levels are high, to a 1 h-exposure to 2 mM nitrofurazone. Consistent with chromosomally-expressed SdsN contributing to resistance against oxidized nitrogen compounds, we always observed fewer colonies for the ΔsdsN mutant strain than the WT parent strain after treatment with nitrofurazone (Figure 5B).

5′ end of SdsN178 inhibits regulation

We noted that none of the mRNAs showing regulation by SdsN137 in the microarray experiments were affected by SdsN178 overexpression. Since the two regions of SdsN137 involved in base pairing with *nfsA*, *hmpA* and *narP* are contained in SdsN178, we tested whether SdsN178 regulates the corresponding lacZ fusions. As seen in Figure 6A, SdsN178 was less effective at repressing all three fusions, particularly *narP-lacZ*.

To elucidate what sequences present in SdsN178 reduce regulatory function, we constructed a number of deletion, mutant and chimeric derivatives from SdsN178. The 5′ end sequence of SdsN178 is extremely AU rich, and previous studies have shown AU-rich sequences are preferentially bound by Hfq and cleaved by RNase E (4). We first generated a series of 5′-truncations of SdsN178 and assayed *narP-lacZ* activity upon overexpression of these derivatives (Figure 6B). All of the truncations were less effective than SdsN137 at repressing the *narP-lacZ* fusion, including the shortest truncation SdsN140, which is only three nucleotides longer than SdsN137. We further mutated the three AU residues at the 5′ end of SdsN140 by changing the residues to GC-rich sequences (AUU to CGG or GGG). With these changes, both of the mutants repress *narP-lacZ* as well as SdsN137 (Figure 6C). It is possible some of the defects in regulation are due to somewhat lower levels of the mutant derivatives (Supplementary Figures S6A and S6B), but the sRNAs expressed from the plasmids are in vast excess. We also fused the 5′ end of SdsN178 (nt 1–41) to the 5′ ends of the well-characterized RyhB and FnRS sRNAs, which both repress sodB. The addition of the SdsN sequence to both sRNAs caused a reduction in sRNA-mediated repression of a *sodB-lacZ* translational fusion despite similar sRNA levels (Supplementary Figure S6C and S6D). Interestingly, we found RyhB also represses the *narP-lacZ* fusion (Figure 6D). This regulation likely is via direct base pairing, given extensive predicted pairing (Supplementary Figure S6E) and high expression of the *narP-lacZ* fusion in a Δ*hfq* mutant, consistent with repression by multiple sRNAs (Supplementary Figure S6F). As for SdsN178, the chimeric form of RyhB did not repress the *narP-lacZ* fusion (Figure 6D). The appended SdsN sequence could alter the structures of base pairing regions of RyhB and FnRS, but because the SdsN 5′ sequence reduces the activities of both sRNAs and the retention of base pairing has been surprisingly robust in other chimeric sRNAs (24), we do not think an altered structure fully explains the reduced repression.

To further dissect the lack of target regulation by SdsN178, we examined SdsN137 and SdsN178 base pairing with target mRNAs in vitro. Radiolabeled SdsN137 and SdsN178 were mixed with Hfq at concentrations to ensure most of the sRNAs were bound by Hfq. The addition of increasing amounts of unlabeled *hmpA* or *narP* mRNA frag-
Figure 4. SdsN\_137 base pairs directly with nfsA, hmpA and narP. (A) Predicted base pairing between SdsN and nfsA. The bases mutated in pBR-SdsN\_137 and nfsA are indicated. (B) ß-galactosidase activity of PM1205-derived strains with nfsA-lacZ (GS0751) or nfsA-2-lacZ (GS0754) carrying pBR control vector, pBR-SdsN\_137 or pBR-SdsN\_137 mutant derivative. (C) Predicted base pairing between SdsN and hmpA. The bases mutated in pBR-SdsN\_137 and hmpA are indicated. (D) ß-galactosidase activity of PM1205-derived strains with hmpA-lacZ (GS0752) or hmpA-2-lacZ (GS0755) carrying pBR control vector, pBR-SdsN\_137 or pBR-SdsN\_137 mutant derivative. (E) Predicted base pairing between SdsN and narP. The bases mutated in pBR-SdsN\_137 and narP are indicated. (F) ß-galactosidase activity of PM1205-derived strains with narP-lacZ (GS0753) or narP-1-lacZ (GS0756) carrying pBR control vector, pBR-SdsN\_137 or pBR-SdsN\_137 mutant derivative. For (A), (C) and (E), base pairing was predicted by IntaRNA (38,39), and numbering for mRNA is relative to start codon. For (B), (D) and (F), the levels of ß-galactosidase activity of the different fusions were assayed after ~1 h of induction with 0.2% arabinose and either 100 µM IPTG (grey bars) or no IPTG (black bars). The average values from three independent assays are shown with error bars corresponding to the standard deviation of those values.
Cleavage leads to SdsN124 capable of regulating hmpA and nfsA

