Acid stress response in *Escherichia coli*: mechanism of regulation of *gadA* transcription by RcsB and GadE

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ABSTRACT

*Escherichia coli* can survive extreme acid stress for several hours. The most efficient acid resistance system is based on glutamate decarboxylation by the GadA and GadB decarboxylases and the import of glutamate via the GadC membrane protein. The expression of the corresponding genes is controlled by GadE, the central activator of glutamate-dependent acid resistance (GDAR). We have previously shown by genetic approaches that as well as GadE, the response regulator of the Rcs system, RcsB is absolutely required for control of *gadA/BC* transcription. In the presence of GadE, basal activity of RcsB stimulates the expression of *gadA/BC*, whereas activation of RcsB leads to general repression of the *gad* genes. We report here the results of various *in vitro* assays that show RcsB to regulate by direct binding to the *gadA* promoter region. Furthermore, activation of *gadA* transcription requires a GAD box and binding of an RcsB/GadE heterodimer. In addition, we have identified an RcsB box, which lies just upstream of the −10 element of *gadA* promoter and is involved in repression of this operon.

INTRODUCTION

*Escherichia coli* is a neutrophilic bacteria that can survive for a long time at very low pH (<2.5). This property is due to three clearly defined acid resistance (AR) systems: glutamate-dependent, arginine-dependent and oxidative systems (1). The glutamate-dependent (Gad) system is the most effective. Two glutamate decarboxylase isoforms, GadA and GadB, consume intracellular protons in decarboxylating glutamate, and GadC, an integral membrane protein, exchanges extracellular glutamate for the decarboxylation product, γ-amino butyric acid (GABA) (2,3). The *gadB* and *gadC* genes are cotranscribed, while *gadA* forms an operon with *gadX*, which encodes an activator of the *gad* system (4). *gadA* and *gadX* belong to the acid fitness island (AFI), a 15-kb region unique to *E. coli* and *Shigella* species, which specifies 12 proteins and a small RNA that contribute to *E. coli* acid resistance in different ways (5). One of these genes, *gadE*, codes for a master regulator of glutamate-dependent acid resistance (GDAR) belonging to the LuxR-like family (6,7). GadE is the key activator of *gadA* and *gadBC* genes. It binds to a GAD box, a 20-bp consensus sequence centered 63 bp upstream of the transcriptional start sites of these genes (8). Regulation of *gadE* expression is extremely complex. At least nine regulators appear to converge on the *gadE* promoter region to either activate or repress its transcription in response to different environmental conditions (1).

Previously, we demonstrated by genetic approaches that RcsB, a response regulator, is another essential regulator of *gadA/BC* transcription (9). RcsB is part of the RcsCDB phosphorelay, a signal transduction system conserved in members of the *Enterobacteriaceae*. This system was first identified as a regulator of capsule synthesis and is involved in pathogenesis, development of biofilms, and the regulation of envelope composition or trafficking (10). RcsB can also be activated independently of the...
phosphorelay, by binding of different co-regulators: RcsA, the main one, and RmpA, TviA and PhoP (11–14). Presumably, this allows multiple inputs into RcsB-mediated regulation of specific promoters.

However, the ability of RcsB to stimulate gadA/B expression is independent of its Rcs partners, both that involved in the phosphorelay and the RcsA activator. In addition, although the activity of RcsB requires a functional gadE allele, its effect is not mediated by activation of gadE transcription, as is the case for the majority of GDAR. In contrast, activation of RcsB, either through the phosphorylation pathway or by RcsA, leads to general repression of gad gene, including gadA, gadB and gadE itself, and a corresponding reduction in acid resistance (9).

The goal of the present study was to investigate the mechanism of regulation of the gad genes by Gde and RcsB. We show that RcsB exerts direct control over gadA/B expression. RcsB is a critical partner of GadE and the binding of both regulators as a heterodimer to the gadA promoter, which contributes to the repression of gadA transcription upon RcsB activation.

**MATERIALS AND METHODS**

**Strains and plasmids**

The bacterial strains and plasmids used in this study are listed in Table 1. The rcsA and rcsDB deletions were constructed as described by Datsenko and Wanner (15). The whole ORFs were deleted and replaced by the chloramphenicol resistance (cat) gene. To construct MPC398 strain, we first transduced ΔrcsCD::cat into MC4100 lon− strain (UGM2). The resistance gene was eliminated by using a FLP helper plasmid (15). Then, we transduced ΔrcsA::cat into the previous strain and finally a ΔgadE::kn (8).

pHGadE plasmid was constructed by amplifying gadE orf from MG1655 strain (gi:948023) using gadEup and gadAdown. The polymerase chain reaction (PCR) product was digested with NdeI and BamHI and cloned in the corresponding sites of pAPT156 (16).

pMRcsB plasmid was constructed by amplifying resB orf from MG1655 strain (gi:947441) using rsBuM and rsBdownM primers. The PCR product and the pMALc2E plasmid were digested by BamHI and HindIII enzymes, and ligated.

pRSgadA-lacZ plasmids were constructed as follows. PCR-generated fragments were cloned between the BamHI and EcoRI sites of pRSS50 (17). The gadA promoter from –101 to +24 relative to the transcription start of the gadA gene was amplified with the primers gadAup and gadAdown. The introduction of the mutations M1, M2 and M3 in the gadAp promoter region was done by PCR using primers carrying the corresponding mutations.