For cells grown to late stationary phase in M63 glucose medium, the levels of a third transcript, SdsN124, were high (Figure 1B). This derivative is derived from processing given the transcript is eliminated when cells are treated with terminator exonuclease (Supplementary Figure S1C). Since a band corresponding to SdsN124 can be detected when SdsN178 or SdsN137 are overexpressed from a plasmid (Figure 7A), we suggest that this derivative can be derived from either of the longer sRNAs. To test whether SdsN124 can serve as a regulator, we again assayed the lacZ fusions (Figure 7B). As expected, given that SdsN124 lacks the region for base pairing with narP, this fusion was not affected by SdsN124 overexpression. In contrast, SdsN124 repressed nfsA-lacZ and hmpA-lacZ as well as or slightly better than SdsN137.

Previous studies have shown that while all sRNAs bind to the proximal face of the Hfq hexamer, interactions with other Hfq surfaces can differ (24). Most sRNAs (Class I) also bind the rim; these contact mRNAs on the distal face and are thus stabilized by mutations of distal face residues. A subset of sRNAs (Class II) binds the distal face; these contact mRNAs on the rim and are stabilized by mutations of rim residues. Given that sRNA binding is reflected in their levels in strains expressing proximal (Q8A), rim (R16A) and distal (Y25D, K31A) face mutants of Hfq, we examined SdsN178, SdsN137, SdsN124 levels in these backgrounds (Figure 7C). The low levels of SdsN124 in the Q8A and R16A mutants together with the elevated levels in the Y25D and K31A mutant, suggest that SdsN124 behaves like a typical Class I binding the proximal and rim surfaces, leaving the distal face free to bind the target mRNA. In contrast, SdsN137 and SdsN178 are present at WT levels in the rim and distal mutants and are only partially decreased in the Q8A mutant, consistent with multiple contact sites including the distal face.

DISCUSSION

The set of SdsN RNAs can be added to a growing list of σ^5^ dependent sRNAs that have been characterized for *E. coli*. In addition to σ^5^, we found that the Crl and NarP transcription factors impact SdsN expression. Crl is not a DNA binding protein and is not known whether σ^5^ and NarP directly bind to the *sdsN* promoters. There is no signal for σ^5^ in the *sdsN* region in a recent chromatin immunoprecipitation-sequencing experiment (42), but there also did not appear to be binding to the *gadY* and *sraL* promoters. We were intrigued to find that multiple transcripts are expressed from the *sdiA-tcyN* intergenic region. Two forms, SdsN137 and SdsN178, are transcribed from two different σ^5^ dependent promoters but share a terminator. These forms can be processed at the 5′ end to generate SdsN124, which accumulates maximally after 20 h growth in M63 glucose media. The relative levels of these three main transcripts vary depending on the growth condition in ways we do not yet fully understand. SdsN124, SdsN137 and SdsN178 all bind Hfq but only SdsN124 and SdsN137 were found to be effective regulators.