**Oligonucleotide sequences (5’ to 3’)**
gadAup (GTTTATATTATTTTTAAAAGTCG), gadAdown (GGAATTCACTTAAATTTT), gadEup (GGACATCTTAAATTTATTTG), gadEdown (CGCGGATCCCCTAAAAATGAAATGTG), lacZ24 (CGCCAGGGTTTTCCCAGTCATGACG), gadEdownM (CGCGGATCCCTAAAAATGAAATGTG), lacBdownM (CGCGGATCCCTAAAAATGAAATGTG), lacBupM (CGCGGATCCCTAAAAATGAAATGTG), lacBdownM (CGCGGATCCCTAAAAATGAAATGTG).

**Purification of MBP-GadE and MBP-RcsB fusion proteins**

*Escherichia coli* MPC398 containing the pMF533 or the pMRcsB plasmid expressing MBP (Mallose Binding Protein product of the malE gene) fused to GadE (Uniprot: P63204) or ResB (Uniprot: P69407) protein respectively (8; our work), was grown at 37°C with aeration in 11 of LB broth supplemented with 0.2% glucose and 100 μg/ml ampicillin. The purification procedure is described in Ma et al. (8).

**Purification of (His)_6-RcsB and (His)_6-GadE fusion proteins**

*Escherichia coli* MPC398 containing pHRcsB or pHGadE was grown at 37°C with aeration in 11 of LB broth
supplemented with 0.2% glucose and 75 µg/ml of spectinomycin. At OD600 ~ 0.3, IPTG was added to a final concentration of 0.5 mM. The culture was incubated for an additional 3 h. Cells were then treated with lysozyme (0.75 mg/ml) for 30 min and disrupted by sonication in 10 ml of column buffer (50 mM NaP buffer pH 7, 300 mM NaCl). Lysates were centrifuged at 12 000g for 30 min. The supernatants were loaded onto 1 ml TALON columns (Ozyme). The loaded columns were washed with 20 ml of column buffer and 5 ml of column buffer plus 10 mM imidazole. The proteins were eluted with 5 ml of column buffer containing 150 mM imidazole. Samples with highest protein contents were combined and dialyzed against column buffer containing 40% glycerol. Protein concentrations were determined by Bio-Rad protein assays.

Electrophoretic mobility shift assay
Probes were PCR-generated with 32P 5’ end-labeled primers and purified using S300 columns (GE Healthcare). With proteins, 5000 c.p.m. per reaction were incubated at room temperature for 30 min in 10 µl of binding buffer (110 mM NaP pH 7, 10 mM EDTA, 20 mM NaCl, 1 mM DTT, 50 mM potassium glutamate, 1 µg poly-(dl-dc) (Sigma), 7 µM bovine serum albumin). Samples were loaded onto 5% TBE non denaturing gels and electrophoresed at room temperature in 0.5 X TBE. After migration, gels were dried, exposed to Fujifilm sensitive screen. Quantifications were made using Multi Gauge Software.

DNase I footprinting
Experiments were performed using protocol described by Francez-Charlot et al. (18). Reactions contained 5–10 nM of purified gadA promoter-containing templates which have been generated by PCR using gadAup and gadAdown primers. gadAup primer was end-labeled with [γ-32P] ATP by polynucleotide kinase.

In vitro transcription assays
Reactions (14 µl) were performed in buffer containing 20 mM Tris–HCl pH 8, 100 mM NaCl, 5 mM MgCl2, 1 mM dithiothreitol (DTT), 50 µg/ml bovine serum albumin (BSA), 5% glycerol, 0.1 mg/ml heparin, 200 µM ATP, 200 µM CTP, 200 µM GTP, 10 µM UTP and 5 µCi of [α-32P] UTP (Promega). Linear DNA templates were generated by PCR using gadAup and lacZ24 primers from pRSgadAlacZ plasmid, gel purified using a Qiagen gel extraction kit; 20 nM of templates were used per reaction. When required GadE and RcsB proteins were added, then the reaction was initiated by the addition of 0.3 U of RNAP (Tebu). After 10 min at 30°C, samples were analyzed by denaturing gel electrophoresis. Transcript products were quantified using a Phosphorimager (Fujifilm) and Multi-Gauge software.

Beta-galactosidase assay
Cells were grown in LBG (LB plus 0.4% glucose) at 37°C. Overnight cultures were diluted 7000-fold, grown for five/10 generations, prior to addition of 500 µM IPTG. The cultures were sampled at different intervals for assay of β-galactosidase activities (19).

RESULTS
Both RcsB and GadE directly regulate gadA transcription
To test whether RcsB acts directly at gad promoters, we carried out an in vitro transcription assay using linear DNA fragment containing the gadA promoter region fused to lacZ as template. This assay was based on His-tagged version of RcsB and a MBP-tagged version of GadE (8,20). With RNA polymerase alone, a transcript of the expected size was visible (Figure 1, lane 1). The signal was weak, in agreement with the observation that in vivo the activity of the gadA promoter is low in the absence of either GadE or RcsB (9). Addition of MBP-GadE to the reaction did not appreciably change the amount of transcript (Figure 1, lane 2). In contrast, in the presence of MBP-GadE, the addition of 3 or 30 nM of (His)6-RcsB (Figure 1, lanes 7 and 8, respectively) strongly stimulated gadA transcription (up to 7-fold). This result therefore indicates that GadE and RcsB act synergistically to stimulate transcription of gadA. At higher concentrations of (His)6-RcsB, stimulation of gadA transcription by RcsB in the presence of GadE declined, essentially disappearing at 3 µM RcsB (Figure 1, lane 10). This behavior implies that the ratio of the two regulators is important for the balance activation/repression. Furthermore, (His)6-RcsB addition alone (Figure 1, lanes 3–6) had a concentration dependent negative effect on gadA transcription, indicating that RcsB alone directly represses the basal level of gadA transcription.

MBP-GadE
(His)6-RcsB

Figure 1. Synergistic regulation of in vitro transcription initiation at the gadA promoter by GadE and RcsB. The gadA promoter-containing linear template was pre-incubated as indicated with RNA polymerase alone (lane 1), plus 780 nM MBP-GadE (lane 2), plus 3, 30, 300 or 3000 nM (His)6-RcsB (lanes 3–6, respectively), or plus MBP-GadE and (His)6-RcsB at the same concentrations (lanes 7–10, respectively). The figure shows a representative autoradiogram.
gadA transcription. These two boxes are strictly conserved in the gadB promoter region (Figure 2A), except for a C instead of a G at the left end of the RcsB box. The reality of the predicted RcsB box in the gadA regulatory region was demonstrated using a DNase I protection assay. As shown in Figure 2B, (His)_6-RcsB protected a 23-bp region containing the putative RcsB box from DNase I digestion (Figure 2B, lane 3). MBP-GadE alone did not protect either the GAD box or the RcsB box (Figure 2B, lane 2). MBP-GadE and (His)_6-RcsB together protected a region extending from −50 to −76, including the GAD box (Figure 2B, lane 4). In these conditions [20 μM of MBP-GadE and 40 μM of (His)_6-RcsB] the binding of (His)_6-RcsB to its box was unaffected (Figure 2B; compare lane 4 to lane 3). Protection of the GAD box was still apparent with 1 μM of MBP-GadE and 0.1 μM of (His)_6-RcsB (data not shown). However, in this case RcsB no longer protected the RcsB box, suggesting that the affinity of RcsB for the GAD box when GadE is present was higher than for the RcsB box. Therefore, there are two binding sites in the gadA regulatory region, the RcsB box next to the −10 element, where RcsB at high concentration binds independently of GadE, and the GAD box, where RcsB acts at lower concentrations provided GadE is present, suggesting a functional interaction between these two regulators.

Binding of RcsB and GadE to the gadA regulatory region

To probe more deeply into the relationship between RcsB, GadE and the two binding sites in the gadA promoter, we used electrophoretic mobility shift assay (EMSA) to analyze binding to a fragment extending from −101 to +24, containing both the GAD and the RcsB boxes. When the DNA was incubated with (His)_6-RcsB protein alone at concentrations 1 μM and above, a shifted complex appeared (Figure 3A; complex I, lanes 4 and 5). This result indicated that RcsB alone could bind stably to the gadA regulatory region, probably to the RcsB box. On the other hand, we detected no retarded complex with MBP-GadE alone, even at 10 μM (Figure 3A, lane 2). With concentrations of RcsB and GadE at or above 0.01 μM (Figure 3A and data not shown), a major retarded complex, named complex II, appeared; furthermore, the limiting factor for complex II formation seems to be GadE since increasing quantities of complex II were obtained only by raising the concentration of MBP-GadE (Figure 3A). This corroborated the DNase I protection result. Other shifted complexes, called complexes III, that migrated more slowly than complex II appeared as the concentration of RcsB rose [Figure 3A; 10 μM of (His)_6-RcsB (lanes 8, 11 and 14)]. Hence, RcsB seems to bind pre-formed complex II, either at the RcsB box or at the GAD box already covered by RcsB and/or GadE.