σ^5^ dependent sRNAs share similar and differing features

There are some interesting similarities and differences among the σ^5^ dependent sRNAs. SraL and SdsR are conserved in a range of enteric bacteria, while SdsN and GadY
Figure 6. 5′ A- and U-rich sequences block SdsN178 function. (A) β-galactosidase activity of PM1205-derived strains with narP-lacZ, nfsA-lacZ or hmpA-lacZ (GSO753, GSO751 and GSO752, respectively) carrying pBR control vector, pBR-SdsN137 or pBR-SdsN178. (B) β-galactosidase activity of PM1205-derived strain with narP-lacZ (GSO753) carrying pBR control vector, pBR-SdsN137, pBR-SdsN178 or plasmids with 5′ truncations of the SdsN178. (C) β-galactosidase activity of PM1205-derived strain with narP-lacZ (GSO753) carrying pBR control vector, pBR-SdsN137, pBR-SdsN178, pBR-SdsN140, pBR-SdsN140-3 (AUU to CGG mutant) and pBR-SdsN140-4 (AUU to GGG mutant). (D) β-galactosidase activity of PM1205-derived strain with narP-lacZ (GSO753) carrying pBR control vector, pBR-SdsN137, pBR-SdsN178, pBR-RyhB or pBR-SdsN1′-RyhB (chimeric RyhB carrying 5′ region of SdsN). For (A), (B), (C) and (D), the levels of β-galactosidase activity of the different fusions were assayed after ∼1 h of induction with 0.2% arabinose and either 100 μM IPTG (grey bars) or no IPTG (black bars). The average values from three independent assays are shown with error bars corresponding to the standard deviation of those values. (E) EMSA of 4 nM of 32P end-labeled SdsN137 with 100 nM Hfq hexamer and the indicated amounts (nM) of unlabeled hmpA or narP RNA. Ternary complexes are indicated with asterisks. (F) EMSA of 4 nM 32P end-labeled SdsN178 with 100 nM Hfq hexamer and the indicated amounts (nM) of unlabeled hmpA or narP RNA.
are restricted to *E. coli* and *Shigella*. SdsN, GadY and SdsR all strongly bind Hfq, while SraL does not. In addition, though synthesis of GadY, SraL, SdsR and SdsN is $\sigma^S$-dependent, they show different patterns of accumulation, with SdsR generally expressed later than the other sRNAs in stationary phase (Figure 1B). This observation suggests that additional factors impact the transcription or stability of the $\sigma^S$-dependent sRNAs as we found for SdsN. Little is known about what other factors might modulate GadY, SraL, and SdsR levels, but it is interesting to note that overlapping transcripts are encoded on the strand opposite each of these sRNAs, *sdhA* mRNA for SdsN, *gadWX* mRNA for GadY, *soxR* mRNA for SraL and RyeA sRNA for SdsR (27).

The mRNA targets of the $\sigma^S$-dependent sRNAs do not show any functional overlap. GadY increases the synthesis of acid response transcription factors and thus may protect against low pH in stationary phase (13). The contribution of the SraL block of the translation of the Trigger Factor chaperone to stationary survival is less clear (14). SdsR represses expression of the MutS component of methyl-directed mismatch repair, possibly enhancing mutagenesis when cells are starved (16). SdsN represses genes involved in the metabolism of oxidized nitrogen compounds. By repressing the synthesis of NfsA, SdsN provides resistance to nitrofurans (Figure 5 and Supplementary Figure S5). The physiological role of SdsN repression of *hmpA* is less clear. The flavohemoglobin eliminates NO under aerobic conditions, but we did not observe any difference in NO sensitivity in the $\Delta$sdsN mutant (data not shown). However the enzyme has also been shown to have other activities (43), which may be detrimental under conditions of SdsN induction.

**Figure 7.** Cleavage activates SdsN$_{178}$. (A) Levels of SdsN$_{178}$, SdsN$_{137}$ and SdsN$_{124}$ expressed from pBR plasmid. Total RNA was isolated from the GSO752 cultures assayed in Figure 7B. (B) $\beta$-galactosidase activity of PM1205-derived strains with narP-lacZ, nfsA-lacZ or hmpA-lacZ (GSO753, GSO751 and GSO752, respectively) carrying pBR control vector, pBR-SdsN$_{137}$, pBR-SdsN$_{178}$ or pBR-SdsN$_{124}$. The levels of $\beta$-galactosidase activity of the different fusions were assayed after $\sim$3 h of induction with 0.2% arabinose and 1 mM IPTG. The average fold difference (for four independent assays) relative to the corresponding pBR vector control samples are shown with error bars corresponding to the standard deviation of the differences. (C) Effect of mutations affecting, rim (R16A), proximal (Q8A) and distal (Y25D, K31A) faces of Hfq. WT cells and strains expressing the indicated mutant Hfq derivatives from the chromosome (20) (DJS2317, DJS2318, DJS2319, DJS2294 and DJS2321) were grown 20 h in M63 glucose. For (A) and (C), RNA was processed for northern analysis as in Figure 1.

**sRNAs are induced by various nitrogen compounds**

Only a few sRNAs whose expression is responsive to the levels of nitrogen compounds have been characterized in bacteria thus far (44–46). One example is RoxS from *Staphylococcus aureus* and *Bacillus subtilis*, whose transcription is induced by the presence of NO by the ResDE two-component transduction system (44). *B. subtilis* cells lacking RoxS have increased expression of genes whose functions are related to oxidative stress and oxidation-reduction reactions. Among these, the *ppnKB* mRNA encoding a NAD+/NADH kinase was confirmed to be a direct target of RoxS. However, apart from a few genes involved in the TCA cycle, there was little overlap in RoxS targets between *S. aureus* and *B. subtilis*. Another example is NrsZ from *Pseudomonas aeruginosa*, whose transcription is induced by nitrogen limitation by the NtrBC two-component transduction system (45). The only confirmed target of NrsZ, *rhlAB* encodes enzymes for the synthesis of rhamnolipid biosurfactants required for swarming motility.