These results contradict published reports that GadE regulator alone could bind to the GAD box (8,21,22). A likely explanation for this discrepancy was obtained when MBP-GadE purified from a wild-type strain was used in the EMSA instead of that purified from a ΔrcsC ΔgadE strain used until now in this work. With 3 μM of this MBP-GadE preparation, we detected a retarded complex migrating at the same position as the RcsB and GadE-dependent complex II (Figure 3B, compare lane 3 with lanes 4 and 6). This result strongly suggests that the binding of MBP-GadE prepared from the wild-type strain is due to the copurification of RcsB with GadE. Finally, the presence of RcsB in the preparation of MBP-GadE purified from wild-type strain was confirmed by western-blot analysis using antibody raised against RcsB (kind provided by Anne Vianney; data not shown).
These results suggested that GadE and RcsB act synergistically in binding to the gadA regulatory region and that both proteins interact directly.

**RcsB/GadE heterodimer binds to the gadA box**

The formation of complex II could result either to binding of both proteins or to binding of only one after modification by the other. The presence of GadE and RcsB in complexes II and III was tested by using combinations of His-tagged and MBP-tagged versions of GadE and RcsB. Owing to the differences in fusion protein molecular weights (24 kDa for (His)_6-GadE versus 62 kDa for MBP-GadE, and 23.6 kDa for (His)_6-RcsB versus 66 kDa for MBP-RcsB), migration patterns were expected to depend on the combination of proteins present in the different complexes. As shown in Figure 4, this was the case. Complex II exhibited lower mobility when an MBP-tagged version of each protein was used instead of the corresponding His-tagged form (Figure 4, compare complex II migrations in lanes 4 and 5, or 4 and 6, or 5 and 7 or 6 and 7), as expected if complex II consisted of a RcsB/GadE oligomer bound to the gadA regulatory region. Combinations of three proteins, both tagged versions of one and one tagged version of the other, gave only two major retarded complexes II in this assay (Figure 4, lanes 8–11). The lack of additional shifted bands indicated that equivalent amounts of RcsB and GadE bound to the gadA promoter region. Taking into account that both regulators belong to protein families known to bind DNA as a dimer (23,24) and the size of the protected region at the GAD box, we could reasonably conclude that complex II is the result of an RcsB/GadE heterodimer sitting on the gadA regulatory region, at the GAD site.

**Binding activities of RcsB and GadE at the gadA promoter**

The affinity of the RcsB/GadE heterodimer for GAD box was estimated by EMSA with increasing concentrations of RcsB in reactions containing a saturating concentration of GadE (2.5 µM). With this approach, the apparent binding constant of the RcsB/GadE heterodimer was calculated to be ~10 nM. We noticed that a large proportion of MBP-GadE formed homodimers in solution (data not shown). Hence, to obtain enough GadE monomers and to favor the RcsB/GadE heterodimer formation, we used a saturating concentration of GadE. We could not estimate the apparent binding constant of the RcsB homodimer for the RcsB box because even with 10 µM RcsB, only 6% of the probe was retarded (Figure 3A; lane 5). This indicates that the activation of gadA

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**Figure 3.** Binding of MalE-GadE and (His)_6-RcsB to the gadA promoter region. (A) EMSA with gadA promoter region-templates (from –101 to +24 relative to the +1 start of transcription). No protein (lane 1), 10 µM MBP-GadE (lane 2), 0.1, 1 and 10 µM (His)_6-RcsB plus 0.1 µM MBP-GadE (lanes 6–8) or plus 1 µM MBP-GadE (lanes 9–11), plus 10 µM MBP-GadE (lanes 12–14). (B) EMSA using protein from wt or rcs mutants with gadA promoter region templates. Proteins were purified from either a wild-type strain (lanes 3 and 4) or a ΔrcsA ΔrcscDBA ΔgadE strain (lanes 2, 5 and 6). No protein (lane 1), 1 µM (His)_6-RcsB (lane 2), 3 µM MBP-GadE (lanes 3 and 5), 3 µM MBP-GadE and 1 µM (His)_6-RcsB (lanes 4 and 6).

**Figure 4.** RcsB and GadE bind GAD box as a heterodimer. EMSA was performed as described in Figure 3 using the following proteins at 1 µM: (His)_6-RcsB, MBP-RcsB, MBP-GadE and (His)_6-GadE. Schematic representations of complexes II obtained are presented on the left-hand side.
transcription could take place at low concentrations of both proteins, whereas repression of gadA transcription would require higher level of RcsB.

**Independent binding on the RcsB and the GAD boxes**

In an effort to dissect protein–protein and DNA–protein interactions, various mutations were introduced into the GAD box or in the RcsB box (Figure 5A) and their effects were analyzed by EMSA (Figure 5B). The M1 mutation changes a highly conserved G to a C. This G is also highly conserved in the RcsB box. As shown by the EMSA in Figure 5B (lanes 5–8), this mutation caused a dramatic diminution of complexes II and III, indicating that this G is critical for the binding of the RcsB/GadE heterodimer to the GAD box. In contrast, the formation of complex I was not compromised, in agreement with the idea that this complex was formed by RcsB bound to the RcsB box. The M2 mutation also introduced a modification TT to CC in the right-hand part of the GAD box, but changes a highly conserved G to a C. This G is also highly conserved in the RcsB box. As shown by the EMSA in Figure 5B, compare lanes 4 and 12), indicating that these nucleotides are not critical for binding RcsB/GadE.

The M3 mutation replaced the conserved A in the RcsB box with a G. This mutation completely inhibited complex I formation by RcsB (Figure 5B, lane 15), but had no impact on the formation of complexes II and III by RcsB and GadE (Figure 5B, lane 16). Taken together, these results indicate that binding to one box was largely independent of binding to the other box. It should be pointed out that, as for the major complex II, the formation of minor complexes III was mainly independent of the RcsB box, indicating that these slow migrating complexes III do not result principally to simultaneous occupation of the Rs and GAD boxes. This was confirmed by EMSA with a shorter DNA fragment containing only the GAD box. This fragment was still able to form two retarded complexes whose migrations were equivalent to that of complexes II and III (Supplementary Figure S1).

**Effects of point mutations on transcriptional activity of gadA in vivo**

The in vivo transcriptional activity of the gadA promoter was monitored using plasmid-borne transcriptional fusions between gadA regulatory region (−101 to +24) and lacZ (Figure 6). As previously reported (9), in a wild-type background, overproduction of (His)₆-GadE activates the transcription of gadA, whereas overproduction of (His)₆-RcsB represses. In contrast, the

![Figure 6. Effects of RcsB or GAD box mutations on the transcriptional regulation of gadA in vivo. (A) β-Galactosidase activities of transcriptional gadA-lacZ fusions (either wild-type or M1 mutant promoter) with or without overexpressed (His)₆-GadE or (His)₆-RcsB. Strains carrying gadAp-lacZ and either pHGadE or pHRcsB plasmids with (white bars) or without (gray bars) 0.5 mM IPTG added for 1 h. (B) Same experiment as in A for gadApwt-lacZ and gadAm1-lacZ fusions with or without induction of RcsB synthesis. Activities were measured 30, 60 and 120 min after IPTG addition.](image)
construction with the inactivated GAD box (mutation M1) displayed a lower intrinsic activity that was no longer stimulated by GadE (Figure 6A). Repression of the β-galactosidase activity was still observed after 1 h of overproduction of RcsB, even if the promoter was no more activated. This repression indicated that the GAD box is not involved in repression of gadA expression by RcsB.

With the M3 fusion (mutation in the RcsB box), the basal activity of the gadA promoter was slightly higher and RcsB repression little affected (Figure 6B). In the case of the mutant promoter, the transcription level was more than twice that of a wild-type promoter after 120 min of RcsB over expression (2000 versus 800 Miller units). However, a repression was still observed with this mutant promoter indicating that at least part of the RcsB-dependent repression of gadA is observed without normal binding of RcsB to the RcsB box. This was, however, consistent with our previous finding that overproduction of RcsB leads to general repression of the gad genes, including those coding for the activators of gadA expression (9). Therefore, in the case of the M3 fusion, the repression observed after RcsB overproduction was probably due to a lower level of GadE and/or GadX(W).

**DISCUSSION**

In this study, we report novel findings that shed light on the highly intricate regulation of glutamate-dependent acid resistance in *E. coli* (Figure 7). In particular, we have provided evidence that RcsB is a critical co-activator along with GadE of the gadA transcription. Genetic approaches had shown that in addition to the central regulator GadE, the response regulator RcsB is strictly required to activate the expression of the three genes gadA/BC and to develop resistance to low pH (9). Here, we demonstrate through *in vitro* assays that RcsB and GadE act directly and synergistically to activate gadA transcription (Figure 1). Localization of the binding site responsible for this activation by genetic (Figure 6) and footprinting (Figure 2) experiments confirmed the identity of the GAD box previously identified (8). However, our data demonstrate that the GadE protein alone is not able to bind this GAD box, and that GadE requires the formation of hetero-oligomers with the co-regulator RcsB to bind this site in the gadA regulatory region (Figures 2–5). These data contradict previous reports that GadE alone could bind to the GAD box (8,21,22). As shown in Figure 3B, this discrepancy can be explained by contamination of MBP-GadE overproduced in wild-type strains by RcsB protein.

Importantly, we demonstrate here that RcsB and GadE both bind to the GAD box. Indeed, retarded complexes II and III, formed in EMSA with gadA promoter region in presence of both RcsB and GadE contain both proteins (Figure 4) and are abolished by mutation of a highly conserved nucleotide in the GAD box (Figure 5). Although our experiments do not define the stoichiometry of the proteins in the protein/DNA complexes, it is likely by analogy with other response regulators and LuxR-like activators (23,24) that the GAD box can accommodate one RcsB/GadE heterodimer. At present, the difference between complexes II and III is not clear, but the GAD box appeared sufficient to generate these complexes (Figures S1 and 5). We note that formation of complex III depended on RcsB concentration (Figure 3), which could be consistent with secondary binding of RcsB to the already bound RcsB/GadE or alternatively to the RcsB box, this latter corroborates the DNase I protection of the two boxes (Figure 2). The RcsB/GadE heterodimer binds the GAD box with an apparent binding constant of 10 nM, which is 10-fold lower than that measured for the RcsA/RcsB heterodimer (25). The point mutations introduced into the GAD box, on either the right or the left side, did not enable definition of the half-binding site for each partner. Although we note the left half-site is very similar to an RcsB site, further studies will be needed to settle this issue.