**Multiple forms of an sRNA allow for additional levels of regulation**

SdsN$_{178}$ showed only partial regulation of *nfsA* and *hmpA* and almost no regulation of *narP* (Figure 6A), despite stronger binding to Hfq (Figure 3C and D). The secondary
structure of SdsN₁₇₈ is similar to SdsN₁₃₇ indicating the base-pairing sites should be accessible. However, the 5’ end of SdsN₁₇₈ is extremely AU-rich. In vitro, Hfq protects the 5’ region present on SdsN₁₇₈ from RNase T1 cleavage (Figure 3B); thus this region is an Hfq binding site not present on SdsN₁₃₇. However, we found SdsN₁₅₇ was better able to form the Hfq-sRNA-mRNA target ternary complex (Figure 6E and F) required for base pairing (47). This difference in the two forms can be explained by the 5’ end of SdsN₁₇₈ competing with the mRNA for the same surface of Hfq.

SdsN₁₂₄ represses nfsA and hmpA substantially better than SdsN₁₇₈ and slightly better than SdsN₁₃₇ (Figure 7B). The stronger regulation is not due to higher abundance since the levels of SdsN₁₂₄ are lower than SdsN₁₃₇ and equal to SdsN₁₇₈ (Figure 7A). Thus, cleavage of SdsN₁₇₈ and SdsN₁₃₇ to generate SdsN₁₂₄ probably improves base pairing with hmpA and nfsA through altered secondary structure or differences in the interaction with Hfq (Figure 7C). Cleavage also leaves a 5’-monophosphate, which may promote RNase E cleavage of the target, as shown for MicC (48).

A number of other sRNAs have been found to be activated by post-transcriptional cleavage of the 5’ end. The first 20 nt of B. subtilis RoxS are removed by RNase Y generating a truncated version, which was found to be an efficient regulator in vivo and form a more extended duplex with the ppnK8 mRNA in vitro, possibly due to disruption of the 5’ stem (44). However, the amount of this cleavage product relative to full-length is quite low under conditions tested. The two forms of E. coli RprA have different stabilities; the unprocessed form is subject to rapid degradation by RNase E, while the shorter cleaved form is more stable. Like SdsN, the relative levels of the two isoforms vary during growth. Intriguingly, each isoform contains seed regions responsible for regulation of different sets of mRNA targets (49). A final example is E. coli ArcZ (50). Again the primary transcript (ArcZ₁₂₁) is processed at the 5’ end to give a shorter form (ArcZ₆₆). The 5’ region of ArcZ₁₂₁ contains AU-rich sequences that are absent in ArcZ₆₆. As seen for SdsN, ArcZ₁₂₁ binds Hfq more tightly than ArcZ₆₆, in vitro, but ArcZ₆₆ forms a more stable ternary complex with Hfq and its mRNA target in vitro. In addition, the levels of the processed form are greatly elevated in strains expressing distal-face Hfq mutants (20), as we also observe for the cleaved derivatives of SdsN as well as GadY (Figure 7C). Given that ArcZ₆₆ shows greater regulation of its target than ArcZ₁₂₁, it is hypothesized that initial ArcZ expression produces a functionally inert sRNA, but is activated upon cleavage that removes the extra Hfq binding site at the 5’ end (50). We suggest that similar activation is occurring with SdsN₁₇₈. However, while ArcZ₁₂₁ is almost entirely processed under most conditions tested, SdsN₁₂₄ levels are still high in the late stationary phase in minimal media with a rich nitrogen source (Figures 1B and 2C).

We speculate additional characterization of SdsN₁₇₈, SdsN₁₅₇ and SdsN₁₂₄, as well as the processed derivatives of other sRNAs, will reveal further roles for these alternative forms. For sRNAs with multiple base pairing regions, alternative transcription and processing can lead to the regulation of different sets of target mRNAs under slightly different environmental conditions. Expression of sRNAs that bind Hfq in an inert state can prevent Hfq binding to competitor sRNAs and perhaps poise the sRNA to serve as a regulator upon cleavage in response to a specific input. These additional levels of regulation, together with tight transcriptional regulation, competition for limiting Hfq and ‘sponge RNAs’ described previously, illustrate the exquisite control of sRNA regulators (2,51).

SUPPLEMENTARY DATA
Supplementary Data are available at NAR Online.

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REFERENCES