It is still not known whether both RcsB and GadE are directly involved in the DNA recognition process or whether one protein stimulates the binding of the other through conformational change triggered by protein–protein interaction. Heterodimerization of transcriptional regulators is prevalent in eukaryotic regulation mechanisms, where it allows the recognition of additional DNA targets (26). However, it is quite uncommon in prokaryotic systems. An *in vitro* study raised the possibility of interaction between hetero-pairs of response regulators from the OmpR/PhoB subfamily (27), and Knusten *et al.* (28) suggested that a ComE/BlpR heterodimer (these proteins belong to the LytR subfamily of response regulator) recognizes a hybrid DNA motif for convergent gene regulation. A RcsB/GadE heterodimer would be the first example of heterodimer formation between a LuxR-like transcription regulator (GadE) and a NarL/FixJ response regulator (RcsB). This noncanonical interaction is sustained by data obtained in the interactome analysis of *E. coli* (29), in which SPA-RcsB was purified with GadE (previously named YhiE). In agreement with this in *vitro* interaction, we found that RcsB co-purified with MBP-GadE (data not shown). All these strongly support

![Figure 7. Regulatory model of gadA expression. Schematic representation of gadA regulatory region with the GadXW (33), GAD and RcsB boxes (gray boxes). The H-NS binding sites responsible for gadA repression are represented as dotted line (37). Direct regulation is shown as a continuous arrow. Repression of gadE transcription by RcsB, in which a direct effect has not been confirmed, is shown as a dotted arrow. This putative feed-forward loop could coordinate gadA expression.](image-url)
that there is a specific interaction between GadE and RcsB. Both regulators displayed in their C-terminal region a motif related to the LuxR-type DNA-binding HTH (Prosite PS0043 HTH_LUXR_2). It is conceivable that these regulators interact through this motif since structural studies indicated that the fourth helix in this motif facilitates dimerization (30, 24). The question arises as to whether GadE ever binds efficiently to DNA on its own or always needs a co-activator or alternatively does it need a signal to become active. As shown by Sayed and Foster (31), this regulator collaborates with a still unknown co-activator to stimulate its own transcription. However, it remains possible that GadE regulates some target genes independently of co-regulators. For example, we noticed that GadE tends to form dimers during purification. Further studies are needed to understand how GadE controls transcription of ~40 genes, including the ones in the AFI (21).

RcsB can function as an activator of gadA/B, although we had previously shown that the overproduction of RcsB or its activation through the Rcs phosphorylase or RcsA pathways represses gadA/BC transcription and results in GDAR reduction (9). In the present work, we identified an RcsB box displaying a sequence characteristic of canonical RcsB binding sites, located just upstream of the −10 element of the gadA promoter (Figures 2 and 7). This box is probably involved in the repression of gadA transcription by obstructing RNA polymerase binding to the promoter. However, the affinity of RcsB for the RcsB box is very low, several orders of magnitude below that of the RcsB/GadE heterodimer for the GAD box, suggesting that the basal level of RcsB is more efficiently oriented for repression of the gadA/BC expression. This is coherent with the results of our in vitro transcription assay where in the presence of the two regulators RcsB behaved as an activator at lower concentration and as a repressor at higher concentration (Figure 1). It is however conceivable that either a cofactor or the phosphorylation of RcsB increases the affinity of RcsB for the RcsB box, thus making the direct repression more efficient. A potential co-activator could be RcsA, since heterodimerization with RcsB was shown to considerably enhance DNA binding efficiency (32, 24). On the other hand, our genetic data indicated that the effect of RcsA is minor for gad repression: its overproduction decreased GDAR 2-fold compared with a 20-fold decrease upon RcsB overexpression (9). Furthermore, repression of gadA/BC transcription seemed to combine a direct effect, probably genetic data indicated that the effect of RcsA is minor.

Finally, what could be the physiological rationale of the dual effect of RcsB on expression of the Gad system? RcsB has shown to be involved in the control of gene expression upon the formation of biofilms and it may control a feed-forward loop involved in gad transcription, allowing repression of GDAR upon Rcs activation following interactions of cells with surfaces, and more generally after envelope perturbation. The purpose of this negative regulation could be to avoid costly runaway expression of gad genes in conditions where cell membrane properties or membrane proteins are modified or damaged, conditions known to activate Rcs system.

SUPPLEMENTARY DATA

Supplementary Data are available at NAR Online.

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REFERENCES

1. Foster, J.W. (2004) Escherichia coli acid resistance: tales of an amateur acidophile. Nat. Rev. Microbiol., 2, 898–907.
2. Castanie-Cornet, M.P., Penfound, T.A., Smith, D., Elliott, J.F. and Foster, J.W. (1999) Control of acid resistance in Escherichia coli. J. Bacteriol., 181, 3525–3535.
3. De Biase, D., Tramonti, A., Bossa, F. and Visca, P. (1999) The response to stationary-phase stress conditions in Escherichia coli: role and regulation of the glutamic acid decarboxylase system. Mol. Microbiol., 32, 1198–1211.
4. Tramonti, A., Visca, P., De Canio, M., Falconi, M. and De Biase, D. (2002) Functional characterization and regulation of gadX, a gene encoding an AraC/XylS-like transcriptional activator of the Escherichia coli glutamic acid decarboxylase system. J. Bacteriol., 184, 2603–2613.
5. Mates, A.K., Sayed, A.K. and Foster, J.W. (2007) Products of the Escherichia coli acid fitness island attenuate metabolite stress at extremely low pH and mediate a cell density-dependent acid resistance. J. Bacteriol., 189, 2759–2768.
6. Tucker, D.L., Tucker, N. and Conway, T. (2002) Gene expression profiling of the pH response in Escherichia coli. J. Bacteriol., 189, 6551–6558.
7. Masuda, N. and Church, G.M. (2003) Regulatory network of acid resistance genes in Escherichia coli. Mol. Microbiol., 48, 699–712.
8. Ma, Z., Gong, S., Richard, H., Tucker, D.L., Conway, T. and Foster, J.W. (2003) GadE (YhiE) activates glutamate decarboxylase-dependent acid resistance in Escherichia coli. Mol. Microbiol., 49, 1309–1320.
9. Castané-Cornet, M.-P., Treffandi, H., Francez-Charlot, A., Gutierrez, C. and Cam, K. (2007) The glutamate-dependent acid resistance system in Escherichia coli: essential and dual role of the His-Asp phosphorylase RcsCDB/AF. *Microbiology*, 153, 238–246.
10. Majdalani, N. and Gottesman, S. (2005) The Rcs phosphorylase: a complex signal transduction system. *Annu. Rev. Microbiol.*, 59, 379–405.
11. Bril, J.A., Quinlan-Walshe, C. and Gottesman, S. (1998) Fine-structure mapping and identification of two regulators of capsule synthesis in *Escherichia coli* K-12. *J. Bacteriol.*, 170, 2599–2611.
12. Nassif, X., Honoré, N., Vasselon, T., Cole, S.T. and Sansonetti, P.J. (1998) Positive control of colanic acid synthesis in *Escherichia coli* by rmpA and rmpB, two virulence-plasmid genes of *Klebsiella pneumoniae*. *Mol. Microbiol.*, 3, 1349–1359.
13. Virlogeux, I., Wexin, H., Ecobichon, C., Lee, J.O. and Popoff, M.Y. (2003) Signal-dependent capsule synthesis in *Salmonella typhi*. *Virol. Microbiol.*, 21, 17–28.
14. Mouslim, C., Latifi, T. and Groisman, E.A. (2003) Signal-dependent regulation of the *Salmonella* Vi antigen synthesis. *Escherichia coli* chromosome genes in *Escherichia coli* K-12 using PCR products. *Proc. Natl Acad. Sci. USA.*, 97, 6640–6645.
15. Polard, P. and Chandler, M. (1995) An *in vivo* transposase-catalyzed single-stranded DNA circularization reaction. *Genes Dev.*, 9, 2846–2858.
16. Simons, R.W., Houman, F. and Kleckner, N. (1987) Improved single and multicopy lac-based cloning vectors for protein and gene fusions. *Gene*, 53, 85–96.
17. Francez-Charlot, A., Laugel, B., Van Gemert, A., Dubarry, N., Wiorowski, F., Castané-Cornet, M.P., Gutierrez, C. and Cam, K. (2003) RcsCDB His-Asp phosphorylase system negatively regulates *Vi* antigen synthesis. *J. Bacteriol.*, 178, 1691–1698.
18. Mouslim, C., Latifi, T. and Groisman, E.A. (2003) Signal-dependent requirement for the co-activator protein RcsA in transcription of the *RcsB*-regulated *ugd* operon. *J. Biol. Chem.*, 278, 50588–50595.
19. Datsenko, K.A. and Wanner, B.L. (2000) One-step inactivation of chromosomal genes in *Escherichia coli* K-12 using PCR products. *Proc. Natl Acad. Sci. USA.*, 97, 6640–6645.
20. Miller, J.H. (1992) A Short Course in Molecular Genetics. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY.
21. Carballes, F., Bertrand, C., Bouché, J.P. and Cam, K. (1999) Regulation of *E. coli* cell division genes *ftsX* and *ftsZ* by the two-component system *rcsC-rcsB*. *Mol. Microbiol.*, 34, 442–450.
22. Hommala, S., Koin, E., Coppee, J.Y., Lacroix, C., Yeraman, E., Dunchin, A. and Bertin, P. (2004) GadE (YhiE): a novel activator involved in the response to acid environment in *Escherichia coli*. *Mol. Microbiol.*, 53, 1349–1359.
23. Itou, Y., Igauchi, Y. and Utsumi, R. (2009) Molecular mechanism of transcriptional cascades initiated by the Evg/EvgA system in *Escherichia coli* K-12. *Biochem. Biophys. Acta Chem.*, 73, 870–878.
24. Ramos, J.L., Martinez-Bueno, M., Molina-Henares, A.J., Terán, W., Watanabe, K., Zhang, X., Gallegos, M.T., Brennan, R. and Tober, R. (2005) The TetR family of transcriptional repressors. *Microbiology*, 150, 61–72.
25. Pristovsek, P., Sengupta, K., Löhr, F., Schäfer, B., von Trebra, M.W., Rüterjans, H. and Bernhard, F. (2003) Structural analysis of the DNA-binding domain of the *Erwinia amylovora* ResB protein and its interaction with the RcsAB box. *J. Biol. Chem.*, 278, 17752–17759.
26. Weiland, M., Kiecker, C., Coplin, D.L., Kelm, O., Saenger, W. and Bernhard, F. (1999) Identification of an RcsA/RcsB recognition motif in the promoters of exopolysaccharide biosynthetic operons from *Erwinia amylovora* and *Pantoea stewartii* subspecies *stewartii*. *J. Biol. Chem.*, 274, 3300–3307.
27. Reményi, A., Schölmerich, H.R. and Wilmanns, M. (2004) Combinatorial control of gene expression. *Nat. Struct. Mol. Biol.*, 11, 812–815.
28. Gao, R., Tao, Y. and Stock, A.M. (2008) System-level mapping of *Escherichia coli* response regulator dimerization with FRET hybrids. *Mol. Microbiol.*, 69, 1358–1372.
29. Knutsen, E., Ween, O. and Hävarstein, L.S. (2004) Two separate quorum-sensing systems upregulate transcription of the same ABC transporter in *Streptococcus pneumoniae*. *J. Bacteriol.*, 186, 3078–3085.
30. Butland, G., Peregrín-Alvarez, J.M., Li, J., Yang, W., Yang, X., Canadien, V., Starostine, A., Richards, D., Beattie, B., Krogan, N. et al. (2005) Interaction network containing conserved and essential protein complexes in *Escherichia coli*. *Nature*, 433, 531–537.
31. Vannini, A., Volparsi, C., Cargioli, C., Muraglia, E., Cortese, R., De Francesco, R., Neddermann, P. and Marco, S.D. (2002) The crystal structure of the quorum sensing protein TraR bound to its autoinducer and target DNA. *EMBO J.*, 21, 4393–4401.
32. Sayed, A.K. and Foster, J.W. (2009) A 750 bp sensory integration region directs global control of the *Escherichia coli* GadE acid resistance regulator. *Mol. Microbiol.*, 71, 1435–1450.
33. Kelm, O., Kiecker, C., Geider, K. and Bernhard, F. (1997) Interaction of the regulator proteins RcsA and ResB with the promoter of the operon for amylovoran biosynthesis in *Erwinia amylovora*. *Mol. Gen. Genet.*, 256, 72–83.
34. Tramonti, A., De Canio, M., Delany, L., Scarlato, V. and Di Biase, D. (2006) Mechanisms of transcription activation exerted by GadX and GadW at the *gadA* and *gadBC* gene promoters of the glutamate-basid acid resistance system in *Escherichia coli*. *J. Bacteriol.*, 188, 8118–8127.
35. Tramonti, A., De Canio, M. and Di Biase, D. (2008) GadX/ GadW-dependent regulation of the *Escherichia coli* acid fitness island: transcriptional control at the *gadY*-gadW divergent promoters and identification of four novel 42 bp GadX/ GadW-specific binding sites. *Mol. Microbiol.*, 70, 965–982.
36. Richard, H. and Foster, J.W. (2007) Sodium regulates *Escherichia coli* acid resistance, and influences GadX- and GadW-dependent activation of *gadE*. *Microbiology*, 153, 3154–3161.
37. Mangan, S. and Alon, U. (2003) Structure and function of the feed-forward loop network motif. *Proc. Natl Acad. Sci. USA.*, 100, 11980–11985.
38. Giangrossi, M., Zattoni, S., Tramonti, A., Di Biase, D. and Falconi, M. (2005) Antagonistic role of H-NS and GadX in the regulation of the glutamate deacetylase-dependent acid resistance system in *Escherichia coli*. *J. Biol. Chem.*, 280, 21498–21505.